

28488

Access DB# _____

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: S. Devi Examiner #: S. Devi Date: 08 May 00
Art Unit: 1641 Phone Number 308-9347 Serial Number: 09/240,675
Mail Box and Bldg/Room Location: CM1-7E15 Results Format Preferred (circle) PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Monoclonal antibodies against the Interferon Receptor
Inventors (please provide full names): Patrick Benoit et al.

Earliest Priority Filing Date: 03.31.92

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please ask Ms. Beverly Shears to perform this search.

Please perform a Sequence & an Interference search on the SEQ ID NO: 1 and 2 and portions or analogues thereof.
Claims are enclosed.

Thanks.

Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 12C14 Tel: 308-4994

SLIS
signature

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STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: Beverly 24995 STN _____
Searcher Phone #: _____ AA Sequence (#) _____ Dialog _____
Searcher Location: _____ Structure (#) _____ Questel/Orbit _____
Date Searcher Picked Up: _____ Bibliographic _____ Dr. Link _____
Date Completed: 06-05-00 Litigation _____ Lexis/Nexis _____
Searcher Prep & Review Time: 12 Fulltext _____ Sequence Systems _____
Clerical Prep Time: _____ Patent Family _____ WWW/Internet _____
Online Time: 20 Other _____ Other (specify) CGN

201 AACTGGATGATTAATGGATAAATTGCTGGGTGCAGATAATACTA 250
|||||
67 sThcGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThS 84
251 GTACCAATGCACTTTTCTTCACGCAAGCTGAATGTTATGAAGAAAT 300
|||||
84 erThrLysCysAsnPhseSerLeuLysLeuAsnValTyrGluGluIle 100
301 AATTCGCTATAGAGCAGAAAAAGAAACACTTCTTCATGATAGAGT 350
|||||
101 LysLeuArGlyIleArGlaGluLysGlnAsnThrSerSerTrpTyrGluVa 117
351 TGACTCATTTACACCATTTTCGCAAGCTCAGATTGCTCCTCAGAGTA 399
|||||
117 lAspSerPheThrProPheArGlyAlaGlnIleGlyProProGluVal 133
seq_name: A_Geneseq_36:R14487

seq_documentation_block:
ID R14487 standard; Protein: 436 AA.
AC R14487;
DT 16-JAN-1992 (first entry)
DE Soluble interferon-alpha/beta receptor.
KW IFN: autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
PN FR265781-A.
PD 09-AUG-1991.
PE 05-FEB-1990; FR-001298.
PR (EUBI-) LAB EURO BIOTECHNO.
PI EId P. Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Tovey M, Uze G;
DR WPI: 91-319778/44.
DR N-PSDB: Q14239.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Claim 2; Page 45; 52pp; French.
CC The transmembrane and cytoplasmic domains of the native IFN receptor
CC have been deleted to obtain a soluble, circulating form of the
CC receptor. Potentially immunogenic epitopes have thus been eliminated.
CC Derivatives obtained by substitution or deletion of this sequence
CC are also claimed as are hybrid molecules comprising the soluble
CC receptor (or deriv.) and an immunoglobulin such as IgG1.
CC See also Q14240.
SQ Sequence 436 AA;

alignment_scores:
Quality: 692.00 Length: 133
Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_27_427 x R14487

Align seg 1/1 to: R14487 from: 1 to: 436

1 ATGATGCTGCTCCTCGGCGGAGACCCCTAGTGTCTGCGCCGTGGG 50
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1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTGTCGCGACCGCAGGTGGAATAATCTTAATCTCTC 100
|||||
17 yProTrpValLeuSerAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTAGAGGTGACATCATAGATGACAACTTATCTGAGGTGAAC 150
|||||
34 lntLysValGluValAspIlelleAspAsnPhseIleleuArGTrpAsn 50
151 AGGAGCATGAGTGTGCGGAATGTGACTTTTCATTCGATTACAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnL 67

201 AACTGGATGATTAATGGATAAATTGCTGGGTGCAGATAATACTA 250
|||||
67 sThcGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThS 84
251 GTACCAATGCACTTTTCTTCACGCAAGCTGAATGTTATGAAGAAAT 300
|||||
84 erThrLysCysAsnPhseSerLeuLysLeuAsnValTyrGluGluIle 100
301 AATTCGCTATAGAGCAGAAAAAGAAACACTTCTTCATGATAGAGT 350
|||||
101 LysLeuArGlyIleArGlaGluLysGlnAsnThrSerSerTrpTyrGluVa 117
351 TGACTCATTTACACCATTTTCGCAAGCTCAGATTGCTCCTCAGAGTA 399
|||||
117 lAspSerPheThrProPheArGlyAlaGlnIleGlyProProGluVal 133
seq_name: A_Geneseq_36:R28495

seq_documentation_block:
ID R28495 standard; Protein: 436 AA.
AC R28495;
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the interferon (IFN) receptor
DE with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-interferon; beta-interferon.
OS Synthetic.
PN WO9218626-A.
PD 29-OCT-1992.
PE 17-APR-1991; F00318.
PR (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI EId P. Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Tovey M, Uze G;
DR WPI: 92-382110/46.
DR N-PSDB: Q30532.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
PT and beta - useful as immunosuppressants, for treating auto-immune
PT diseases and transplant rejection
PS Claim 2; Fig 1; 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
CC IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template. For example,
CC bacteriophage lambda ZAP, containing the entire coding sequence of
CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
CC lacks the transmembrane and cytoplasmic domains. Both forms bind
CC IFN in the same way as antibodies so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 436 AA;

alignment_scores:
Quality: 692.00 Length: 133
Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_27_427 x R28495

Align seg 1/1 to: R28495 from: 1 to: 436

1 ATGATGCTGCTCCTCGGCGGAGACCCCTAGTGTCTGCGCCGTGGG 50
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTGTCGCGACCGCAGGTGGAATAATCTTAATCTCTC 100
|||||
17 yProTrpValLeuSerAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTAGAGGTGACATCATAGATGACAACTTATCTGAGGTGAAC 150
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34  InLysValGluValAlaSpIleIleAspAspAsnPhelIleuArGTrpAsn 50
151 AGGAGCGATGAGTCTGGCGGAGATGACTTTTATTCGATATCAAAA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLys 67
201 AACTGGCATGATTAATGATTAATGATGCTGCTGATGATATTA 250
67 sThcGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleHis 84
251 GTACCAAAATGCAACTTTTCTTCACTCAAGCTGAATGTTATGAGA 300
84 eThrLysCysAsnPheserSerLeuLysLeuAsnValTyrGlnLulle 100
301 AAATGGCTATTAAGAGCAGAAAAAAGAACTTCTTCAATGATGAGCT 350
101 LysLeuArGlyIleArGAlaGluLysGlnAsnThrSerSerTyrGluVa 117
351 TGACTCATTTACACCATTTGCGAAAGCTCAGATGCTGCTCCAGAA 399
117 LAspSerPheThrProPheArGlyAlaGlnIleGlyProProGluVal 133

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seq_name: A_Geneseq_36:R71723

seq_documentation_block:

ID R71723 standard; Protein: 436 AA.
AC R71723;
DT 16-OCT-1995 (first entry)
DE IFN receptor extracellular domain.
KW IFN receptor; interferon receptor; interferon-alpha;
KM Interferon-beta; monoclonal antibody; immunomodulator; AIDS.
OS Homo sapiens.
PN W09507716-A.
PD 23-MAR-1995.
PF 16-SEP-1994; EP-402279.
PR 17-SEP-1993; EP-402279.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benlari EJ, Tovey MG;
DR WPI: 95-131187/17.
N-PSDB: Q86437.
PT Compn. of monoclonal antibodies against interferon receptor -
PT useful as immuno:modulator, eg. for treating AIDS
PS Disclosure: Fig.2A-2B; 105pp; English.
CC A recombinant soluble form of the human interferon class I receptor
CC protein extracellular domain, given in R71723, was expressed in
CC either E. coli or COS cell hosts. The protein was used to raise
CC immunomodulatory monoclonal antibodies.
SQ Sequence 436 AA;

alignment_scores:

Quality: 692.00 Length: 133
Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_427 x R71723

Align seg 1/1 to: R71723 from: 1 to: 436

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1  ATGATGCTGCTCTCTCGGCGGAGACCTAGTCTGTCGCGCTGG 50
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17  yProtrpValIleuSerAlaAlaIleGlyGlyAsnLeuLysSerPro 34
1  MetheValValIleuLeuGlyAlaIleThrThrIleuValIleValAl 17
51  CCATGAGTGTGTCTCGAGCCGAGGTGGAATAAATATCTCTCTC 100
|||||
17  yProtrpValIleuSerAlaAlaIleGlyGlyAsnLeuLysSerPro 34
101  AAAAAGTAGAGTGCACATCATAGTACACTTATCTGAGTGGAGAC 150
|||||
34  InLysValGluValAlaSpIleIleAspAspAsnPhelIleuArGTrp 50
151  AGGAGCGATGAGTCTGGCGGAGATGACTTTTATTCGATATCAAAA 200

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|||||
51  ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnL 67
201  AACTGGCATGATTAATGATTAATGATGCTGCTGATGATATTA 250
67  sThcGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleHis 84
251  GTACCAAAATGCAACTTTTCTTCACTCAAGCTGAATGTTATGAGA 300
84  eThrLysCysAsnPheserSerLeuLysLeuAsnValTyrGlnLulle 100
301  AAATGGCTATTAAGAGCAGAAAAAAGAACTTCTTCAATGATGAGCT 350
101  LysLeuArGlyIleArGAlaGluLysGlnAsnThrSerSerTyrGluVa 117
351  TGACTCATTTACACCATTTGCGAAAGCTCAGATGCTGCTCCAGAA 399
117  LAspSerPheThrProPheArGlyAlaGlnIleGlyProProGluVal 133

```

seq_name: A_Geneseq_36:W21806

seq_documentation_block:

ID W21806 standard; Protein: 496 AA.
AC W21806;
DT 23-SEP-1997 (first entry)
DE Spliced-deleted interferon alpha-receptor form 2.
KW Interferon alpha-receptor; IFNAR.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..419
FT /label= "Extracellular domain
FT /note= "Comprises amino acid residues 1-413 and
FT 422-427 of transmembranal IFNAR"
FT domain 420..496
FT /label= "Intracellular domain
FT /note= "Comprises amino acids 481-557 of
FT transmembranal IFNAR"

PN AU9475977-A.
PD 11-MAY-1995.
PF 20-OCT-1994; 075977.
PR 24-OCT-1993; IL-107378.
PA (YEDR) YEDA RES & DEV CO LTD.
PA (ABBR/) ABRAMOVICH C.
PI Abramovich C, Racovitski E, Revel M;
DR WPI: 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Example 3; Fig 7; 46pp; English.
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2
CC (W21806) is characterised by a double deletion when compared to
CC transmembranal IFNAR (W21804). The extracellular domain is
CC shortened by 6 amino acid residues and is followed by a truncated
CC intracellular domain. There is no transmembrane region. The amino
CC acid sequence is predicted from a cDNA clone (see also J73521) obtd.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 (see also W21805) and 2 may regulate the
CC response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating IFN activities. They can be expressed
CC in host cells and used to inhibit, modulate or modify the
CC activities of IFNs alpha and beta in cells, tissues and organisms,
CC or for diagnostic purposes.
SQ Sequence 496 AA;

alignment_scores:

Quality: 692.00 Length: 133
Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_427 x W21806

Align seg 1/1 to: W21806 from: 1 to: 496

alignment_scores:

Quality: 692.00 Length: 133
 Ratio: 5.203 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_427 x R14488 ..

Align seg 1/1 to: R14488 from: 1 to: 557

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1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTTGTCGCCAGCCGAGGTGGAATAAATCTAAATCTCTC 100
| | | | | | | | | | | | | | | | | | | | | | | | | | |
17 YProTPrValLeuSerAlaAlaAlaGlyGlyAsnLeuLysSerProG 34
101 AAAAAGTAGAGGTGCACATCATAGATGACAACTTATCTCGAGTGAAC 150
| | | | | | | | | | | | | | | | | | | | | | | | | | |
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArGTrpAsn 50
151 AGGAGCGATGAGTCGTGCGGGAATGACTTTTCATTCGATTATCAAAA 200
| | | | | | | | | | | | | | | | | | | | | | | | | | |
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrpGlnL 67
201 AACTGGGATGATTAATTGATTAATAATTGCTGGGTGCAGATATTACTA 250
| | | | | | | | | | | | | | | | | | | | | | | | | | |
67 sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThr 84
251 GTACCAATGCAACTTTTCTTCACTCAAGCTGAATGTTATGAGAAATT 300
| | | | | | | | | | | | | | | | | | | | | | | | | | |
84 eThrIlyCysAsnPheserSerLeuLysLeuAsnValTyrgLInLile 100
301 AAATTCGCTATAGAGCAGAAAAGAAACACTTCTTCATGATGAGCT 350
| | | | | | | | | | | | | | | | | | | | | | | | | | |
101 LysLeuArGlyIleArGAlaGluLysGlnAsnThrSerTrpTrpGluVa 117
351 TGACTCATTTACACCATTTCCGCAAGCTCAGATTGGTCTCCAGAACTA 399
| | | | | | | | | | | | | | | | | | | | | | | | | | |
117 LAspSerPheThrProPheArGlyAlaGlnIleGlyProProGluVal 133

```

seq_name: A_Geneseq_36:R28496

seq_documentation_block:

ID R28496 standard; Protein: 557 AA.

AC R28496:
 DT 31-MAR-1993 (first entry)
 DE Sequence of a soluble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta.
 KW Interferon receptor; alpha-interferon; beta-interferon.
 OS Synthetic.
 PN MO9218626-A.
 PD 29-OCT-1992.
 PF 17-APR-1991: F00318.
 PR 17-APR-1991: WO-F00318.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
 PI Eid P, Gresser I, Luftalla G, Meyer F, Mogensen KE, Tovey M, Uze G.
 PI Tovey M, Uze G.
 DR MPI: 92-382110/46.
 DR N-PDB: Q30533.
 PT Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating auto-immune diseases and transplant rejection
 PS Claim 3: Fig 2: 58pp. English.
 CC DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos Q30534 and Q30535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind

CC IFN in the same way as antibodies so are immunosuppressants e.g. for
 CC treating autoimmune diseases and graft rejection. They lack the
 CC toxic side-effects of known immunosuppressants such as steroids.
 SQ Sequence 557 AA:

alignment_scores:

Quality: 692.00 Length: 133
 Ratio: 5.203 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_427 x R28496 ..

Align seg 1/1 to: R28496 from: 1 to: 557

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1 ATGATGTCGTCCTGCGGCGGAGACCCCTAGTCGTCGCGCGTGGG 50
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1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTTGTCGCCAGCCGAGGTGGAATAAATCTAAATCTCTC 100
| | | | | | | | | | | | | | | | | | | | | | | | | | |
17 YProTPrValLeuSerAlaAlaAlaGlyGlyAsnLeuLysSerProG 34
101 AAAAAGTAGAGGTGCACATCATAGATGACAACTTATCTCGAGTGAAC 150
| | | | | | | | | | | | | | | | | | | | | | | | | | |
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArGTrpAsn 50
151 AGGAGCGATGAGTCGTGCGGGAATGACTTTTCATTCGATTATCAAAA 200
| | | | | | | | | | | | | | | | | | | | | | | | | | |
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrpGlnL 67
201 AACTGGGATGATTAATTGATTAATAATTGCTGGGTGCAGATATTACTA 250
| | | | | | | | | | | | | | | | | | | | | | | | | | |
67 sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThr 84
251 GTACCAATGCAACTTTTCTTCACTCAAGCTGAATGTTATGAGAAATT 300
| | | | | | | | | | | | | | | | | | | | | | | | | | |
84 eThrIlyCysAsnPheserSerLeuLysLeuAsnValTyrgLInLile 100
301 AAATTCGCTATAGAGCAGAAAAGAAACACTTCTTCATGATGAGCT 350
| | | | | | | | | | | | | | | | | | | | | | | | | | |
101 LysLeuArGlyIleArGAlaGluLysGlnAsnThrSerTrpTrpGluVa 117
351 TGACTCATTTACACCATTTCCGCAAGCTCAGATTGGTCTCCAGAACTA 399
| | | | | | | | | | | | | | | | | | | | | | | | | | |
117 LAspSerPheThrProPheArGlyAlaGlnIleGlyProProGluVal 133

```

seq_name: A_Geneseq_36:R42635

seq_documentation_block:

ID R42635 standard; Protein: 557 AA.

AC R42635:
 DT 20-APR-1994 (first entry)
 DE Human Interferon Receptor.
 KW IFN-R; extracellular domain; monoclonal antibody; viral infection; cell proliferation; allograft rejection; systemic lupus erythematosus; psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia; immunodeficiency; measles virus; interferon-alpha-beta.
 KW Homo sapiens.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 1..436
 FT /label= extracellular domain
 FT /note= "soluble, immunogenic form of IFN-R"
 PN EP-563487-A.
 PD 06-OCT-1993.
 PF 31-MAR-1992: 400902.
 PR 31-MAR-1992: EP-400902.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey M.
 DR MPI: 93-312951/40.
 DR P-PDB: R42635.
 PT Monoclonal antibody to human interferon type-I receptor - having

PT neutralising activity against human type I interferon, used for
 PT therapy and diagnosis
 PS Disclosure; Fig 3; 21pp; English.
 CC Monoclonal antibodies produced against soluble forms of the human
 CC interferon alpha-beta receptor based on the full-length human IFN-
 CC sequence are claimed. The antibodies are useful for treatment and
 CC prophylaxis of disorders involving cell proliferation and/or viral
 CC infection.
 SQ Sequence 557 AA;

alignment_scores:
 Quality: 692.00 Length: 133
 Ratio: 5.203 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

us-09-240-675-1_copy_27_427 x R42635 ..

Align seg 1/1 to: R42635 from: 1 to: 557

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1 ATGATGTCGTCCTCTGCGCGGAGACCCCTAGTGTCTGCGCGG 50
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1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTGTCGCCGCGGAGGTGGAAAAATCTAAATCTCTC 100
|||||
17 yPrrtPrAlLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAAGTAGAGTCGATCATAGATGACAACTTATCTGAGGTGGAAC 150
|||||
34 InLysValGluValAspIleIleAspAspAsnPhelIleuArgTrpAsn 50
151 AGGAGCGATGAGTCGTGCGGAAATGACTTTTCATTCGATTATCAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGluL 67
201 AACCTGGATGATTAATGGATAAATGTCGGGTCTGAGATATTACTA 250
|||||
67 sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleHis 84
251 GTACCAATGCAACTTTCTTCACTCAAGCTGAATGTTATGAAGAAAT 300
|||||
84 eThrLysCysAsnPheserSerLeuLysLeuAsnValTyrGluGluIle 100
301 AAATTCGCTATAAGACGAGAAAAAAGAAACACTTCTTCATGTGATGAG 350
|||||
101 LysLeuArgIleArgAlaGluLysGlnAsnThrSerSerTrpTyrGluVa 117
351 TGACATATTACACCATTTGCGAAGCTCAGATTGTCCTCCAGAAATA 399
|||||
117 lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133

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seq_name: A_Geneseq_36:R75356

seq_documentation_block:

ID R75356 standard; Protein; 557 AA.
 AC R75356;
 DT 16-OCT-1995 (first entry)
 DE Human IFN receptor.
 KW IFN receptor; interferon receptor; interferon-alpha;
 KW interferon-beta; monoclonal antibody; immunomodulator; AIDS.
 OS Homo sapiens.
 FH Key
 FT domain Location/Qualifiers
 FT 1..436
 FT /label= Extracellular_domain
 PN W0507716-A.
 PD 23-MAR-1995.
 PE 16-SEP-1994; E03114.
 PF 17-SEP-1993; EP-402279.
 PR (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benizri EJ, Tovey MG;
 DR WPI, 95-131187/17.

DR N-PSDB; 086458.
 PT Compsn. Of monoclonal antibodies against interferon receptor
 PT useful as immuno-modulator, eg. for treating AIDS
 PS Disclosure; Fig.3A-2B; 105pp; English.
 CC The amino acid sequence of human interferon class I receptor is
 CC given in R75356. A recombinant soluble form of the extracellular
 CC domain of this receptor (R71723) has been used to raise
 CC immunomodulatory monoclonal antibodies.
 SQ Sequence 557 AA;

alignment_scores:
 Quality: 692.00 Length: 133
 Ratio: 5.203 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

us-09-240-675-1_copy_27_427 x R75356 ..

Align seg 1/1 to: R75356 from: 1 to: 557

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1 ATGATGTCGTCCTCTGCGCGGAGACCCCTAGTGTCTGCGCGG 50
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTGTCGCCGCGGAGGTGGAAAAATCTAAATCTCTC 100
|||||
17 yPrrtPrAlLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAAGTAGAGTCGATCATAGATGACAACTTATCTGAGGTGGAAC 150
|||||
34 InLysValGluValAspIleIleAspAspAsnPhelIleuArgTrpAsn 50
151 AGGAGCGATGAGTCGTGCGGAAATGACTTTTCATTCGATTATCAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGluL 67
201 AACCTGGATGATTAATGGATAAATGTCGGGTCTGAGATATTACTA 250
|||||
67 sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleHis 84
251 GTACCAATGCAACTTTCTTCACTCAAGCTGAATGTTATGAAGAAAT 300
|||||
84 eThrLysCysAsnPheserSerLeuLysLeuAsnValTyrGluGluIle 100
301 AAATTCGCTATAAGACGAGAAAAAAGAAACACTTCTTCATGTGATGAG 350
|||||
101 LysLeuArgIleArgAlaGluLysGlnAsnThrSerSerTrpTyrGluVa 117
351 TGACATATTACACCATTTGCGAAGCTCAGATTGTCCTCCAGAAATA 399
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117 lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133

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seq_name: A_Geneseq_36:W21804

seq_documentation_block:

ID W21804 standard; Protein; 557 AA.
 AC W21804;
 DT 23-SEP-1997 (first entry)
 DE Transmembranal interferon alpha-receptor.
 KW Interferon alpha-receptor; IFNAR.
 OS Homo sapiens.
 FH Key
 FT domain Location/Qualifiers
 FT 1..436
 FT /label= Extracellular_domain
 FT 437..457
 FT /label= Transmembrane_domain
 FT 458..557
 FT /label= Intracellular_domain
 PN A09475977-A.
 PD 11-MAR-1995.
 PE 20-OCT-1994; 075977.
 PF 24-OCT-1993; IL-107378.

PA (YEDA) YEDA RES & DEV CO LTD.
 PA (ABRA/) ABRA/ MOVIC C.
 PI Abramovich C, Ratovitski E, Revel M;
 DR WPI: 95-200634/27.
 PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Disclosure: Fig 7: 46pp; English.
 CC Human transmembrane Interferon alpha receptor (IFNAR) (W21804)
 CC includes a 21-amino acid transmembrane region. Novel, splice-
 CC deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected
 CC that lack this transmembrane domain. These, soluble non-membrane
 CC bound polypeptides can be expressed in host cells and used to
 CC inhibit, modulate or modify the activities of interferons alpha
 CC and beta in cells, tissues and organisms, or for diagnostic
 CC purposes.
 SQ Sequence 557 AA;

alignment_scores:
 Quality: 692.00 Length: 133
 Ratio: 5.203 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-240-675-1_COPY_27_427 x W21804 ..

Align seg 1/1 to: W21804 from: 1 to: 557

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17 ProTyrValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
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51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrpGlnLyl 67
201 AACTGCGATGATTAATGATTAATTTCTGCGTGTGATATATCTACTA 250
|||||
67 sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS 84
251 GTACCAATGCACTTTTCTCTCACTCAAGCTGAATGTTATGAGAAT 300
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84 eTrThrLysCysAsnPheserSerLeuLysAsnValTyrGlnIle 100
301 AATTCGCTATTAAGAGCAAAAAAGAAACCTTCTCATGGTATGAGT 350
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101 LysLeuArgIleArgAlaGlnLysGlnAsnThrSerTrpTyrGlnVal 117
351 TGACATTTACACCATTTCCAAAGCTCAGATTGCTCTCCAGAGA 399
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117 IAspSerPheThrProPheArgGlyAlaGlnIleGlyProProGlnVal 133

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seq_name: A_Geneseq_36:W79159

seq_documentation_block:

ID W79159 standard; Protein; 553 AA.
 AC W79159;
 DT 20-NOV-1998 (first entry)
 DE Zcytor7 cytokine receptor polypeptide.
 KW Zcytor7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas;
 KW type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;
 KW agonist; cell proliferation; cell differentiation; renal disease; human;
 KW neural disease; pancreatic disease.
 OS Homo sapiens.
 PH key Location/Qualifiers

FT Domain 30..250
 FT /note= "extracellular (ligand-binding) domain;
 FT sequence claimed in claim 1."
 FT Domain 275..553
 FT /note= "intracellular domain"

PN WO9837193-A1.
 PD 27-AUG-1998.
 PF 18-FEB-1998; 003029.
 PR 02-OCT-1997; US-943087.
 PR 20-FEB-1997; US-803305.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RU, Farran TM, Jelmeberg AC, Kho CJ, Lok S,
 PI Whitmore TE;
 DR WPI: 98-480798/41.
 DR N-PSDB: V57515.
 PT Novel human zcytor7 DNA encodes a type 2 cytokine receptor - useful
 PT for treating renal, neural, pancreatic and prostatic diseases
 PS Claim 1, Pages 55-59, 72pp; English.
 CC This represents the zcytor7 cytokine receptor. Zcytor7 is a ligand-
 CC binding receptors the zcytor7 polypeptide and is a novel member of the type 2 cytokine
 CC receptor family (CRF2). An expression vector containing the zcytor
 CC polynucleotide, operably linked to transcription promoter, a sequence
 CC encoding a transmembrane and intracellular domain, or both, and a
 CC transcriptional terminator can be used to transform host cells for the
 CC recombinant production of the polypeptide. The sequences can be used to
 CC study the zcytor7 gene and to isolate ligands binding to it. Zcytor7 is
 CC preferentially expressed in the kidney, pancreas, prostate or nervous
 CC tissue. Agonists of zcytor7 can be used to stimulate proliferation and
 CC differentiation of cell in these organs. The antagonists and agonists can
 CC also be used in the treatment of renal, neural, pancreatic and prostate
 CC diseases.
 SQ Sequence 553 AA;

alignment_scores:
 Quality: 146.00 Length: 127
 Ratio: 1.848 Gaps: 4
 Percent Similarity: 62.205 Percent Identity: 29.921

alignment_block:
 US-09-240-675-1_COPY_27_427 x W79159 ..

Align seg 1/1 to: W79159 from: 1 to: 553

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75 AGGTGAAAAAATTAATCTCCTCAAAAAGTAGAGGTGACATCATAG 124
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34 rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
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49 snMetLysAsnValLeuGlnIleThrProProGlnLysLeuGlnLysVal 65
172 AATGTCATTTTTCATTCGATTAATCAAAAACTGAGTGAATGATGAT 221
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222 AAAATGCTGCGGTGTCAGAAATATTAATGACCAATGCAACTTTCTT 271
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82 uAsnLysSerGlnLysArgAsnIleAsnArgThrTyrCysAspLeuSerA 99
272 CACGCAAGCTGAATGTTATGAGAAGAAATTAATTCGCTATTAAGCA... 318
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99 IagLutThrSerAspTyrGlnIleGlnTyrTyrAlaLysValLysAlaIle 115
319 GAAAAAAGAAACACTTCTTCATGATGATGATGATGATGATGATGAT 368
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116 TrpLysThrLysCysSerLysTyrPheAlaGlnLysSerGlyArgPheThrPro 132
369 TCGCAAGCTCAGATTTGCTCTCCAGAGA 399

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receptor for a helical cytokine or one

184 TCATTCGATTATCAAAAACCTGGATGGATTAATTGGATAAATTGTCTGG 23

CC. receptor for a neutral cytokine or the interaction of

34 InlysvaIgluValasplllelleaspsaspnphelleuargtrpsn 50
151 AGGAGGATGAGTCTGTCGGAATGTGACTTTTCATGATATCAAAA 200
51 ArgserAspGluserValglYasnValthrPheSerPheAspTylGlnly 67
201 AACTGGATGATATGATATAAATGTCTGGGTGTCAGATATATCTA 250
67 sThrglYMetaspasntrpIleLysleuSerGlyCysGlnasnIleThrs 84
251 GTACCAAAATGCAACTTTTCTCCTCAGCTGAGTGTATGAGAAAT 300
84 eThrlYscYasnpheserSerleuLysleuasnValtyrGlnGluIle 100
301 AAATTCGCTATAAGACAGCAAAAAAGAAACACTTCTTCATGTAGAGT 350
101 LysleuArgIleargIagluLysGlnasnThrSerSerTrpTyrGlnVal 117
351 TGACGTATTACACCTTCGCAAAAGCTGAGTGTGCTCCGAGAGTA 399
117 LaspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133
seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-307-588-2
seq_documentation_block:
Sequence 2, Application US/08307588
Patent No. 5919453
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/GUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-588-2

alignment_scores:
Quality: 692.00 Length: 133
Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-307-588-2 ..
Align seg 1/1 to: US-08-307-588-2 from: 1 to: 436
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51 CCCATGGGTGTTCGCCGAGCCGAGGTGAAAAAATCTAAATCTCTC 100
17 yProTrpAlleuSerAlaAlaAlaGlyGlyLysasnleuLysSerProG 34
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101 LysleuArgIleargIagluLysGlnasnThrSerSerTrpTyrGlnVal 117
351 TGACGTATTACACCTTCGCAAAAGCTGAGTGTGCTCCGAGAGTA 399
117 LaspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133
seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-12
seq_documentation_block:
Sequence 12, Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
ZIP: 20004
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: REVEL-13
 REFERENCE/DOCKET NUMBER: 25,618
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 496 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-328-256-12

alignment_scores:
 Quality: 692.00 Length: 133
 Ratio: 5.203 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-240-675-1_copy_27_427 x US-08-328-256-12 ..

Align seg 1/1 to: US-08-328-256-12 from: 1 to: 496

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34 InlysvaIguValaAspIlelleAspAspAsnPhelleuAlaGtrPasn 50
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101 LysLeuArgIleArgAlaGluLysGluAsnThrSerSertrPtyrGluva 117
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seq_documentation_block:

; Sequence 10, Application US/08328256
 ; Patent No. 5643749

; GENERAL INFORMATION:

; APPLICANT: REVEL, Michel

; APPLICANT: ABRAMOVICH, Carolina

; APPLICANT: RATOVIJSKI, Edward

; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NETMARK

STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/328,256

FILING DATE: 24-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 107378

FILING DATE: 24-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: REVEL-13

REFERENCE/DOCKET NUMBER: 25,618

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-328-256-10

alignment_scores:

Quality: 692.00 Length: 133
 Ratio: 5.203 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-240-675-1_copy_27_427 x US-08-328-256-10 ..

Align seg 1/1 to: US-08-328-256-10 from: 1 to: 557

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17 yProtpValLeuSerAlaAlaIagIyGlyAsnLeuLysSerProG 34
101 AAAAGAGAGGTCGACATCATAGATGACAACTTATCCCTGAGTGAAC 150
34 InlysvaIguValaAspIlelleAspAspAsnPhelleuAlaGtrPasn 50
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101 LysLeuArgIleArgAlaGluLysGluAsnThrSerSertrPtyrGluva 117
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seq_name: /cgn2_6/ptodata/1/laa/5A_COMB.pep:us-08-471-454-2

seq_documentation_block:

Sequence 2, Application US/08471454

Patent No. 5731169

GENERAL INFORMATION:

APPLICANT: MOGENSEN, Knud E.

APPLICANT: UZE, Gilles

APPLICANT: LUTFALLA, Georges

APPLICANT: GRESSER, Ion

TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

NUMBER OF SEQUENCES: 2

PREPARATION OF THE CORRESPONDING PROTEIN

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,454

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/900,642

FILING DATE: 15-JUN-1992

APPLICATION NUMBER: FR 89/13770

FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 960-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-471-454-2

alignment_scores:

Quality: 692.00

Ratio: 5.203

Percent Similarity: 100.000

Percent Identity: 100.000

Length: 133

Gaps: 0

Alignment block:

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Align seg 1/1 to: US-08-471-454-2 from: 1 to: 557

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351 TGACTATTACACCATTTGCGAAGCTCAGATTGTCCTCCGAGAGTA 399
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117 lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133
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seq_documentation_block:

Sequence 2, Application US/08466974

Patent No. 5861258

GENERAL INFORMATION:

APPLICANT: MOGENSEN, Knud E.

APPLICANT: UZE, Gilles

APPLICANT: LUTFALLA, Georges

APPLICANT: GRESSER, Ion

TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

NUMBER OF SEQUENCES: 2

PREPARATION OF THE CORRESPONDING PROTEIN

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,974

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/900,642

FILING DATE: 15-JUN-1992

APPLICATION NUMBER: FR 89/13770

FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 960-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids

TYPE: amino acid

STRANDEDNESS: single

US-08-471-454-2

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-974-2

alignment_scores:

Quality: 692.00 Length: 133
Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_427 x US-08-466-974-2 ..

Align seg 1/1 to: US-08-466-974-2 from: 1 to: 557

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17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerPro 34
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|||||
101 LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVal 117
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seq_name: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:US-08-471-453-2

seq_documentation_block:

Sequence 2, Application US/08471453

Patent No. 5886153

GENERAL INFORMATION:

APPLICANT: NOGENSEN, Knud E.

APPLICANT: UZE, Gilles

APPLICANT: LUTFALLA, Georges

APPLICANT: GRESSER, Ion

TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

NUMBER OF SEQUENCES: 2 PREPARATION OF THE CORRESPONDING PROTEIN

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHUYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,453

FILING DATE: 06-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/900,642

FILING DATE: 15-JUN-1992

APPLICATION NUMBER: FR 89/13770

FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 960-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-471-453-2

alignment_scores:

Quality: 692.00 Length: 133
Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_427 x US-08-471-453-2 ..

Align seg 1/1 to: US-08-471-453-2 from: 1 to: 557

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1 ATGATGTCGTCTCTCTGCGCGGAGACCTAGTGTCTGCGCGTGGG 50
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1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
51 CCCATGGGTGTGTCGCCAGCCGAGTGGAAAAAATCTAAATCTCTC 100
|||||
17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerPro 34
|||||
101 AAAAGTAAAGTCGACATCATAGATGACAACTTTATCTGAGTGGAAC 150
|||||
34 InLysValGluValAlaSpIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
151 AGAGCGATGAGTCGTGCGGAGATGTGACTTTTCATTCGATATCAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnL 67
201 AACTGGATGATTAATGGATAAATGTCTGGTGTGACAAATATTACTA 250
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67 sTrpGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThs 84
251 GTACCAATGCACTTTCTTCACTCAAGCTGAATGTTATGAAGAAAT 300
|||||
84 erThrLysCysAsnPheserSerLeuLysLeuAsnValTyrGluGluIle 100
301 AAATTCGCTTAAGACGAGAAAAAGAAACACTTCTTCATGATGATGAGT 350
|||||
101 LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVal 117
351 TGACTCATTTACACACTTTCGCAAGCTGATGGTCTCTCCAGAAAGTA 399
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117 LaspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133
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seq_name: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:US-08-307-588-4

seq_documentation_block:

Sequence 4, Application US/08307588

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: Patent No. 5919453
: GENERAL INFORMATION:
: APPLICANT: BENOIT, Patrick
: APPLICANT: MEYER, Francois
: APPLICANT: MAGUIRE, Deborah
: APPLICANT: PLAVEC, Ivan
: APPLICANT: TOVEY, Michael G.
: TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
: TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
: TITLE OF INVENTION: INTERFERON
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley & Lardner
: STREET: 3000 K Street, N.W., Suite 500
: CITY: Washington
: STATE: D.C.
: ZIP: 20007
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: FILING DATE: 05-DEC-1994
: APPLICATION NUMBER: US/08/307,568
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: PCT/EP93/00770
: FILING DATE: 30-MAR-1993
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: EP 92400902.0
: FILING DATE: 31-MAR-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Saxe, Bernhard D.
: REGISTRATION NUMBER: 28,665
: REFERENCE/DOCKET NUMBER: 17283/117/GUPL
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)672-5300
: TELEFAX: (202)672-5399
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 557 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-307-588-4

alignment_scores:
      Quality: 692.00      Length: 133
      Ratio: 5.203        Gaps: 0
      Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-307-588-4 ..
Align seg 1/1 to: US-08-307-588-4 from: 1 to: 557

1 ATGATGGTGTCTGCTCGGCGCGACCTAGTGTCTGCGCGGTGG 50
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1 Metetvalvalleuueuglyalathrthrleuvalleuvalalaalagl 17
51 CCATGGGTGTGTCGCCGACCGCGAGGTGAAAAAATCTAAATCTCTC 100
|||||
17 yProtrpvalleuseralaalaalagllyllysasnleuylserserpro 34
101 AAAAGTAGAGTGTGACATCATAGTGAACAATTATCTAGAGTGAAC 150
|||||
34 Inlysvaigluvalaspllelleaspaspasnphelileuairgtrpasn 50
151 AGGAGCGATGAGTGTGCGGAATGTGACTTTTCATTCGATTATCAAAA 200
|||||
51 Argseraspgluservalaglyasnvalthrpheserpheasprtyrglnly 67

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seq_name: /cgn2.6/ptodata/1/1aa/PCTUS_COMB.pep: PCT-US94-14277-3
seq_documentation_block:
: Sequence 3, Application PC/TUS9414277
: GENERAL INFORMATION:
: APPLICANT: Aguet, Michel
: APPLICANT: Bohm, Ruth
: APPLICANT: Hemmi, Silvio
: TITLE OF INVENTION: Receptor subunit Polypeptides
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/14277
: FILING DATE: 07-DEC-1994
: CLASSIFICATION:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/164596
: FILING DATE: 09-DEC-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: 866PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-5530
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 202 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: PCT-US94-14277-3

alignment_scores:
      Quality: 273.50      Length: 107
      Ratio: 3.552        Gaps: 1
      Percent Similarity: 71.963      Percent Identity: 48.598

alignment_block:
US-09-240-675-1_COPY_27_427 x PCT-US94-14277-3 ..
Align seg 1/1 to: PCT-US94-14277-3 from: 1 to: 202

82 AAAAATCTAAATCTCTCAAAAAGAGAGTGCAGATCATGATGACAAA 131
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1 GluAsnLeuysProProGluAsnIleAsp***TyrIleIleAspSps 17
132 CTTTATCCGAGGTGGAAGAGAGCGATGCTGTGCGGAATGTGACTT 181
17 nTyrIleLeuysTirPserHisGlyUserMetGlySerValIhrp 34
182 TTTCATTCGATTATCAAAAACTGGGATGATTAATGGATTAATGTCT 231
34 heserIleGlyTyrArgThrLysAspGluArgLysTirPleuys**Pro 50
232 GGGTCGACAGATATTAAGTACCAATGCACTTTCTCTCACTCAAGCT 281
51 GlucySGlnHisThrIhrThrLysCysGluPheSerLeuAspThr 67
282 GAATGTTATGAAGAAATTAATGCGCTATAGAGAGCAAAAAAGAAC 330
67 rAsn**TyrIleLysThrGlnPheArgValArgIleGluGlyAsn 84
331 .ACTTCTCATGGTATGAGGTGACTCATTTACACCATTTCCCAAGCT 378
84 erThrSerSerTrpAsnGluValAspProPheIleProPheTyrThrAla 100
379 CAGATGTCTCTCCAGAGTA 399
101 HisMetSerProProGluVal 107
seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-943-087-2
seq_documentation_block:
; Sequence 2, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Fairah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-08-943-087-2
alignment_scores:
  Quality: 146.00      Length: 127
  Ratio: 1.848        Gaps: 4
  Percent Similarity: 62.205      Percent Identity: 29.921
alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-943-087-2 ..
Align seg 1/1 to: US-08-943-087-2 from: 1 to: 553
31 CAGTGTCTGCGCGCGGCCATGCG...GTTTCCGACGCCGC 74
18 LeuLeuLeuLeuLeuAlaIleProItrpGlyArgIleValProCysValSe 34
75 AGGTGAAAAAATCTAAATCTCTCAAAAAGTAGAGTGCATCATAG 124
34 rGlyGly.....LeuProLysProIleAsnIleThrPheLysSerIleA 49
125 ATGCAACACTTATCTGAGGTGGAAGAGAGCGATGACTGTCCGG... 171
49 smetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
172 AATGCACTTTTTCATTCGATTCATCAAAAAAGTGGATGATTAATGAT 221
66 LysValThrTyrThrValGlnItrPheIleTyrGlyGlnLysLysTrpLe 82
222 AAATGTCGTGGGTGACAGATATTAAGTACCAAAATGCACTTTCTT 271
82 uAsnLysSerGlyCysArgAsnIleAsnArgTrpTyrCysAspLysSerA 99
272 CACTCAAGCTGAATGTTTATGAAGAAATTAATGGCTTAAGAGA... 318
99 IadIuThrSerAspTyrGluHisGlnTyrTyrAlaLysValLysAlaIle 115
319 GAAAAAGAAACACTCTTCATGATGATGAGGTGACTCATTTACACATT 368
116 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProh 132
369 TCCGAAAGCTCAGATTGTCCTCCAGAGTA 399
132 eleuGluThrGlnIleGlyProProGluVal 142
seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-943-087-14
seq_documentation_block:
; Sequence 14, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Fairah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
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```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-14

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alignment_scores:
Quality: 146.00      Length: 127
Ratio: 1.848         Gaps: 4
Percent Similarity: 62.205      Percent Identity: 29.921

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alignment_block:
US-09-240-675-1_copy_27_427 x US-08-943-087-14

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Align seq 1/1 to: US-08-943-087-14 from: 1 to: 553

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18 LeuLeuLeuLeuLeuAlaAlaProTTPGlyArgAlaValProCysValSe 34
75 AGGTGGAAGAAAATCTAAATCTCTCAAAAAGTAGAGTGCACATCATAG 124
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 TGLYGLY.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
125 ATGACACATTATCTCGAGTGAAGACAGACGATGATGATGATGATGAT 171
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
49 smetLysAsnValLeuGlnTTPhrProProGluGlyLeuGlnGlyVal 65
172 AATGTGACATTTCATTCGATTATCAAAAACTGGGATGATTAATGGAT 221
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
66 LysValThrThrValGlnTTPhrPheIleTyrGlyGlnLysLysTyrPle 82
222 AAAATTCCTGCGTCTGAGATATATACAGTACCAAAAGCAACTTTCTT 271
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
82 uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA 99
272 CACTCAAGCTGAATGTTATGAAGAAATTAATGCGTATAAGACA... 318
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
99 IagLutHisSerAspTyrGlnHisGlnTyrTyrAlaLysValLysAlaIle 115
319 GAAAAAGAAAACACTTCTTCATGCTGATGAGTGTGACATTCATTACAC 368
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
116 TTPGlyThrLysCysSerLysTyrPalaGlnSerGlyArgPheTyrProPh 132
369 TCGCAAGCTCAGATTGCTCTCCAGAAAGTA 399
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132 eLeuGlnThrGlnIleGlyProProGlnVal 142

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seq_name: /cgn2_6/prodata/1/laa/5B_COMB.pep:US-08-943-087-16

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seq_documentation_block:
; Sequence 16, Application US/08943087
; Patent No. 5945311

```

```

GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelnberg, Anna C.
APPLICANT: Adams, Rodyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-16

```

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alignment_scores:
Quality: 146.00      Length: 127
Ratio: 1.848         Gaps: 4
Percent Similarity: 62.205      Percent Identity: 29.921

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alignment_block:
US-09-240-675-1_copy_27_427 x US-08-943-087-16

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Align seq 1/1 to: US-08-943-087-16 from: 1 to: 553

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18 LeuLeuLeuLeuAlaAlaProTTPGlyArgAlaValProCysValSe 34
75 AGGTGGAAGAAAATCTAAATCTCTCAAAAAGTAGAGTGCACATCATAG 124
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34 TGLYGLY.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
125 ATGACACATTATCTCGAGTGAAGACAGACGATGATGATGATGATGAT 171
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49 smetLysAsnValLeuGlnTTPhrProProGluGlyLeuGlnGlyVal 65
172 AATGTGACATTTCATTCGATTATCAAAAACTGGGATGATTAATGGAT 221
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
66 LysValThrThrValGlnTTPhrPheIleTyrGlyGlnLysLysTyrPle 82

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222 AAAATGCTCTGGGTGTCAGAAATATTACTAGTACCAAAATGCAACTTTCTT 271
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82 uasnlysserlucysargasnilleasnargthryrcysaspleusera 99
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272 CACTCAAGCTGAATGTTATGAGAAATTAATGCGTATAGACA... 318
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99 lagluthserasptyrghlughisgintyrrtyralalysvalysalalle 115
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319 GAAAAAGAAAACACTTCTCATGTATGAGGTTGACTCATTTACACATT 368
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
116 trpglythrlyscysserlystrpialagluserglyargphetyrproph 132
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
369 TCGCAAGCTCAGATTGCTCTCCAGAAAGTA 399
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132 eleugluthrghlughisgintyrrtyrprogluval 142
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seq_documentation_block:
: Sequence 18, Application US/08943087
: Patent No. 5945511
: GENERAL INFORMATION:
: APPLICANT: Lok, S1
: APPLICANT: Kho, Choon J.
: APPLICANT: Jelmeberg, Anna C.
: APPLICANT: Adams, Robyn L.
: APPLICANT: Whitmore, Theodore E.
: APPLICANT: Farrah, Theresa M.
: TITLE OF INVENTION: CYTOKINE RECEPTOR
: NUMBER OF SEQUENCES: 60
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Zymogenetics, Inc.
: STREET: 1201 Eastlake Avenue East
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98102
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/943,087
: FILING DATE:
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/803,305
: FILING DATE: 20-FEB-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Lunn, Paul G
: REGISTRATION NUMBER: 32,743
: REFERENCE/DOCKET NUMBER: 96-24C1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-442-6627
: TELEFAX: 206-442-6678
: TELEX:
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 553 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FRAGMENT TYPE: internal
: US-08-943-087-18

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alignment_scores:
Quality: 146.00      Length: 127
Ratio: 1.848         Caps: 4
% Similarity: 62.205   Percent Identity: 29.921

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alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-943-087-18 ..
Align seg 1/1 to: US-08-943-087-18 from: 1 to: 553

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31 CTAGTCTCTGTCGCCGCGGCCCATG....GTGTGTCGCCAGCCGC 74
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
18 leuleuleuleuleualalaprotpolylargalavalprocyvalise 34
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
75 AGGTGGAATAATCTAAATCTCCCAAAAAGTAGAGTGCACATCATAG 124
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
34 rlygly....leuprolsproalaasnilerhrpheluserilea 49
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
125 ATGCAACTTATCTGAGTGGAACAGAGCATGAGTCTGTGGG... 171
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
49 smetlyasnvalleuglntprhrproprogluglyleuglnclyal 65
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
172 AATGTGACTTTTTCATTCGATTATCAAAAACCTGGGATGATTAATGGAT 221
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
66 lysvalthrtyrthrvalglnlyrphelleyrglyglnlystlystrple 82
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
222 AAAATGCTCTGGGTGTCAGAAATATTACTAGTACCAAAATGCAACTTTCTT 271
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
82 uasnlysserlucysargasnilleasnargthryrcysaspleusera 99
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
272 CACTCAAGCTGAATGTTATGAGAAATTAATGCGTATAGACA... 318
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
99 lagluthserasptyrghlughisgintyrrtyralalysvalysalalle 115
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
319 GAAAAAGAAAACACTTCTCATGTATGAGGTTGACTCATTTACACATT 368
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
116 trpglythrlyscysserlystrpialagluserglyargphetyrproph 132
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
369 TCGCAAGCTCAGATTGCTCTCCAGAAAGTA 399
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
132 eleugluthrghlughisgintyrrtyrprogluval 142
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

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seq_name: /cgn2_6/prodata/1/laa/5B_COMB.pep:US-08-943-087-20

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seq_documentation_block:
: Sequence 20, Application US/08943087
: Patent No. 5945511
: GENERAL INFORMATION:
: APPLICANT: Lok, S1
: APPLICANT: Kho, Choon J.
: APPLICANT: Jelmeberg, Anna C.
: APPLICANT: Adams, Robyn L.
: APPLICANT: Whitmore, Theodore E.
: APPLICANT: Farrah, Theresa M.
: TITLE OF INVENTION: CYTOKINE RECEPTOR
: NUMBER OF SEQUENCES: 60
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Zymogenetics, Inc.
: STREET: 1201 Eastlake Avenue East
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98102
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/943,087
: FILING DATE:
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/803,305
: FILING DATE: 20-FEB-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Lunn, Paul G
: REGISTRATION NUMBER: 32,743

```

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REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-20

alignment_scores:
Quality: 146.00 Length: 127
Ratio: 1.848 Gaps: 4
Percent Similarity: 62.205 Percent Identity: 29.921

alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-943-087-20 ..

Align seg 1/1 to: US-08-943-087-20 from: 1 to: 553

31 CTAGTCTGCGCGCGCGCCATGG.....GTGTGTCGCGACGCCG 74
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18 LeuLeuLeuLeuLeuAlaAlaProTIPGlyArgAlaValProCysValSe 34
75 AGGTGAAAAAATCTAAATCTCTCAAAAAGTAGAGGTGACATCATAG 124
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
125 ATGCACACTTATCTGAGGTGGAACAGAGCGATGAGTCTGCGG... 171
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
49 smetLysAsnValLeuGlnIleThrProProGluGlyLeuGlnGlyVal 65
172 AATGTGACTTTTCATTCGATTATCAAAAAAAGTGGATGATTAATGAT 221
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
66 LysValThrThrValGlnIleThrPheIleTyrlGlyGlnLysLysTyr 82
222 AAAATGCTGGGTGTCAGAAATATTAAGTACCAAAATGCAACTTTCTT 271
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
82 uAsnLysSerGluCysArgAsnIleAsnArgThrTyrcysAspLeuSerA 99
272 CACCTCAAGCTCAATGTTTATGAAGAATAATTAATGCGTATAGACA... 318
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
99 lAcIuThrSerAspTyrGlnHisGlnIleTyrAlaLysValLysAlaIle 115
319 GAAAAAGAAACACTTCTTCATGATGATGAGGTGACATTCATTCACCAT 368
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
116 TrpGlyThrLysCysSerLysTyrAlaLysSerLysArgPheTyrProPh 132
369 TCGCAAGCTCAGATTGGTCTCCAGAAAGTA 399
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
132 eleuGluThrGlnIleGlyProProGluVal 142

seq_name: /cgn2_6/prodata/1/1aa/5B_COMB.pep:US-08-943-087-22

seq_documentation_block:
; Sequence 22, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jeimberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theodore M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTED for Windows Version 2.6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-22

alignment_scores:
Quality: 146.00 Length: 127
Ratio: 1.848 Gaps: 4
Percent Similarity: 62.205 Percent Identity: 29.921

alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-943-087-22 ..

Align seg 1/1 to: US-08-943-087-22 from: 1 to: 553

31 CTAGTCTGCGCGCGCGCCATGG.....GTGTGTCGCGACGCCG 74
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
18 LeuLeuLeuLeuLeuAlaAlaProTIPGlyArgAlaValProCysValSe 34
75 AGGTGAAAAAATCTAAATCTCTCAAAAAGTAGAGGTGACATCATAG 124
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
125 ATGCACACTTATCTGAGGTGGAACAGAGCGATGAGTCTGCGG... 171
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
49 smetLysAsnValLeuGlnIleThrProProGluGlyLeuGlnGlyVal 65
172 AATGTGACTTTTCATTCGATTATCAAAAAAAGTGGATGATTAATGAT 221
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
66 LysValThrThrValGlnIleThrPheIleTyrlGlyGlnLysLysTyr 82
222 AAAATGCTGGGTGTCAGAAATATTAAGTACCAAAATGCAACTTTCTT 271
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
82 uAsnLysSerGluCysArgAsnIleAsnArgThrTyrcysAspLeuSerA 99
272 CACCTCAAGCTCAATGTTTATGAAGAATAATTAATGCGTATAGACA... 318
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
99 lAcIuThrSerAspTyrGlnHisGlnIleTyrAlaLysValLysAlaIle 115
319 GAAAAAGAAACACTTCTTCATGATGATGAGGTGACATTCATTCACCAT 368
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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116 TTPGlyThrIysCysSerIysTTPAlaGluSerGlyArgPheTyrProPh 132
369 TCCGAAGCTCAGATTGTCCTCCAGAACTA 399
I :::::::::::::::::::::::
132 eLeuGluThrGlnIleGlyProProGluVal 142

OM of: US-09-240-675-1_COPY_27_427 to: PIR-63:*

out-format : pfs

Date: Jun 1, 2000 12:36 AM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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-MODEL=frame+12p_model -DEV=xlp
-O=gsn2.1/USPTO_spool/US09240675/runat_30052000.164312.24623/app_query.fasta.1
-DB=PIR-63 -OPT=fastan -SUFFIX=modif.rpr -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -IOPECL=0.000 -IOPEXT=0.000
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blomsu62
-TRANS=human40.ccd1 -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US09240675 -NCPU=6 -ICPU=3 -NO_XLPHY -WAIT
-THREADS=1
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Search information block:

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Query: US-09-240-675-1_COPY_27_427
Query length: 401
Database: PIR-63:*
Database sequences: 168808
Database length: 58629743
Search time (sec): 85.570000
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score_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
PIR2:A32694	+	692.00	5.3e-69	557	Interferon alpha/beta receptor
PIR2:427387	+	454.00	1.8e-42	560	Interferon alpha/beta receptor type
PIR2:445237	+	366.50	7.1e-32	590	Interferon alpha/beta receptor
PIR2:401418	+	136.50	260.76	273	Cytokine receptor family II, me
PIR2:447003	+	136.50	259.27	325	Cytokine receptor family class
PIR2:449947	+	127.00	239.67	349	Interferon receptor class II cy
PIR2:138500	+	120.00	226.06	332	Interferon gamma receptor beta
PIR2:431555	+	104.50	194.90	337	Interferon gamma receptor acces
PIR2:427934	+	85.50	153.68	489	Interferon gamma receptor precu
PIR2:557242	+	84.00	128.17	6831	hypothetical protein ZK617.1a
PIR2:127935	+	84.00	128.16	6839	hypothetical protein ZK617.1b
PIR2:425698	+	84.00	127.77	7150	hypothetical protein ZK617.1b
PIR2:404591	+	83.50	153.68	306	probable 5-hydroxylase (EC 1.-)
PIR2:404239	+	82.50	149.87	378	hypothetical protein P14M19.130
PIR2:420106	+	81.50	138.36	1152	hypothetical protein 2 - slime
PIR1:138344	+	80.00	108.46	2626	titin, cardiac muscle - human
PIR2:404240	+	79.50	136.82	1.03	hypothetical protein P14M19.140
PIR2:444237	+	79.50	143.29	1.12	interleukin-6 signal transducin
PIR2:561165	+	79.00	141.53	1.19	hypothetical protein YDR370c -
PIR2:156215	+	78.00	137.24	1.57	interleukin-10 receptor - human
PIR2:423031	+	78.00	131.88	1.67	hypothetical protein T01G1.3 -
PIR2:567208	+	77.50	130.59	1.91	hypothetical protein Y0R504w -
PIR2:126351	+	76.50	143.56	2.09	hypothetical protein Y105C5B -
PIR1:SL4222	+	76.50	139.42	2.18	chalcone reductase (EC 1.-.-.-)
PIR2:449667	+	76.50	134.28	2.31	interleukin-10 receptor - mouse
PIR2:436337	+	76.50	130.29	2.42	membrane glycoprotein gp130 pre
PIR2:422836	+	75.50	133.34	2.95	hypothetical protein P57B7.4 -
PIR2:137892	+	75.50	131.08	3.03	IL12 receptor component - human
PIR2:420901	+	75.00	111.19	3.78	titin - rabbit (fragment)
PIR2:540037	+	74.50	137.79	4.00	protein p11 - mouse
PIR2:536638	+	73.50	131.61	4.81	glycoprotein EPI - carrot
PIR2:420265	+	73.50	129.83	5.52	hypothetical protein C56A3.3 -
PIR2:420648	+	71.50	127.05	8.08	hypothetical protein T1P1.150
PIR2:406017	+	71.50	122.05	8.56	subtilisin-like protease homo
PIR2:109337	+	71.00	128.71	8.94	choline kinase (EC 2.7.1.32) -
PIR2:AC2034	+	71.00	120.17	9.50	trp3 protein - rat
PIR2:JS5807	+	71.00	123.16	9.83	peroxidase (EC 1.11.1.7) 1 pred
PIR2:561405	+	70.50	127.38	10.44	beta-galactoside alpha-2,6-sial
PIR2:AA1734	+	70.50	125.24	10.46	hypothetical protein T12A2.15
PIR2:W3435	+	70.50	122.31	10.79	hypothetical protein T12A2.15

```
PIR1:164231 + 70.00 125.08 11.76 368 | high affinity transport s
PIR2:A48584 + 70.00 106.79 14.41 313 | transmission blocking ta
PIR2:A45731 + 69.50 132.26 12.21 141 | comc-alpha protein - phag
PIR2:JC2339 + 69.50 129.41 12.61 197 | neutrophil gelatinase-ass
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seq_name: PIR2:A32694

seq_documentation_block:

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Interferon alpha/beta receptor precursor - human
C.Species: Homo sapiens (man)
C.Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 22-Oct-1999
C.Accession: A32694; S17112
R.Uze, G.; Lutfalla, G.; Gresser, I.
Cell 60, 225-234, 1990
A.Title: Genetic transfer of a functional human interferon alpha receptor into mou
A.Reference number: A32694; MUID:90124632
A.Accession: A32694
A.Molecule type: mRNA
A.Residues: 1-557 <U>Z>
A.Cross-references: GB:J03171; NID:q184645; PID:AAA52730.1; PID:g306914
R.Lutfalla, G.
Submitted to the EMBL Data Library, July 1991
A.Description: The structure of the human interferon alpha/beta receptor gene.
A.Reference number: S17112
A.Accession: S17112
A.Molecule type: DNA
A.Residues: 1-16, 'A', '18-329, 'V', '343-557 <U>T>
A.Cross-references: EMBL:X60459; NID:g32671
C.Genetics:
A.Gene: GDB:IFNAR1; IFNAR; IFRC
A.Cross-references: GDB:120078; OMIM:107450
A.Map position: 21q22.1-21q22.1
A.Intons: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
F.1-3/Domain: cytokine receptor; glycoprotein; transmembrane protein
F.437-455/Domain: transmembrane #status predicted <R>N>
F.50,58,81,88,110,172,254,313,314,416,433,507,518,537/Binding site: carboxydra
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alignment_scores:

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Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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alignment_block:

US-09-240-675-1_COPY_27_427 x A32694

Align seg 1/1 to: A32694 from: 1 to: 557

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1 ATGATGTCCTCTCTGCGGCGGACGACCTAGTCTCTCGCGCGTGGG 50
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1 MethetValValLeuLeuGlyAlaThrThrLeuValValValAlaValG1 17
51 CCATGGGCTTGTTCGCGACCCGAGTGGAAAAATCTTAATCTCTC 100
|||||
17 yProTrpValLeuSerAlaAlaAlaGlyLyValSAsnLeuLysSerProG 34
101 AAAAAGTAGAGTGCACATCATGATGACAACTTATCTCGAGTGAAC 150
|||||
34 InlySValGluValAspIleIleAspAspAsnPhelleLeuAlaGTTpAsn 50
|||||
151 AGAGGCGATGCTGTGCGGAATGTGACTTTTTCATTCGATTACAAA 200
|||||
51 ArgSerAspIleSerValGlyAsnValThrPheSerPheAspPyrgInly 67
201 AACTGCGATGATTAATGATAAATTTGTGGGTGTCAGAAATTAACTA 250
|||||
67 sTrngIlyMeCAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrs 84
251 GTACCAATGCACTTTCTTCACTCAAGCTGATGATGTTATGAAGAATT 300
|||||
84 ertHrlyScsAsnPheserSerLeuLysLeuAsnValTyrGluGluIle 100
```

301 AATTCGCTATAGAGCAGAAAAACACTTCTTCATGATGAGT 350
 |||
 101 LysleuAargileAargAlaGluLysGluAsnThrSerTyrGluVal 117
 351 TGACTCATTTACACCATTTGCCAAAGCTCAGATTGGTCTCCAGAGTA 399
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 117 LaspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133
 seq_name: p1r2:S27387

seq_documentation_block:
 Interferon alpha receptor type 1 precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S27387; S33770
 R:Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
 FEBS Lett. 313, 255-259, 1992
 A:Title: Specific antiviral activities of the human alpha interferons are determined at
 A:Reference number: S27387; MUID:93076908
 A:Accession: S27387
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-560 <MOU>
 A:Cross-references: EMBL:X68443; NID:9431; PIDN:CAA48484.1; PID:9432
 A:Experimental source: MDBK cells
 R:Lim, J.K.; Langer, J.A.
 Blochim. Biophys. Acta 1173, 314-319, 1993
 A:Title: Cloning and characterization of a bovine alpha interferon receptor.
 A:Reference number: S33770; MUID:93305725
 A:Accession: S33770
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-421, 'V', 423-560 <LIU>
 A:Cross-references: EMBL:L06320; NID:9163187; PIDN:AA02571.1; PID:9163188
 A:Experimental source: Lung
 C:Keywords: antiviral; cytokine receptor; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>

alignment_scores:
 Quality: 454.00 Length: 134
 Ratio: 3.914 Gaps: 4
 Percent Similarity: 86.567 Percent Identity: 69.403

alignment_block:
 US-09-240-675-1_COPY_27_427 x S27387 ..

Align seg 1/1 to: S27387 from: 1 to: 560

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4 ATGCGTCCTCTCTGCGCGAGCGACCTAGTCTGCGCGGCGCC 53
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1 MetLeuAlaLeuLeuGluAlaThrThrLeuLeuValAla...GLYAr 16
54 ATGGGTGTTGTCGCGAGCGCGAGGTGGAATAAATCTAAATCTCTCAAA 103
|||  

16 gtrValleuProAlaAlaSerGlyLysAlaAsnLeuLys...ProGluA 32
104 AACTAGAGTCGACATCATGATGACAACTTATCTCTGAGTGGAGACAG 153
|||  

32 snValGluIleLysIleLeuAspAsnPhePheLeuLysTrpAsnSer 48
154 AGGAGATGCTGTGCGGAATGAGCTTTTCATTCGATATCAAAAAC 203
|||  

49 SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGlnIleLe 65
65 uGlyThrAspAsnTyrLysLysSerGlyCysGlnIleIleThrSer 82
254 CCAATTCGACTTTCTCTCACTCAAGCTG...AATGTTTGAAGAAT 300
|||  

82 hrLysCysAsnPheSerSerValGluLeuGluAsnValPheGluLysIle 98

```

301 AATTCGCTATAGAGCAGAAAA...GAAACACTTCTTCATGATGATGA 347
 |||
 99 GluLeuAargileAargAlaGluGluLysAsnAsnThrSerThrTyrGrl 115
 348 GGTGACTCATTTACACCATTTGCCAAAGCTCAGATTGGTCTCCAGAG 397
 |||
 115 uValGluProPheValProPheLeuGluAlaGlnIleGlyProProAspV 132
 398 TA 399
 |||
 132 at 132
 seq_name: p1r2:A45283

seq_documentation_block:
 Interferon alpha/beta receptor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C:Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429
 R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
 Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
 A:Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in hon
 A:Reference number: A45283; MUID:92262522
 A:Accession: A45283
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-590 <UZE>
 A:Cross-references: GB:M89641; NID:9194111; PIDN:AAA37890.1; PID:9194112
 A:Note: Sequence extracted from NCBI backbone (NCBIN:102354, NCBIPI:102357)
 R:Lutfalla, G.; Uze, G.
 Gene 148, 343-346, 1994
 A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high
 A:Reference number: I48423; MUID:95047447
 A:Accession: I48423
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 127-224 <RES2>
 A:Cross-references: EMBL:U06238; NID:9497104; PIDN:AA01749.1; PID:9755811
 A:Accession: I48425
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 243-264 <RES3>
 A:Cross-references: EMBL:U06239; NID:9497106; PIDN:AAA65004.1; PID:9510261
 A:Accession: I48426
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 265-375 <RES4>
 A:Cross-references: EMBL:U06240; NID:9497108; PIDN:AAA65005.1; PID:9510262
 A:Accession: I48427
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 397-424 <RES5>
 A:Cross-references: EMBL:U06241; NID:9497110; PIDN:AAA65006.1; PID:9755812
 A:Accession: I48428
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 426-445 <RES6>
 A:Cross-references: EMBL:U06242; NID:9497112; PIDN:AAA65007.1; PID:9755813
 A:Accession: I48429
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 473-590 <RES7>
 A:Cross-references: EMBL:U06244; NID:9497114; PIDN:AAA65008.1; PID:9510265
 C:Genetics:
 A:Gene: IFNAR
 A:Introns: 177/3; 331/1
 C:Keywords: cytokine receptor; transmembrane protein

alignment_scores:

Quality: 366.50 Length: 133
Ratio: 3.524 Gaps: 1
Percent Similarity: 78.195 Percent Identity: 52.632

alignment_block:

US-09-240-675-1_copy_27_427 x A45283 ..

Align seg 1/1 to: A45283 from: 1 to: 590

```

4 ATGCTGCTCCCTCGCGCGAGACCCCTAGTCTGCTGCGCGGCGCC 53
1 MetLeuAlaValValGlyAlaAlaLeuValAlaGlyAlaPr 17
54 ATGGGTGTGTCGCGCGAGCGGAGAAAATCTAAATCTCTCAA 103
17 OTPrValLeuProSerAlaAlaGlyGlyGluAsnLeuLysProProGluA 34
104 AAGTAGAGGTGACATCATAGATGACAATTATCTGAGGTGAGACAG 153
34 snLeuAspValTyrIleIleAspAspAsnTyrThrLeuLysTyrSer 50
154 AGCCATGAGTCTGCGGAGATGACATTTTCATTCGATTTCAGAAAAC 203
51 HisGlyLysSerMetGlySerValThrPheSerAlaGluTyrArgThrLy 67
204 TGGGATGATATGATATAAATGTGCGGTGACAGATATTTACTGTA 253
67 sAspGluAlaLysTyrPheLysValProGluCysGlnHisThrThrThrT 84
254 CCAATGCCAATTTCTTCTCACTCAAGTGAATGTTATGAGAATAA 303
84 hTyrCysGluPheSerLeuLeuAspThrAsnValTyrIleLysThrGln 100
304 TTGGCTATAGACGCAAAAAGAAAAC...ACTTCTTCATGCTATGAGCT 350
101 PheArgValAlaGlyAlaGluGlnGlyAsnSerThrSerSerTyrPasnGluVa 117
351 TGACTCATTTTACACCATTTGSCAAGCCACATGGTCTCCAGAGTA 399
117 lAspProPheIleProPheTyrThrAlaHisMetSerProGluVal 133

```

seq_name: p1r2:G01418

seq_documentation_block:

Cytokine receptor family II, member 4 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C:Accession: G01418
R:Lutilla, G.
submitted to the EMBL Data Library, April 1994
A:Reference number: G06935
A:Accession: G01418
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-273 <LUT>
A:Cross-references: EMBL:U08988; NID:g571295; PID:g571296
C:Genetics:
A:Gene: GDB:CRF4; CRF2-4
A:Cross-references: GDB:138166; OMIM:123889
A:Map position: 21q22.1-21q22.2
A:introns: 17/1; 58/2; 111/1; 166/3; 216/1

alignment_scores:

Quality: 136.50 Length: 121
Ratio: 1.896 Gaps: 5
Percent Similarity: 59.504 Percent Identity: 33.058

alignment_block:

US-09-240-675-1_copy_27_427 x G01418 ..

Align seg 1/1 to: G01418 from: 1 to: 273

```

55 TGGGTGTGTCGCGCGAGCGGAGAAAATCTAAATCT..... 96
3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuG 19
97 .....CTCAAAAGTAGAGTGCATCATAGATGAGACACT 133
19 yMetValProProProGluAsnValArgMetAsnSerValAsnPhelysA 36
134 TTATCTGAGGTGGAACAGGAGCATGCTGTCGGGAATGACTTTT 183
36 snLeuLeuGlnTyrGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
184 TCATTCGATATCAAAAAACTGGATGATATGCTAAATGCTCG 233
53 ThrAlaGlnTyr.....LeuSerTyrArgIlePheGlnAspLy 65
234 GTGTCAGATATATTAGTACCAATGCACTTTCTTCACTCAAGCTGA 283
65 sCysMetAsnThrThrLeuThrGluCysAspPheSerSer.....LeuS 80
284 ATGTTTATGAGAAATTAATTCGCTATTAAGACAGAA...AAGAAAAC 330
80 eLysTyrGlyAspPheThrLeuArgValArgAlaGluPheAlaAspGln 96
331 ACTTCTTCATGCTATGAGTGTGACTCATTTACACCATTTGCAAGCTCA 380
97 HisSerAspTyrValAsnIle...ThrPheCysProValAspAspThrI 112
381 GATTGCTCTCA 393
112 eLleGlyProPro 116

```

seq_name: p1r2:A47003

seq_documentation_block:

Cytokine receptor family class II protein CRF2-4 precursor - human
C:Species: Homo sapiens (man)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1997
C:Accession: A47003
R:Lutilla, G.; Gardiner, K.; Uze, G.
Genomics 16, 366-373, 1993
A:Title: A new member of the cytokine receptor gene family maps on chromosome 21 at
A:Reference number: A47003; MUID:93930510
A:Accession: A47003
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-325 <LUT>
A:Cross-references: GB:217227; NID:g393378; PID:g393379
C:Genetics:
A:Map position: 21q
C:Keywords: transmembrane protein

alignment_scores:

Quality: 136.50 Length: 121
Ratio: 1.896 Gaps: 5
Percent Similarity: 59.504 Percent Identity: 33.058

alignment_block:

US-09-240-675-1_copy_27_427 x A47003 ..

Align seg 1/1 to: A47003 from: 1 to: 325

```

55 TGGGTGTGTCGCGCGAGCGGAGAAAATCTAAATCT..... 96
3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuG 19
97 .....CTCAAAAGTAGAGTGCATCATAGATGAGACACT 133
19 yMetValProProProGluAsnValArgMetAsnSerValAsnPhelysA 36

```

```

134 TTATCTGAGGTGAGACAGACGATGCTGTCCGGAATGACTTT 183
    |||||
36 snlleuGlnTrpGlnSerProAlaPheAlaLysGlyAsnLeuPhe 52
    |||||
184 TCATTGATATCAAAAACTGCGATGATTAATGATTAATGCTGCG 233
    |||||
53 ThrAlaGlnTyr.....LeuSerTyrArgIlePheGlnAspLys 65
    |||||
234 GTGTCAGAAATTAATTAAGTACCAAAATGCACTTTCTTCACTCA 283
    |||||
65 scyGlnSerThrThrLeuThrGlnCysAspPheSer.....LeuS 80
    |||||
284 ATGTTAGAGAAATTAATGCTGATTAAGACAGAGA...AAGAAAC 330
    |||||
80 eLysTyrGlyAspHisThrLeuArgValArgAlaGlnPheAlaSer 96
    |||||
331 ACTTCCTGATGATGAGTTCACATTCATTCACCATTCGCCAAAGCTCA 380
    |||||
97 HisSerAspTrpValAsnIle...ThrPheCysProValAspAspThr 112
    |||||
381 GATTGCTCTCCA 393
    |||||
112 eileGlyProPro 116

```

```

seq_documentation_block:
Interferon receptor class II cytokine receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: J06311
R:Gibbs, V.C.; Pennica, D.
Gene 186, 97-101, 1997
A:Title: CRF2-4: Isolation of cDNA clones encoding the human and mouse proteins.
A:Reference number: J06311
A:Accession: J06311
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-349 <GIB>
A:Cross-references: GB:U53696

```

```

alignment_scores:
Quality: 127.00 Length: 121
Ratio: 1.693 Gaps: 6
Percent Similarity: 61.983 Percent Identity: 30.579

```

```

alignment_block:
US-09-240-675-1_COPY_27_427 x J06311 ..

```

```

Align seg 1/1 to: J06311 from: 1 to: 349

```

```

46 GTGGGCCCATGGGTGTGCCGACGCGAGGTGAAAAATCTAAATC 95
    |||||
9 LeuGlyGlyPheLeuLeuValProAlaLeuGly.....MetIleProPr 23
    |||||
96 TCCTCAAAAGTAGTAGTGCACATCATAGATGCAACTTATCTAGAGG 145
    |||||
23 oProGluLysValArgMetAsnSerValAsnPheLysAsnIleLeuGln 40
    |||||
146 GGAACAGGACGATGAGTCTGTCCGGAATGATGATTTTCATTCGATT 195
    |||||
40 TrpAlaValProAlaPheProLysThrAsnLeuThrPheThrAlaGlnTyr 56
    |||||
196 CA.....AAACGTGGATGATTAATGATTAATTTGCTGGGTCA 239
    |||||
57 GluSerTyrArgSerPheGlnAspHis.....CysLys 67
    |||||
240 GATTATTACTAGTACCAAAATGCACTTTCTTCACTCAAGCTGATGTT 289
    |||||
67 SarGlnAlaSerThrGlnCysAspPheSer.....HisLeuSerLys 82

```

```

290 ATGAGAAATTAATTCGATTAAGACAGAGA...AAGAAACACTGCT 336
    |||||
82 TrpGlyAspTyrThrValArgValArgAlaGlnLeuAlaAspHisSer 98
    |||||
337 TCATGATGAGGTGATGATTCATTCATTCACCATTCGCCAAAGCTG 386
    |||||
99 GluTrpAlaValAsnVal...ThrPheCysProValGlnAspThrIleLeu 114
    |||||
387 TCCTCCAGAGTA 399
    |||||
114 YProProGlnMet 118

```

```

seq_name: p1r2:A49947
seq_documentation_block:
Interferon gamma receptor beta subunit - mouse
N:Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor; ty
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A49947
R:Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M.
Cell 76, 803-810, 1994
A:Title: A novel member of the interferon receptor family complements functionality
A:Reference number: A49947; MUID:94170381
A:Accession: A49947
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-332 <HEM>
A:Cross-references: GB:S69336; NID:9545841; PIDN:AAB30165.1; PID:9545842
A:Experimental source: early B-cell line Y16
A:Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBI:145656)
C:Keywords: cytokine receptor

```

```

alignment_scores:
Quality: 120.00 Length: 130
Ratio: 1.500 Gaps: 8
Percent Similarity: 61.538 Percent Identity: 30.769

```

```

alignment_block:
US-09-240-675-1_COPY_27_427 x A49947 ..

```

```

Align seg 1/1 to: A49947 from: 1 to: 332

```

```

61 TTGTCGCGACGCGAGGTGGA.....AAAACTTAAATCTCC 98
    |||||
16 LeuGlyAlaAlaAlaSerProAspSerPheSerGlnLeuAlaLys 32
    |||||
99 TCAAAAGTAGTAGTGCACATCATAGATGACAACTTTTCCTGAGGTG 148
    |||||
32 OLeuAsnProArgLeuHisLeuTyrAsnAspGlnGlnIleLeuThrTrp 49
    |||||
149 ACAGAGCGATGAGTCT.....GTCCGGAATGTCAGT 180
    |||||
49 LuProSerProSerSerAsnAspProArgProValValTyrGlnValGlu 65
    |||||
181 TTTTCATTCGATTATCAAAAACTGGATGAT...AATGATTAATTT 227
    |||||
66 TyrSerPhe.....IleAspGlySerTrpHisArgLe 76
    |||||
228 G.....TCTGGGTCTCAAAATTAATTAAGTACCAAAATGCACTTTCT 271
    |||||
76 uLeuGlnProAsnCysThrAspIleThrGlnThrLysCysAspLeuTrp 93
    |||||
272 CA.....CTCAAGCTGAATGTTATGA...GAATTAATTTGCGT 309
    |||||
93 TrpGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeuArg 109
    |||||
310 ATTAGAGCAGAAAAAGAAAC...ACTTCCTCATGATGATGAGTTGATC 356
    |||||
110 ValArgAlaLysArgGlyAsnLeuThrSerLysTrpValGlyLeuGlnPr 126
    |||||
357 ATTACACCATTTCCGCAAGCTCAAGATTGTCCTCAGAGA 396

```


126 oPhcGlnH1stYrGluAsnValThrValGlyProProlys 139
seq_name: p1r2:138500

seq_documentation_block:
Interferon gamma receptor accessory factor-1 precursor - human
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 05-Nov-1999
C:Accession: 138500; 138501
R:Sch, J.; Donnelly, R.J.; Kosenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S.
Cell 76, 793-802, 1994
A:Title: Identification and sequence of an accessory factor required for activation of
A:Reference number: A49946; MUID:94170380
A:Accession: 138500
A:Molecule type: mRNA
A:Residues: 1-337 <RES>
A:Cross-references: EMBL:U05875; NID:g463549; PIDN:AAA16955.1; PID:g463550
A:Experimental source: clone pSK1
A:Accession: 138501
A:Molecule type: mRNA
A:Residues: 1-63, 'Q', 65-337 <RE2>
A:Cross-references: EMBL:U05877; NID:g463551; PIDN:AAA16956.1; PID:g463552
C:Genetics:
A:Map position: 21
C:Keywords: cytokine receptor

alignment_scores:
Quality: 104.50 Length: 145
Ratio: 1.393 Gaps: 7
Percent Similarity: 51.724 Percent Identity: 25.517

alignment_block:
US-09-240-675-1_COPY_27_427 x 138500 ..
Align seg 1/1 to: 138500 from: 1 to: 337

```
34 GTGCTCGCCGCGGCGCCATGGGCTGTTCGCGAGCGCAGTGGA.. 81
9 LeuLeuLeuLeuLeuGlyValPheAlaAlaAlaAlaAlaAlaProPheAs 25
82 .....AAAAATCTAAATCTCCTCAAAAAGTAGAGTCGACATCATAG 124
25 ProLeuSerGlnLeuProAlaProGlnHisProLysIleArgLeuTyrA 42
125 ATGCAACTTATCTCTGAGTGG.....ACACGAGC 156
42 snAlaGlnGlnValLeuSerTrpGluProValAlaAlaLeuSerAsnSerThr 58
157 GATAGTCTGTGGGAATGTGACTTTTCATTCGATTATCAAAAACGCG 206
59 ArgProValValTyrArgValGlnPheLysTyrThrAspSerLys.... 73
207 GATGATTAATGGATAAAATGTCT.....GGGTCTC 238
74 .....TriPheThrAlaAspIleMetSerIleGlyValAsnCyst 87
239 AGAATATTACAGTACCAATGCAACTTTTCTCA..... 273
87 hrgInIleThrAlaThrGlnLysAspPheThrAlaAlaSerProSerAla 103
274 .....CTCAGCTGAATGTTTATGAGAAGAAATTAATGCGTATAG 314
104 GlyPheProMetAspPheAsnVal.....ThrLeuAspGlnLeuArg 116
315 ACAGAAAAAGAAAAACACT...TCTCATGCTATGAGGTTGACTCATTTA 361
116 gAlaGlnLeuGlnValAlaLeuHisSerAlaTrpValThrMetProTrpPheG 133
362 CACCATTTCCGAAGCTCAGATGTGCTCTCCAGAA 396
```

133 InH1stYrArgAsnValThrValGlyProProGlu 144
seq_name: p1r2:A31555

seq_documentation_block:
Interferon gamma receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Jul-1999
C:Accession: A31555
R:Agnet, M.; Dembic, Z.; Merlín, G.
Cell 55, 273-280, 1988
A:Title: Molecular cloning and expression of the human interferon-gamma receptor.
A:Reference number: A31555; MUID:89003065
A:Accession: A31555
A:Molecule type: mRNA
A:Residues: 1-489 <AGD>
A:Cross-references: GB:J03143; NID:g184650; PIDN:AAA52731.1; PID:g306915
C:Genetics:
A:Gene: GDB:IFNGR1; IFNGR
A:Cross-references: GDB:120688; OMIM:107470
A:Map position: 6q23-6q24
C:Superfamily: Interferon gamma receptor
C:Keywords: cytokine receptor; transmembrane protein

alignment_scores:
Quality: 85.50 Length: 136
Ratio: 1.018 Gaps: 5
Percent Similarity: 61.765 Percent Identity: 24.265

alignment_block:
US-09-240-675-1_COPY_27_427 x A31555 ..
Align seg 1/1 to: A31555 from: 1 to: 489

```
7 GTGCTCTCTGCGGCGGCGACACCTAGTCTGTCGCGCGCGCCATG 56
1 MetAlaLeuLeuPheLeuLeuProLeuValMetGlnGlyAlaSerArgAl 17
57 GGTCTTCTCCGCAACC...GCAGTGGAAAAAATCTAAATCTTCCTAAA 103
17 gAluMetGlyThrAlaAspLeuGlyProSerSerValProThrProThra 34
104 AAGTAGAGCGACATCATGATGACAACTTATCCGAGGTGGAACAGC 153
34 snValThrIleGlnSerTyrAsnMetAsnProIleValTyrTrpGluTyr 50
154 AGCGATGATCTGTGCGGAATGTG...ACTTTTCATTCGATTATGAAA 200
51 .....GlnIleMetProGlnValProValPheThrValGlnValLysAs 65
201 AACTGGGATGATTAATGATTAATTCGTCTGGGTGTCACAAATTTACTA 250
65 nTyrGlyValLysAsnSerGlnTrpIleAspAlaCysIleAsnIleSerH 82
251 GTACCAATGCAACTTTCTTCACGTCAGCTGATGTTTATGAAGAAT 300
82 ISh1stYrCysAsnIleSerAspHisValGlnLysProSerAsnSerLeu 98
301 AAATTCGGTAAAGACA.....GAAAAAGAAAACCTTCTTCATG 341
99 TrpValArgValLysAlaArgValGlnGlnLysGlu.....SerAlaTy 113
342 GATAGGAGTACTCAATTTACACACTTTGCAAGCGACATGCGCTC 391
113 fAlaLysSerGlnGlnPheAlaValAlaCysArgAspGlyLysIleGlyPro 130
392 CAGAGTA 399
130 rOlyLysLeu 132
seq_name: p1r2:T27934
```

seq_documentation_block:
 hypothetical protein ZK617.1a - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 15-Oct-1999 #sequence-revision 15-Oct-1999 #text-change 29-Oct-1999
 C:Accession: T27934; T28030
 R:White, S.
 Submitted to the EMBL Data Library, May 1996
 A:Reference number: 220442
 A:Accession: T27934
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-6831 <M12>
 A:Cross-references: EMBL:Z27897; PIDN:CAA98064.1; GSPDB:GN00022; CESP:ZK617.1a
 R:Harris, B. the EMBL Data Library, May 1996
 Submitted to the EMBL Data Library, May 1996
 A:Reference number: 220458
 A:Accession: T28030
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-6831 <M12>
 A:Cross-references: EMBL:Z27899; PIDN:CAA98081.1; GSPDB:GN00022; CESP:ZK617.1a
 A:Experimental source: clone ZK829
 C:Genetics:
 A:Gene: CESP:ZK617.1a
 A:Map position: 4
 A:Introns: 10/3; 61/3; 135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 542/3; 574/3; 59
 144/3; 6683/3; 6768/1; 6800/3

alignment_scores:
 Quality: 84.00 Length: 117
 Ratio: 1.151 Gaps: 8
 Percent Similarity: 62.393 Percent Identity: 26.496

alignment_block:
 US-09-240-675-1_COPY_27_427 x T27934 ..

Align seg 1/1 to: T27934 from: 1 to: 6831

```

88 CTAATAATCTCTCAAAA.....GTAGAGTC...GACATCAT 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1856 LeuAspArgProSerLysProAsnGlyProLeuGluValSerAspValph 1872
123 AGATGCAATTTATCTGTGAGTGAACAGCAGCAGTGTGCTGGGGA 172
   :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1872 egiuAspAsnLeuAsnLeuSerTyrProAspAspAspGlyGlyG 1889
173 ATGTGACTTTTCATTCGATTATCAAAA.....ACTGGATGATTAAT 216
   :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1889 IurolleGluTyrTyrGluValGluLysLeuAspThrAlaThrGlyArg 1905
217 TGGATAAAATTTGCTGGGTCTGAGAAATATTACTAGTCAAAATGCAACT 266
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1906 TrpValPro.....CysAlaLysValLysAspThrLysAlaHisI 1919
267 TTTTCACTCAAGCTGAATGTTATTAAGAAATTAATTGCGATTAAGAG 316
   :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1919 eaSpGlyLeuLysLysGly.....GlnThrTyrGlnPheArgValLysA 1934
317 CA...GAAAAAGAAACACTTCTCATGTATGAGGTGACATTTACA 363
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1934 IuValAsnLysGluGlyAlaSerAspAlaLeuSerThrAspLysAspThr 1950
364 .....CCATT...CGCAAAGTCAGATGCTGCTCCAGAACT 398
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1951 LysAlaLysAsnProTyrAspGluProGlyLysThrGlyThrProAspVa 1967
399 A 399
1967 1 1967
seq_name: p1r2:S57242

```

seq_documentation_block:
 twitchin - *Caenorhabditis elegans*
 N:Alternate names: myosin-regulating protein
 N:Contains: Protein kinase (EC 2.7.1.-)
 C:Species: *Caenorhabditis elegans*
 C>Date: 28-Oct-1995 #sequence-revision 24-Oct-1997 #text-change 18-Jun-1999
 C:Accession: S57242; S07571; S06797; S57218
 R:Benlian, G.M.; L'Hernault, S.W.; Morris, M.E.
 Submitted to the EMBL Data Library, February 1993
 A:Description: Additional sequence complexity within twitching of *Caenorhabditis ele*
 A:Reference number: S57242
 A:Accession: S57242
 A:Molecule type: DNA
 A:Residues: 1-6839 <BEN1>
 A:Cross-references: EMBL:L10351
 R:Benlian, G.
 Submitted to the EMBL Data Library, November 1989
 A:Reference number: S07571
 A:Accession: S07571
 A:Molecule type: DNA
 A:Residues: 792-6839 <BEN2>
 A:Cross-references: EMBL:X15423; NID:96897; PIDN:CAA33463.1; PID:96898
 R:Benlian, G.M.; Kiff, J.E.; Neckelmann, N.; Moerman, D.G.; Waterston, R.H.
 Nature 342, 45-50, 1989
 A:Title: Sequence of an unusually large protein implicated in regulation of myosin
 A:Reference number: S06797; MUID:90044042
 A:Accession: S06797
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 806-1175; 1178-1998; 'Y', 2000-3040; 'I', 3042-3335; 'I', 3337-5693; 5696-6359,
 A:Cross-references: EMBL:X15423
 A:Experimental source: var. Bristol
 R:Benlian, G.M.; L'Hernault, S.W.; Morris, M.E.
 Genetics 134, 1097-1104, 1993
 A:Title: Additional sequence complexity in the muscle gene, unc-22, and its encoded
 A:Reference number: S57218; MUID:93387664
 A:Accession: S57218
 A:Molecule type: DNA
 A:Residues: 2-99; 108-194; 'Q', 196-206; 374-468; 658-753 <BEN4>
 A:Experimental source: var. Bristol
 C:Comment: Lack of unc-22 leads to a constant twitching of the body muscles.
 C:Genetics:
 A:Gene: unc-22
 A:Map position: IV
 A:Introns: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/
 152/3; 6691/3; 6776/1; 6808/3
 C:Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homol
 C:Keywords: ATP; autophosphorylation; duplication; muscle; phosphotransferase; seril
 F:806-898, 899-990, 991-1083, 1084-1175, 1178-1273, 1474-1567, 1770-1864, 2066-2158, 2358-2
 96-5790, 6283-6356, 6386-6478, 6541-6635, 6649-6742, 6745-6838/Region: motif 2
 F:1274-1372, 1373-1473, 1568-1670, 1671-1769, 1865-1964, 1965-2065, 2159-2258, 2259-2357, 2
 23, 4215-4313, 4314-4415, 4416-4516, 4612-4710, 4811, 4908-5009, 5010-5109, 5110-5210,
 F:5948-5956/Region: protein kinase homology <kin>
 F:5948-5956/Region: protein kinase ATP-binding motif
 F:5971/Active site: Lys #status predicted

alignment_scores:
 Quality: 84.00 Length: 117
 Ratio: 1.151 Gaps: 8
 Percent Similarity: 62.393 Percent Identity: 26.496

alignment_block:
 US-09-240-675-1_COPY_27_427 x S57242 ..

Align seg 1/1 to: S57242 from: 1 to: 6839

```

88 CTAATAATCTCTCAAAA.....GTAGAGTC...GACATCAT 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1864 LeuAspArgProSerLysProAsnGlyProLeuGluValSerAspValph 1880

```

```

123 AGATGACAACTTTATCTGAGCTGACAGACGAGTCTGTGCGGA 172
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
1880 egluaspasnleuasnleuSerTrpProProaspaspGlyGlyG 1897
173 ATGTGACTTTTCATTCATATCAAAA.....ACTGGATGATMAT 216
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
1897 luprollelglutyrtygluvalglulysleuasprthralatnrglyArg 1913
217 TGCATTAATAATGCTGCTGCTGACAGATTTACTAGTACCAATGCAACTT 266
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
1914 TrpValPro.....CysAlaLysValLysAspThrLysAlaHisI 1927
267 TTCTCACTCAAGCTGAATGTTATGAAGAAATTAATGCTATAGAG 316
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
1927 easpGlyLeuLysLysGly.....GlnThrTyrGlnPheArgValLysA 1942
317 CA...GAAAAAGAAACACTTCTTCATGATGATGAGTGCATCTTACA 363
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
1942 lavalasnLysgluGlyAlaSeraspAlaLeuSerThrAspLysAspThr 1958
364 .....CCATT...CGCAAGCTCAGATTGCTCCTCCAGAGT 398
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
1959 LysAlaLysasnProTyrAspGluProGlyLysThrGlyThrProaspVa 1975
399 A 399
    |
1975 1 1975

```

seq_name: p1r2:T27935

```

seq_documentation_block:
  hypothetical protein ZK617.1b - Caenorhabditis elegans
  C:Species: Caenorhabditis elegans
  C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
  C:Accession: T27935; T28031
  R:White, S.
  submitted to the EMBL Data Library, May 1996
  A:Reference number: Z20442
  A:Accession: T27935
  A:Status: preliminary; translated from GB/EMBL/DBD
  A:Molecule type: DNA
  A:Residues: 1-7160 <MIL>
  A:Cross-references: EMBL:Z73897; PIDN:CAA98065.1; GSPDB:GN00022; CESP:ZK617.1b
  R:Harris, B.
  submitted to the EMBL Data Library, May 1996
  A:Reference number: Z20458
  A:Accession: T28031
  A:Status: preliminary; translated from GB/EMBL/DBD
  A:Molecule type: DNA
  A:Residues: 1-7160 <W12>
  A:Cross-references: EMBL:Z73899; PIDN:CAA98082.1; GSPDB:GN00022; CESP:ZK617.1b
  A:Experimental source: clone ZK829
  C:Genetics:
  A:Gene: CESP:ZK617.1b
  A:Map position: 4
  A:Insertions: 10/3; 61/3; 135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 542/3; 574/3; 59
  3067/1; 3141/3; 3269/1; 6473/3; 7012/3; 7097/1; 7129/3

```

alignment_scores:

```

  Quality: 84.00      Length: 117
  Ratio: 1.151      Gaps: 8
  Percent Similarity: 62.393      Percent Identity: 26.496

```

alignment_block:

US-09-240-675-1_COPY_27_427 x T27935 ..

Align seg 1/1 to: T27935 from: 1 to: 7160

```

88 CTAATAATCTCTCAAAAA.....GTAGAGCTC...GACATCAT 122
   ||| |||:||||| |||:||||| |||:|||||

```

```

2185 leuaspargProSerLysProasnGlyProleuGluValSeraspValPh 2201
123 AGATGACAACTTTATCTGAGCTGACAGACGAGTCTGTGCGGA 172
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
2201 egluaspasnleuasnleuSerTrpProProaspaspGlyGlyG 2218
173 ATGTGACTTTTCATTCATATCAAAA.....ACTGGATGATMAT 216
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
2218 luprollelglutyrtygluvalglulysleuasprthralatnrglyArg 2234
217 TGCATTAATAATGCTGCTGCTGACAGATTTACTAGTACCAATGCAACTT 266
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
2235 TrpValPro.....CysAlaLysValLysAspThrLysAlaHisI 2248
267 TTCTCACTCAAGCTGAATGTTATGAAGAAATTAATGCTATAGAG 316
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
2248 easpGlyLeuLysLysGly.....GlnThrTyrGlnPheArgValLysA 2263
317 CA...GAAAAAGAAACACTTCTTCATGATGATGAGTGCATCTTACA 363
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
2263 lavalasnLysgluGlyAlaSeraspAlaLeuSerThrAspLysAspThr 2279
364 .....CCATT...CGCAAGCTCAGATTGCTCCTCCAGAGT 398
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
2280 LysAlaLysasnProTyrAspGluProGlyLysThrGlyThrProaspVa 2296
399 A 399
    |
2296 1 2296

```

seq_name: p1r2:A25698

seq_documentation_block:

probable protein kinase KIN28 (EC 2.7.1.-) - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: protein D2330; protein YDL108w

C:Species: *Saccharomyces cerevisiae*

C>Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 18-Jun-1999

C:Accession: A25698; S67650; S67410; S72098

R:Simon, M.; Seraphin, B.; Faye, G.

EMBO J. 5, 2697-2701, 1986

A:Title: KIN28, a yeast split gene coding for a putative protein kinase homologous

A:Reference number: A25698; MUID:87053839

A:Accession: A25698

A:Molecule type: DNA

A:Residues: 1-306 <SIM>

A:Cross-references: EMBL:X04423; NID:q3848; PIDN:CAA28019.1; PID:q3849

R:Ballestra, J.P.G.; Remacha, M.; Soler-Mira, A.; Jimenez, A.; Garcia-Cantalejo, J.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67629

A:Accession: S67650

A:Molecule type: DNA

A:Residues: 1-306 <BAL>

A:Cross-references: EMBL:Z74156; NID:q1431153; PIDN:CAA8675.1; PID:e253036; PID:g

R:Poskovic, J.; Saliz, J.E.; Soler-Mira, A.; Garcia-Cantalejo, J.; Revuelta, J.L.;

submitted to the EMBL Data Library, February 1996

A:Reference number: S67406

A:Accession: S67410

A:Molecule type: DNA

A:Residues: 1-306 <BOS>

A:Cross-references: EMBL:X95644; NID:g1199535; PIDN:CAA64904.1; PID:e223186; PID:g

Yeast 12, 1077-1084, 1996

A:Title: The sequence of a 20.3 kb DNA fragment from the left arm of *Saccharomyces*

A:Reference number: S72094; MUID:97051597

A:Accession: S72098

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-306 <SAI>

A:Cross-references: EMBL:X95644; NID:g1199535; PIDN:CAA64904.1; PID:e223186; PID:g

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1

C:Genetics:

A:Gene: SGD:KIN28

A:Cross-references: MIPS:YDL108w; SGD:S0002266
A:Map position: 4L
A:Introns: 10/1
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:5-259/Domain: protein kinase homology <KIN>
F:13-21/Region: protein kinase ATP-binding motif

Alignment_scores:
Quality: 83.50 Length: 102
Ratio: 1.606 Gaps: 4
Percent Similarity: 50.980 Percent Identity: 26.471

Alignment_block:
US-09-240-675-1_COPY_27_427 x A25698

Align seg 1/1 to: A25698 from: 1 to: 306

```
115 GACATCATGATGACACTTATCCGAGGTGGAACAGGAGCATGATC 164
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
159 GUILLEUTHSerAsnValAlaThrArgTyrArgAlaProGlu.. 174
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
165 TGTGGGAATGTGACTTTTTCATTCGATTATCAAAAAGTGGATGATA 214
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
175 .....LeuLeuPheGlyAlaIshsYrThrSerAlaIleAspI 188
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
215 ATTGATTAATTTGCTGGGTGTCAGATATTCTAGTACCAATTCAC 264
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
188 lerp.....SerValGlyValIle 194
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
265 TTTTCTCACTCAAGCTG.....AATGTTTA 290
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
195 PheAlaGluMetLeuArgIleProTyrLeuProGlyGlnAsnAsp 211
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
291 TGAAGAATTAATTCGATTAAGACAGAAAAAACAACCTCT..T 337
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
211 lAspGlnMetGluValThrPheArgAlaLeuGlyThrProThrAspArg 228
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
338 CATGATATGAGTTGACTCTATTCACACCATTTGGCAAGCTGATG 387
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
228 sPrpProGluValSerSerPheMetThrTyrAsnLysLeuGlnIleTyr 244
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
388 CCTCA 393
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
245 ProPro 246
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
```

seq_name: p1r2:T04591

seq_documentation_block:

ferulate-5-hydroxylase (EC 1.-.-.-) - Arabidopsis thaliana
N:Alternate names: cytochrome P450-dependent monooxygenase; protein F23E13.110
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 29-Sep-1999
C:Accession: T04591
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse, T.
submitted to the Protein Sequence Database, March 1998
A:Reference number: 215378
A:Accession: T04591
A:Molecule type: DNA
A:Residues: 1-520 <BEV>
A:Cross-references: EMBL:AL022141
A:Experimental source: cultivar Columbia; BAC clone F23E13
C:Genetics:
A:Map position: 4
A:Introns: 11/1; 314/3
A:Note: F23E13.110
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: heme; iron; oxidoreductase
F:458/Binding site: heme iron (Cys) (axial ligand) #status predicted

alignment_scores:

Quality: 83.00 Length: 156
Ratio: 1.137 Gaps: 6
Percent Similarity: 46.795 Percent Identity: 21.154

Alignment_block:

US-09-240-675-1_COPY_27_427 x T04591

Align seg 1/1 to: T04591 from: 1 to: 520

```
1 ATGATGCTGCTCCTCCGCGCGACGACCCCTATGCTGTCGCGCGG 50
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
313 lIleMetAspValMetPheGlyGlyThrGluThrValAlaSerAlaIle.. 328
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
51 CCCATGGGTGTTCGCCAGCCGAGGTGGAAAAATCTAAATCTCCTC 100
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
329 .GluThrAlaLeuThr.....GluLeuLeuArgSerProG 340
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
101 AAAAAAGTAGAGTCGACATCATAGATGACAACTTATCTGAGGTGAC 150
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
340 lAspLeuLys..... 343
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
151 AGAGCGCATGATGCTGCGGAGATGACTTTTCATTGATATCAAAA 200
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
344 ArgValGlnGlnGluLeuAlaGluVal..... 352
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
201 AACTGGATGATATATGATTAATTTGCTGGGTGTCAGAAATATCTA 250
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
353 .ValGlyLeuAspArgValGluGluSerAspIleGlyLysLeuThr 369
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
251 GTACCAATGCAACTTTCTTCACTCAAGCTGAATGTTTANGAANAAT 300
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
369 yLeuLysCysThrLeuLysGlu...ThrLeuArgMetHisProProlle 384
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
301 AATGCGCTATAGAGCAGAAAAAACAACCTCT..... 336
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
365 ProLeuLeuLysGluThrAlaGlnAspThrSerIleAspGlyPhePh 401
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
336 ..... 336
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
401 eIleProLysLysSerArgValMetIleAsnAlaPheAlaIleGlyArg 418
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
337 .....TCATGATGAGTTGACTCTATTCACACCATTTGCCAAACT 378
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
418 sPrpThrSerThrPheAspProAspThrPheArgProSerArgPheLeu 434
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
379 CAGATTGTCCTCCAGAA 396
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
435 GluProGlyValProAsp 440
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
```

seq_name: p1r2:T04239

seq_documentation_block:

hypothetical protein F14M19.130 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C:Accession: T04239
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Hohenseel, J.
submitted to the Protein Sequence Database, March 1999
A:Reference number: 215262
A:Accession: T04239
A:Molecule type: DNA
A:Residues: 1-578 <BEV>
A:Cross-references: EMBL:AL049480
A:Experimental source: cultivar Columbia; BAC clone F14M19
C:Genetics:
A:Map position: 4
A:Introns: 47/3; 130/3; 163/1; 262/2
A:Note: F14M19.130

alignment_scores:
Quality: 82.50 Length: 111
Ratio: 1.269 Gaps: 6

Percent Similarity: 58.559 Percent Identity: 29.730

Alignment block:

US-09-240-675-1_copy_27_427 x T04239

Align seg 1/1 to: T04239 from: 1 to: 378

```
73 GCAGGTGAAAAAATCTAAATCTCTCA.....AAAGTAGAGT 113
||||| .....||| |||:| :|||:|
205 AlaGlyLysValLysIleLysCysProGluThrAspLeuAlaGluLe 221
|||:| :|||:| :|||:| :|||:|
114 CGACATCATGATGACAACTTATCTGAGGTG.....AACA 151
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
221 uHisLeuIleSerAspSerPheIleGluArgPheArgGlyAsnAsnAsnA 238
152 GGAGC.....GATGAGTCTCGGGAATGTGACTTT 183
||||| .....||| |||:| :|||:|
238 rGserIleLysGlyLysIlePheGluSerSerGlyAsnGlnLeuTyr 254
|||:| :|||:| :|||:| :|||:|
184 TCATTC.....GATTATCAAAAACTGGATGATAATGATAAAATT 227
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
255 AsnIlePheGlyHisTrpAspArgThrValMetAlaLysAsnIleLysTh 271
|||:| :|||:| :|||:| :|||:|
228 GTCGTGGGTGCAGAAATATTAATGACAAATGCACTTTCTTCACTCA 277
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
271 rGlyGluLeuGluValIleTyrAsnAlaLysGluAsnIlePheGlyLeuL 288
278 AG.....CTGAATGTTTATGAGAAATTAATTCGATTAAGAGCA 318
|||:| :|||:| :|||:| :|||:|
288 ysProPThrValLysAsnLeuGluGluVal.....Thr 299
319 GAAAAAGAAACACTCTCTCATGATGAGGT 351
|||:| :|||:| :|||:| :|||:|
300 GluSerGluSerThrMetValTrpSerGluVal 310
```

OM of: US-09-240-675-1_COPY_27_427 to: SwissProt_38: * out_format: pfs
Date: Jun 1, 2000 12:37 AM
About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+12p_model -DEV=xlp
-O=/gen2.1/USP0_spool/US09240675/runat.30052000.164313.24686/app_query.fasta.1
-DB=SwissProt_38 -QFMT=fastan -SUFFIX=modif.rsp -GAPOP=12.000
-CAPEXT=4.000 -MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US09240675 -NCPU=6 -ICPU=3 -NO_XLPHY -WAIT
-THREADS=1

Search information block:
Query: US-09-240-675-1_COPY_27_427
Query length: 401
Database: SwissProt_38: *
Database sequences: 83857
Database length: 30454973
Search time (sec): 45.030000

score_list:

Sequence	Strid Orig	Zscore	Escore Len	Documentation
SwissProt_38:INRI_HUMAN +	692.00	1368.21	2.3e-69	1 P17181 homo sapiens (human).
SwissProt_38:INRI_BOVIN +	454.00	891.17	8.6e-43	560 1 O04790 bos taurus (bovine).
SwissProt_38:INRI_SHEEP +	439.00	861.11	4.0e-41	560 1 O28589 ovis aries (sheep).
SwissProt_38:INRI_MOUSE +	366.50	715.34	5.0e-33	590 1 P33896 mus musculus (mouse).
SwissProt_38:CRF4_HUMAN +	136.50	259.66	2.2e-07	325 1 O08334 homo sapiens (human).
SwissProt_38:INRS_HUMAN +	104.50	195.20	0.0008	337 1 P38484 homo sapiens (human).
SwissProt_38:INRS_HUMAN +	85.50	153.83	0.0151	489 1 P15260 homo sapiens (human).
SwissProt_38:K18_YEAST +	83.50	153.97	0.1808	306 1 P06242 saccharomyces cerevisiae
SwissProt_38:CP84_ARATH +	83.00	148.28	0.2207	520 1 O42600 arabidopsis thaliana
SwissProt_38:IL1B_RAT +	79.50	136.24	0.5854	918 1 P40180 rattus norvegicus (rat)
SwissProt_38:IL1OR_HUMAN +	78.00	137.32	0.8091	578 1 O16361 homo sapiens (human).
SwissProt_38:6DCS_SOYBN +	76.50	139.68	1.10	315 1 P26690 glycine max (soybean).
SwissProt_38:11OR_MOUSE +	76.50	134.36	1.19	575 1 O61728 mus musculus (mouse).
SwissProt_38:IL1B_HUMAN +	76.50	130.23	1.27	918 1 P40189 homo sapiens (human).
SwissProt_38:VNS3_ROTHM +	75.50	131.11	1.57	662 1 P43701 homo sapiens (human).
SwissProt_38:K1CH_YEAST +	71.00	123.23	4.90	486 1 P35424 human rotavirus (sero
SwissProt_38:CA01_HUMAN +	70.50	125.41	5.31	406 1 P15907 homo sapiens (human).
SwissProt_38:5230_PLAFO +	70.00	106.34	7.93	3135 1 O08372 plasmodium falciparu
SwissProt_38:COMA_BPTA +	69.50	132.76	5.96	141 1 O01438 bacteriophage t4, comc
SwissProt_38:NGAL_HUMAN +	69.50	129.76	6.23	198 1 P80188 homo sapiens (human).
SwissProt_38:IDEP_HAEIN +	69.50	129.36	6.27	207 1 P46291 haemophilus influenzae
SwissProt_38:RRRA_CWJH +	69.50	102.17	9.46	4488 1 P19751 murine coronavirus m
SwissProt_38:VE2_HPV42 +	68.50	121.58	8.85	398 1 P27223 human papillomavirus t
SwissProt_38:TYO3_RAT +	68.50	114.57	9.84	880 1 P55166 rattus norvegicus (rat)
SwissProt_38:YD83_SCHPO +	67.00	111.40	12.95	1004 1 O10408 schistosomaccharomyces
SwissProt_38:VE2_HPV23 +	67.00	117.87	13.15	431 1 P50769 human papillomavirus t
SwissProt_38:HPRI_YEAST +	67.00	112.95	14.17	752 1 P17629 saccharomyces cerevisiae
SwissProt_38:VPEH_NPVAC +	66.50	121.61	13.92	252 1 P24728 autographa californic
SwissProt_38:ICED_HUMAN +	66.50	118.05	14.69	377 1 P49662 homo sapiens (human).
SwissProt_38:CAG1_RAT +	66.50	117.46	14.82	403 1 P13721 rattus norvegicus (rat)
SwissProt_38:YCF0_MARPO +	66.50	108.85	16.88	1068 1 P12221 marcanthia polymorpha
SwissProt_38:Y060_MYCGE +	66.00	119.16	16.18	297 1 P43306 mycoplasma genitalium
SwissProt_38:Y107_METJA +	66.00	114.12	17.46	525 1 O57571 methanococcus jannasch
SwissProt_38:PD12_RAT +	66.00	111.93	18.05	673 1 O08642 mus musculus (mouse).
SwissProt_38:PHLC_MOUSE +	66.00	111.21	18.25	730 1 P06200 pseudomorus aegyptius
SwissProt_38:CTFD_STRMG +	66.00	105.07	20.02	1462 1 P49331 streptococcus mutans
SwissProt_38:KYL1_DICDI +	66.00	104.36	20.24	1584 1 P18160 dictyostellium disco
SwissProt_38:IDPOE_YEAST +	65.50	100.37	24.08	2222 1 P21951 saccharomyces cerevisiae

seq_name: SwissProt_38:INRI_HUMAN

seq_documentation_block:	seq_documentation_block:	seq_documentation_block:	seq_documentation_block:	seq_documentation_block:
ID	INRI_HUMAN	STANDARD:	PRT:	557 AA.
AC	P17181:			
DT	01-AUG-1990 (rel. 15. Created)			
DT	01-AUG-1990 (rel. 15, last sequence update)			
DT	15-FEB-2000 (rel. 39, last annotation update)			
DE	INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).			
GN	IFNAR1 OR IFNAR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
RP	(1)			
RP	SEQUENCE FROM N.A.			
RP	Medline: 90124632.			
RA	Uze G., Lutfalla G., Gresser I.;			
RT	"Genetic transfer of a functional human interferon alpha receptor			
RT	into mouse cells: cloning and expression of its cDNA."			
RT	Cell 60:225-234(1990).			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RP	Medline: 92129376.			
RA	Lutfalla G., Gardner K., Proudhon D., Viel E., Uze G.;			
RT	"The structure of the human interferon alpha/beta receptor gene."			
RT	J. Biol. Chem. 267:2802-2809(1992).			
RL	(3)			
RP	PHOSPHORYLATION BY TYK2.			
RX	Medline: 95059042.			
RA	Colmanick O., Van H., Domanski P., Handa R., Smalley D.,			
RA	Mullersman J., Witte W., Krishnan K., Krolewski J.;			
RT	"Direct binding to and tyrosine phosphorylation of the alpha subunit			
RT	of the type I interferon receptor by p135tyr2 tyrosine kinase."			
RT	Mol. Cell. Biol. 14:8133-8142(1994).			
CC	- FUNCTION: RECEPTOR FOR INTERFERON ALPHA AND BETA. BINDING TO TYPE			
CC	I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS			
CC	INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-			
CC	SUBUNITS THEMSELVES.			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND			
CC	EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.			
CC	- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.			
CC	- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.			
CC	-----			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (see http://www.isb-sdb.ch/announce/			
CC	or send an email to license@isb-sdb.ch).			
CC	-----			
DR	EMBL: J03171; AA52730.1; -			
DR	EMBL: X60459; CA942992.1; -			
DR	PIR: A32694; A32694.			
DR	PIR: S17112; S17112.			
DR	MIM: 107450; -			
KW	Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;			
FT	Phosphorylation.			
FT	SIGNAL	1	27	POTENTIAL.
FT	CHAIN	1	557	INTERFERON-ALPHA/BETA RECEPTOR ALPHA
FT	DOMAIN	28	436	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	437	457	POTENTIAL.
FT	DOMAIN	458	557	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	79	87	BY SIMILARITY.
FT	DISULFID	199	220	BY SIMILARITY.

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FT MOD_RES 466 466 PHOSPHORYLATION (BY TYR2) (PROBABLE).
FT MOD_RES 481 481 PHOSPHORYLATION (BY TYR2) (PROBABLE).
FT CARBOHYD 50 50 POTENTIAL.
FT CARBOHYD 58 58 POTENTIAL.
FT CARBOHYD 81 81 POTENTIAL.
FT CARBOHYD 88 88 POTENTIAL.
FT CARBOHYD 110 110 POTENTIAL.
FT CARBOHYD 172 172 POTENTIAL.
FT CARBOHYD 254 254 POTENTIAL.
FT CARBOHYD 313 313 POTENTIAL.
FT CARBOHYD 314 314 POTENTIAL.
FT CARBOHYD 376 376 POTENTIAL.
FT CARBOHYD 416 416 POTENTIAL.
FT CARBOHYD 433 433 POTENTIAL.
FT VARIANT 168 168 'L->V'
FT CONFLICT 17 17 /FtId-VAR.002717,
SO SEQUENCE 557 AA; 63525 MW; 0F6744CBADBE73 CRC64;
  G -> A (IN REF. 2).

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Alignment_scores:
  Quality: 692.00      Length: 133
  Ratio: 5.203        Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

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Alignment block:

US-09-240-675-1_COPY_27_427 x INR1_HUMAN ..

Align seg 1/1 to: INR1_HUMAN from: 1 to: 557

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1 ATGATGTCGTCCTCTGGGCGGCGAGACCTAGTGTGTCGCGCGGCGG 50
1 MetMetValValLeuLeuValAlaThrThrLeuValLeuValAlaValAl 17
51 CCCATGGGTGTGTCCGCGCGCGAGGCGGAGGAGGAGGAGGAGGAGG 100
17 yProTrrValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerPirG 34
101 AAAAGTACAGTCGACATCATAGAGACACTTTCCTGAGGCGGAGC 150
34 LbLysAlaGluValAspLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 50
151 AGGAGCGATGAGTCTGTGCGGAGATGACTTTTCATTCGATATCAAAA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGln 67
201 AACTGGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 250
67 sThrGlyMetAspAsnTrrPileLysLeuSerGlyGlyGlnAsnIle 84
251 GTCACAAATGCAACTTTTCTCAGCTCAGCTGAAATGTTATGAAGAA 300
84 eThrLysCysAsnPheSerSerLeuLysLeuAsnValIlyrGluGlu 100
301 AATTCGCTATAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 350
101 LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrrPyrGlu 117
351 TGACTATTTTACACATTCGCAAGTTCAGATGTCCTCCCGAGAGTA 399
117 LAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133

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seq_name: SwissProt_38:INR1_BOVIN

seq_documentation_block:

ID INR1_BOVIN STANDARD: PRT: 560 AA.

AC Q04790:

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).

GN IFNAR1 OR IFNAR.

OS Bos taurus (Bovine).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
OC [1]
RN SEQUENCE FROM N.A.
RP TISSUE=LUNG;
RX Medline: 93076908.
RA Mouchel-Vieilh E., Lutfalla G., Mogenssen K.E., Uze G.;
RT "Specific antiviral activities of the human alpha interferons are
  determined at the level of receptor (IFNAR) structure.";
RL FEBS Lett. 313:255-259(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX Medline: 93305725.
RA Lym J.-R., Langer J.A.;
RT "Cloning and characterization of a bovine alpha interferon receptor.";
CC Blochm. Biophys. Acta 1173:314-319(1993)
CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYR2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
DR EMBL: X68443; CAA48484.1; -
DR EMBL: L06320; AA02571.1; -
DR PIR: S33770; S33770.
DR PIR: S27387; S27387.
DR PIR: PF00041; fn3; 1.
KM Receptor: Transmembrane; Glycoprotein; Signal.
FT FT 1 24 BY SIMILARITY.
FT FT 25 560 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
FT FT CHAIN
FT FT 25 437 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 438 458 POTENTIAL.
FT FT DOMAIN 459 560 CYTOPLASMIC (POTENTIAL).
FT FT DISULFID 76 84 BY SIMILARITY.
FT FT DISULFID 199 220 BY SIMILARITY.
FT FT CARBOHYD 47 47 POTENTIAL.
FT FT CARBOHYD 55 55 POTENTIAL.
FT FT CARBOHYD 85 85 POTENTIAL.
FT FT CARBOHYD 109 109 POTENTIAL.
FT FT CARBOHYD 172 172 POTENTIAL.
FT FT CARBOHYD 254 254 POTENTIAL.
FT FT CARBOHYD 313 313 POTENTIAL.
FT FT CARBOHYD 377 377 POTENTIAL.
FT FT CARBOHYD 434 434 POTENTIAL.
FT FT CONFLICT 422 422 F -> V (IN REF. 2).
SO SEQUENCE 560 AA; 63818 MW; 66D76B72861E1D11 CRC64;

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Alignment_scores:
  Quality: 454.00      Length: 134
  Ratio: 3.914        Gaps: 4
  Percent Similarity: 86.567  Percent Identity: 69.403

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Alignment block:

US-09-240-675-1_COPY_27_427 x INR1_BOVIN ..

Align seg 1/1 to: INR1_BOVIN from: 1 to: 560

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4 ATGTCGTCCTCTGGGCGGCGAGACCTAGTGTGTCGCGCGGCGG 53
1 MetLeuAlaLeuLeuGlyAlaThrThrLeuLeuValAla...GlyAr 16

```

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54 ATGGCTGTTCCGCGAGCCGAGTGGAAAAATCTAAATCTCCCTCAAA 103
16 gtrpvalleuproalaalaserglyalaasnleuys...ProGluA 32
104 AAGTAGAGTCGACATCATAGACACTTATCCAGAGTGGAGACAG 153
32 snvalglullehstleilaspaspasnpheluleuylstrpanser 48
154 AGCGATGAGTCTGTGCGGAGTGTGACTTTTCATTCGATTATCAAAAAC 203
49 SerSerGluSerValLysasnValThrPheSerAlaAspTyrGlnIlele 65
204 TGGGATGATTAATGATTAATGATTTCTGGGTGTGAGAAATTAAGTA 253
65 ucglythraspansrplyslyseuserglycysglnhstlethrsert 82
254 CCAATGCACTTTCTTCTACCTCAAGCTG...AATGTTATGAAGAAT 300
82 hrlscysasnpheserSerValGluLeuGlnasnValPheGluLysile 98
301 AATTCGCTATAAGACAGAAAAA...GAACAACATCTTCATGATGATGA 347
99 GluleuargileargalaglulguglyasnasnThrserThrtrpTyrG1 115
348 GGTGACTCATTTACACCACTTTCGCAAGCTCAGATTGCTCCAGAGAG 397
115 uvalgluprophevalprophleuglualaglnhstleglyprothraspy 132
398 TA 399
132 al 132

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seq_name: Swlssprot_38:INRL_SHEEP

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seq_documentation_block:
ID INRL_SHEEP STANDARD: PRT: 560 AA.
AC 028589; 095206;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
DE (INTERFERON ALPHA/BETA RECEPTOR-1).
GN IFNARI OR IFNAR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OC (1)
RN SEQUENCE FROM N.A.
RP TISSUE-ENDOMETRIUM;
RX MEDLINE: 97135690.
RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
RT "Structure of an ovine interferon receptor and its expression in
endometrium."
RT J. Mol. Endocrinol. 17:207-215(1996).
RN (2)
RN SEQUENCE FROM N.A.
RP TISSUE-ENDOMETRIUM;
RX MEDLINE: 98006426.
RA Han C.-S., Machuga N., Klemann S.W., Roberts R.M.;
RT "Molecular cloning of ovine and bovine type I interferon receptor
RT subunits from uteri, and endometrial expression of messenger
RT ribonucleic acid for ovine receptors during the estrous cycle and
RT pregnancy."
RT Endocrinology 138:4757-4767(1997).
RN (1)
RN FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC (1)
CC SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC (1)
CC TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
CC CONCEPTUS AT DAY 15 OF PREGNANCY.

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CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X95939; CA65183.1; -.
DR EMBL: U65978; AAB84231.1; -.
DR PIRAM: PF00041; fn3; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 560
FT DOMAIN 25 437
FT TRANSMEM 438 458
FT DOMAIN 459 560
FT DISULFD 76 84
FT DISULFD 199 220
FT CARBOHYD 47 47
FT CARBOHYD 55 55
FT CARBOHYD 85 85
FT CARBOHYD 108 108
FT CARBOHYD 109 109
FT CARBOHYD 172 172
FT CARBOHYD 222 222
FT CARBOHYD 285 285
FT CARBOHYD 313 313
FT CARBOHYD 359 359
FT CARBOHYD 377 377
FT CARBOHYD 434 434
FT CONFLICT 352 522
FT CONFLICT 522 522
SQ SEQUENCE 560 AA; 63918 MW; E7198A1905D4805C CRC64;

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alignment_scores: Quality: 439.00 Length: 134
Ratio: 3.851 Gaps: 4
Percent Similarity: 85.075 Percent Identity: 67.910

alignment_block:

US-09-240-675-1_COPY_27_427 x INRL_SHEEP ..

Align seg 1/1 to: INRL_SHEEP from: 1 to: 560

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4 ATGGCTGCTCTCTGCGGCGAGACCGAGTGCCTGCGCGCGGCGCC 53
||||| ||||||| ||||||| ||||||| |||
1 MetLeuSerLeuLeuGlyAlaThrThrLeuMetLeuValAla...GlyAr 16
54 ATGGGTGTTCCGCGAGCCGCGAGTGGAAAAATCTAAATCTCCCTCAAA 103
||||| ||||||| ||||||| ||||||| |||
16 gtrpvalleuproalaalaserglyalaasnleuys...GluA 32
104 AAGTAGAGTCGACATCATAGACACTTATCCAGAGTGGAGACAG 153
||||| ||||||| ||||||| ||||||| |||
32 snvalglullehstleilaspaspasnpheluleuylstrpanser 48
154 AGCGATGAGTCTGTGCGGAGTGTGACTTTTCATTCGATTATCAAAAAC 203
||||| ||||||| ||||||| ||||||| |||
49 SerSerGluSerValLysasnValThrPheSerAlaAspTyrGlnIlele 65
204 TGGGATGATTAATGATTAATGATTTCTGGGTGTGAGAAATTAAGTA 253
||||| ||||||| ||||||| ||||||| |||
65 ucglythraspansrplyslyseuserglycysglnhstlethrsers 82
254 CCAATGCACTTTCTTCTACCTCAAGCTG...AATGTTATGAAGAAT 300
||||| ||||||| ||||||| ||||||| |||
82 ertlyscysasnpheserSerValGluLeuLysasnValPheGluLysile 98

```



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301 AAATGCGGTATAAGCAGAAAA...GAAGAATTCTTCAATGSTATGA 347
:::|||||.....:|||||
99 GIUEUAAGLIEARGLAGIUGLIYLSANANTIRSETHPTTYRGL 115
348 GATTACATTTATTCAGCCATTCGCCAAGCATGATGGTCTGCAGAA 397
||||: ||::::||| |||||||||
115 UVALGIURPHEVAIPROPHLEULYSALAIINLEGYPROPPOASPY 132

398 TA 399
||
132 AL 132

seq_name: SwissProt_38:INRL_MOUSE
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seq_documentation_block:
ID INRL_MOUSE STANDARD; PRT; 590 AA.
AC P33896;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON- $\alpha$ /BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN- $\alpha$ -REC).
GN IFNARI OR IFNAR OR IFAR.
OS MUS MUSCULUS (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
NC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE: 92262522.
RA USE G., Luftalla G., Bandu M.T., Proudron D., Mogensen K.E.;
RT "Behavior of a cloned murine interferon alpha/Beta receptor expressed
in homospesific or heterospecific background."
RL Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).
FC I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
I INFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
SUBUNITS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBROECTIN TYPE II-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
-----
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DR EMBL; M89641; AAA37890.1; -.
DR PIR; A45283; A45283.
DR MGD; MG1:107658; IFNAR.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 590 INTERFERON- $\alpha$ /BETA RECEPTOR ALPHA
CHAIN.
FT DOMAIN 27 429 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 430 449 POTENTIAL.
FT DOMAIN 450 590 CYTOPLASMIC (POTENTIAL).
FT DISULFID 78 86 BY SIMILARITY.
FT DIISULFID 199 220 BY SIMILARITY.
FT CARBOHYD 43 43 POTENTIAL.
FT CARBOHYD 109 109 POTENTIAL.
FT CARBOHYD 181 181 POTENTIAL.
FT CARBOHYD 214 214 POTENTIAL.
FT CARBOHYD 314 314 POTENTIAL.
FT CARBOHYD 370 370 POTENTIAL.
FT CARBOHYD 409 409 POTENTIAL.
FT CARBOHYD 413 413 POTENTIAL.
SO SEQUENCE 590 AA; 65776 MW; 7EC6DEF370185D3A CRC64;
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Quality: 366.50 Length: 133
Ratio: 3.524 Gaps: 1
Percent Similarity: 78.195 Percent Identity: 52.632

alignment_block:
US-09-240-675-1_COPY_27_427 x INR1_MOUSE ..

Align seg 1/1 to: INR1_MOUSE from: 1 to: 590

4 ATGTCGTCCTCTCGGGCGGACGACCCCTAGTGCTGTCGCCGTGGGCC 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MetLeuAlaValAlaGlyAlaAlaAlaLeuValLeuValAlaGlyAla 17
54 ATGGGTGTCTCCCGACCCCGAGGTGGAAAAAATCTAAATCTCCCTAAA 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 CTTPAlaLeuProSerAlaAlaGlyGlyGluAlaLeuLysProGluAla 34
104 AAGTAGAGATCGACATCATAGATACAACTTATCTGAGGTGGAAAGC 153
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 snIleAspValTyrIleIleAspAspSrnTyrIleLysTyrSerSer 50
154 AGCGATGAGTGTGTGGGAAATGACATTTTCATTCATTATCAAAAAAC 203
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 HisGlyGluSerMetGlySerValThrPheSerIleGluTyrGlnThr 67
204 TGGGATGGATTAATGGATAAATGTCTGGGTGCACAAATTAATCTAGTA 253
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 sAspAluAlaLysTyrLeuLysValAlaProGluCysGlnHisThrThr 84
254 CCAATTCGAACTTTTCTCACTCAAGCGATGATGTTATGAAAGAAATAAA 303
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 hTrpLysCysGluPheSerLeuLysAspThrAsnValTyrIleLysThrGln 100
304 TTGCCTATAGACGAGAAAAAGAAAAC...ACTCTTCATGATGATGAGT 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 PheArgValAlaGlyAlaGluGlnGlyAsnSerThrSerSerTrpAsnGluVala 117
351 TGACATCATTTACACCATTTCCCAAGAGCACAATGTGCTCCACAAAGTA 399
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
117 IAspProPheIleProPheTyrThrAlaHisMetSerProProGluVala 133

seq_name: SwissProt_38:CRF4_HUMAN

seq_documentation_block:
ID CRF4_HUMAN STANDARD; PRT; 325 AA.
AC Q08334;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.
DE CRFB4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
CC [1]
CC SEQUENCE FROM N.A.
CC RP TISSUE=FETAL BRAIN;
CC RX MEDLINE; 93300510.
CC RA Lutfalla G., Gardiner K., Uze G.;
CC "A new member of the cytokine receptor gene family maps on chromosome
CC RT 21 at less than 35 kb from IRNAR.";
CC RL Genomics 16:366-373(1993).
CC [2]
CC SEQUENCE FROM N.A.
CC RP MEDLINE; 96054036.
CC RA Lutfalla G., McInnis M.G., Antonarakis S.E., Uze G.;
CC "Structure of the human CRFB4 gene: comparison with its IFNAR
CC RT neighbor.";
CC J. Mol. Evol. 41:338-344(1995).
CC -1- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS

```


RA Meyer K., Cusumano J.C., Somerville C.R., Chapelle C.C.S.:
 RT "Ferulate-5-hydroxylase from Arabidopsis thaliana defines a new
 family of cytochrome P450-dependent monooxygenases.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:6869-6874(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RA Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
 RA Hohnselt J., Jesse T., Heijnen L., Vos P., Mewes H.-W., Mayer K.,
 RA Schaefer C.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- PATHWAY: GENERAL PHENYLPROPANOID PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U38416; AAC9389.1; ..
 DR EMBL: AL022141; CA18128.1; ..
 DR PRINTS: PR00385; P450.
 DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 DR PFAM: PF00067; P450; 1.
 KM Oxidoreductase; Monooxygenase; Membrane; Heme.
 FT BINDING 458 458 HEME (By SIMILARITY).
 SO SEQUENCE 520 AA; 58720 MW; E81279AF5BF01BC CRC64;

alignment_scores:

Quality: 83.00 Length: 156
 Ratio: 1.137 Gaps: 6
 Percent Similarity: 46.795 Percent Identity: 21.154

alignment_block:

US-09-240-675-1_COPY_27_427 x CP84_ARATH ..

Align seg 1/1 to: CP84_ARATH from: 1 to: 520

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1 ATGATGTCGTCCTCTCGGCGGCGAGCCCTAGTCTGTCGGCGGCGG 50
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
313 IlemetaspValmetPheglyGlyThrGluThrValAlaSerAlaIle.. 328
51 CCCATGGGTGTTGTCGCCGCGGAGGTGGAATAAATCTAAATCTCTC 100
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
329 GluThrPalaLeuThr.....GluLeuLeuArgSerProG 340
101 AAAAAGTAGAGGTGCATCATAGTGAACAATTATCTGAGTGAAC 150
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
340 LuAsPLeuLys..... 343
151 AGGAGCGATGAGTCTGTCGGGAGTGAATTTCATTCGATTATCAAAA 200
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
344 ArgValGlnGlnGlnLeuAlaGluVal..... 352
201 AACTGGGATGATTAATGATTAATTTGTCGGGTGTCAGAAATATACTA 250
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
353 ValGlyLeuAspArgArgValGlnGlnSerPrlLeuSerLeuThr 369
251 GACCAAGTGCACACTTCTTCACATCAAGTCGATGTTATGACAAAT 300
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
369 yLeuLysCysThrLeuLysGlu...ThrLeuArgMetHisProPrlle 384
301 AAATGCGTATGAGAGCAGAAAAAGAAAACACTTCT..... 336
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
389 ProLeuLeuLeuHisGluThrAlaGlnAspThrSerIleAspGlyPhePh 401
336 ..... 336
401 eileProLysLysSerArgValMetIleAsnAlaPheAlaIleGlyArgA 418

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337 .....TCATGATGAGTGTGACTCATTTACACCATTTGCAAAAGCT 378
  ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
418 sPProthreSerThrPthAspProAspPthPheArgProSerArgPheLeu 434
379 CAGATTGCTCTCCAGAA 396
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
435 GluProGlyValPProasp 440
seq_name: SwissProt_38:IL6B-RAT
seq_documentation_block:
ID IL6B-RAT STANDARD; PRT; 918 AA.
AC P40190;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
GN IL6ST.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheraia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE: 93052397.
RA Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;
RT "Molecular cloning and characterization of the rat liver IL-6 signal
transducing molecule, gp130.";
RL Genomics 14:666-672(1992).
CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES.
AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
EMBRYONIC DEVELOPMENT (By SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
AND ENDOTHELIAL CELLS.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M92340; -; NOT_ANNOTATED_CDS.
DR PIR: A44257; A44257.
DR HSSP: P40189; LBQU.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
DR PFAM: PF00041; fn3; 3.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
Repeat.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT DOMAIN 23 618 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 619 640 POTENTIAL.
FT DOMAIN 641 918 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 120 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 124 221 FIBRONECTIN TYPE-III.
FT DOMAIN 222 323 FIBRONECTIN TYPE-III.
FT DOMAIN 324 422 FIBRONECTIN TYPE-III.
FT DOMAIN 423 516 FIBRONECTIN TYPE-III.
FT DOMAIN 517 612 FIBRONECTIN TYPE-III.
FT DOMAIN 724 754 SER-RICH.
FT DISULFID 134 144 BY SIMILARITY.

```

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CC 013651:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
GN IL10RA OR IL10R.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOMA.
RX MEDLINE: 94165477.
RA Liu Y., Wei S.H.-Y., Ho A.S.-Y., de Waal Malefyt R., Moore K.W.;
RT Expression cloning and characterization of a human IL-10 receptor.";
J. Immunol. 152:1821-1829(1994).
RL
CC -1- FUNCTION: RECEPTOR FOR IL-10. BINDS IL-10 WITH A HIGH AFFINITY.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: SPLEEN, THYMUS, AND PMNC. FAINT EXPRESSION
CC IN PANCREAS, SKELETAL MUSCLE, BRAIN, HEART, AND KIDNEY. PLACENTA,
CC LUNG, AND LIVER SHOWED INTERMEDIATE LEVELS. MONOCYTES, B CELLS,
CC LARGE GRANULAR LYMPHOCYTES, AND T CELLS EXPRESS HIGH LEVELS OF IL-
CC 10R.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on ways
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U00672; AAA17896.1; -.
DR MIM: 146933; -.
KM Receptor: Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 578 INTERLEUKIN-10 RECEPTOR.
FT DOMAIN 22 235 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 236 256 POTENTIAL.
FT DOMAIN 257 578 CYTOPLASMIC (POTENTIAL).
FT DISULFID 202 223 POTENTIAL.
FT CARBOHYD 50 50 POTENTIAL.
FT CARBOHYD 74 74 POTENTIAL.
FT CARBOHYD 110 110 POTENTIAL.
FT CARBOHYD 154 154 POTENTIAL.
FT CARBOHYD 177 177 POTENTIAL.
FT CARBOHYD 189 189 POTENTIAL.
SQ SEQUENCE 578 AA; 62903 MW; E81B29064338157C CRC64;

Alignment_scores:
Quality: 78.00 Length: 129
Ratio: 1.026 Gaps: 6
Percent Similarity: 58.915 Percent Identity: 24.031

Alignment_block:
US-09-240-675-1_COPY_27_427 x IL10R_HUMAN ..

Align seg 1/1 to: IL10R_HUMAN from: 1 to: 578

4 ATGTCGTCCTCTGGGCGGAGCAGACCTAGTCTGTCGCGCGGAGGCC 53
:::|||||:::|||||:::|||||
5 LeuValValLeuLeuAlaAla.....LeuLeuSerLeuArgLeuGly.. 18
54 ATGGGTGTTCGCCGACGCCGAGGTGGAAGAAATTAATAATCTCTCAAA 103
:::|||||:::|||||
19 .....SerAspAlaHisGlyThrClnLeuProSerProPro 31
104 AAGTAGAGGTGAGCATCATAGATGACACTTATCTGAGGAGGGAACAGG 153
:::|||||:::|||||
31 erValTrpPheGlnAlaGlnPhePheHisHisLeuValHisTrpHisPro 47

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154 ACCGATGACTCTGCGAATGACTTTTCATTCGATTATCAAAAAC 203
      :::::  :::::  :::::  :::::
48 IIEPRAENGINSERGLUSERHRCYRGLVALALALEULEAIGTY 64
      :::::  :::::  :::::  :::::
204 TGGATGCGATTAATGATAAATTTCTGGGCTGCAGATAATTACTAGT 253
      |||  |||  |||  |||  |||  |||
64 rGlyleGuserTIPASerSILeSerASnCySerGInThrLeuSer 80
      |||  |||  |||  |||  |||  |||
254 CCAATGCACTTTCTCAGTCAGCAATGCTTATGAGAA..... 297
      :::::  :::::  :::::  :::::  :::::  :::::
81 .... TyrAspLeuThrAlaValAlaThrLeuAspLeuThrHisSerSngly 95
      :::::  :::::  :::::  :::::  :::::  :::::
298 ATTAATTCGCTATAAGACA...GAAAAAGAAAACACTTCTTCATGC 342
      :::::  |||  |||  |||  |||  |||
96 TyrArgAlaArgValArgAlaValAspGlySerArgHisSerAsnTrpH 112
      :::::  |||  |||  |||  |||  |||
343 .....TATGAGCTTGACTACTTTACA 363
      :::::  |||  |||  |||  |||  |||
112 rValThrAsnThrArgPheSerValAspGlyValAlaThr 124

seq_name: SwissProt_38:6DCS_SOYBN
seq_documentation_block:
ID 6DCS_SOYBN STANDARD: PRT: 315 AA.
AC P26690:
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE NAD(P)H DEPENDENT 6'-DEOXYCHALCONE SYNTHASE (EC 1.-.-.-).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
  core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
  Glycine.
OC [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP STRAIN-CV. HAROSOV 63;
RA MEDLINE: 91177016.
RX Welle R., Schroeder G., Schlitz E., Grisebach H., Schroeder J.;
  "Induced plant responses to pathogen attack. Analysis and
  heterologous expression of the key enzyme in the biosynthesis of
  phytoalexins in soybean (Glycine max L. Merr. cv. Harosoy 63).";
  Eur. J. Biochem. 196:423-430(1991).
RL CC -1- FUNCTION: CO-ACTS WITH CHALCONE SYNTHASE IN FORMATION OF
  4,2',4'-TRIHYDROXYCHALCONE, INVOLVED IN THE BIOSYNTHESIS OF
  GLYCETOLIN TYPE PHYTOALEXINS.
CC CC -1- PATHWAY: THIS IS THE KEY ENZYME IN THE BIOSYNTHESIS OF
  PHYTOALEXINS IN SOYBEAN.
CC CC -1- SUBUNIT: MONOMER.
CC CC -1- INDUCTION: BY PATHOGEN ATTACK.
CC CC -1- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE FAMILY.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC CC EMBL: X55730; CAA39261.1;
DR DR PIR: S14222; S14222.
DR HSSP: P14550; 2ALR.
DR PRINTS: PRO0069; ALDKETREDTASE.
DR PROSITE: PS00062; ALDO-KETO REDUCTASE 2; 1.
DR PROSITE: PS00063; ALDO-KETO REDUCTASE 3; 1.
DR PROSITE: PS00798; ALDO-KETO REDUCTASE_1; 1.
DR PFAM: PF00248; aldo_ket_red; 1.
DR Flavonoid biosynthesis; Oxidoreductase; NADP.
KW SEQUENCE 315 AA; 35490 MW; C3A6BE07EF330F47 CRC64;

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      Quality: 76.50 Length: 132
      Ratio: 1.048 Gaps: 8
      Percent Similarity: 55.303 Percent Identity: 23.485
alignment_block:
05-09-240-675-1_COPY_27_427 x 6DCS_SOYBN ..
Align seg 1/1 to: 6DCS_SOYBN from: 1 to: 315
82 AAAATCTAAATCTCTCAAAAAGTAGAGTGACATCATAGATGACA 131
      |||  |||  |||  |||  |||  |||
105 LysSerLeuYsTrnLeuGlnLeuGluTyrLeuAspLeu..... 117
      :::::  :::::  :::::  :::::  :::::  :::::
132 CTTATTCCTGAGTGGAACAGACCGATGATGCTGTCGGAATGACTT 181
      :::::  |||  |||  |||  |||  |||
118 TyrLeuIleHisTrpProLeuSerSerGlnPro..GlyLysPheSer 133
      :::::  |||  |||  |||  |||  |||
182 TTTCATTCGAT.....TATCAAAAAGCTGGATGAT 213
      ||  ||  ||  ||  ||  ||
133 heProIleGluValGluAspLeuProPheAspValLysGlyVal... 148
      :::::  :::::  :::::  :::::  :::::  :::::
214 AATGATTAATATGCTGGTGTGCAATATTACTGATCAAAATGC 261
      |||  |||  |||  |||  |||  |||
149 ...TrpGluSerMetGluGluCysGlnLysLeuGlyLeuThrySAlaIl 164
      :::::  :::::  :::::  :::::  :::::  :::::
262 .....ACCTTTCTTCACCTCAAGCTGAAT..... 285
      |||  |||  |||  |||  |||  |||
164 eGlyValSerAsnPheSerValLysLysLeuGlnAsnLeuSerValA 181
      :::::  |||  |||  |||  |||  |||
286 .....GTTATGACAAATTAATTCGCTATTAAGACGCGAA 321
      |||  |||  |||  |||  |||  |||
181 IatHrIleArgProValAlaAspGlnValAlaGluMetAsnLeuAlaTrpGln 197
      :::::  :::::  :::::  :::::  :::::  :::::
322 AAAGAAAGCACTTCTCATGATGATGAG.....GTTGACTC 356
      :::::  :::::  :::::  :::::  :::::  :::::
198 GlnLysLysLeuArgGluPheCysLysGluAsnGlyIleLeuValTrAl 214
      :::::  |||  |||  |||  |||  |||
357 ATTACACCATTTGCGAAA...GCTCAGATTGGTCTCTCAGCAAGTA 399
      |||  |||  |||  |||  |||  |||
214 aPheSerProLeuArgLysGlyAlaSerArgGlyProAsnGluVal 229

seq_name: SwissProt_38:IL10R_MOUSE
seq_documentation_block:
ID IL10R_MOUSE STANDARD: PRT: 575 AA.
AC O61727:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
GN IL10RA OR IL10R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
  Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6 X AJ F1; TISSUE=HEMATOPOIETIC;
RX MEDLINE: 94068585.
RA Ho A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;
  "A receptor for Interleukin 10 is related to interferon receptors.";
  Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).
RL CC -1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
CC CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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  or send an email to license@isb-sib.ch).
CC CC

```

alignment_scores:

EMBL: L12120; AAA16156.1; -
 DR MGD; MGI:96538; IL10RA.
 KM Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 16 POTENTIAL.
 FT CHAIN 17 575 INTERLEUKIN-10 RECEPTOR.
 FT DOMAIN 17 241 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 242 262 POTENTIAL.
 FT DOMAIN 263 575 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 204 225 POTENTIAL.
 FT CARBOHYD 50 66 POTENTIAL.
 FT CARBOHYD 113 66 POTENTIAL.
 FT CARBOHYD 182 182 POTENTIAL.
 FT CARBOHYD 238 238 POTENTIAL.
 SQ SEQUENCE 575 AA; 64248 MW; 820B9CD576F686B7 CRC64;

alignment_scores:
 Quality: 76.50 Length: 118
 Ratio: 1.062 Gaps: 5
 Percent Similarity: 61.017 Percent Identity: 23.729

alignment_block:

US-09-240-675-1_COPY_27_427 x IL10R_MOUSE ..

Align seg 1/1 to: IL10R_MOUSE from: 1 to: 575

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37 CTCGCGCCGCGGCATGCTGTGGCGACGCCAGCGGAAAAA 86
   |||||.....|.....|.....|.....|.....|
9  LeuValAlThrIleSerSerLeuSerLeuGluPheIleAlaIlyrIlythrgI 25
87 TCATAAATCTCTCAAAAGTAGAGTCGACATCATAGATGACAACTT 136
   |||||.....|.....|.....|.....|.....|
25  uleuProSerProSerTyrValItrPheGluAlaIargPheGlnHisI 42
137 TCCTGAGAGTGG.....AACAGAGCGATGAGTGTGCGGAAAT 174
   |||||.....|.....|.....|.....|.....|
42  leuHnIstrPluysProIleProHnIleSerIlySerThrIlyTyrGlu 58
175 GTACATTTTCATTCGATGATCAAAAAACGGGATGATTAATGATTA 224
   |||||.....|.....|.....|.....|.....|
59  ValAlaIleu.....LysGlnTyrGlyAsnSerThrItrPnasas 71
225 ATTGTGTGGGTCTCAGAAATATTAATACCAAACTTTCTTCTCAC 274
   |||||.....|.....|.....|.....|.....|
71  pIleHnIleCysArgIysIaGlnAlaIleuSerCysAspLeuThrP 88
275 TCAAGCTGAATGTTATGAAGAA.....ATTAAATGCGTATNAGA 315
   ::|||.....|.....|.....|.....|.....|
88  heThrIleuAspLeuTyrHisArgSerTyrGlyTyrArgAlaArgValArg 104
316 GCA.....GAAAGAAAAAACTTCTTCATGATAGAGGTATACCA...TT 359
105  AlValAlaPnasSerGlnTyrSerAsnItrPthThrThrgIuThrArgp 121
360 TACA 363
   ||||
121  ethr 122

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seq_name: SwissProt_38: IL6B_HUMAN

seq_documentation_block:

IL6B_HUMAN STANDARD; PRT; 918 AA.

AC P40189;
 DT 01-FEB-1995 (rel. 31, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
 DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130) (ONCOSTATIN M
 DE RECEPTOR) (CD130) (CD130 ANTIGEN).
 GN IL6ST.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

```

OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MYELOMA, AND PLACENTA;
RX MEDLINE; 91084844.
RA Hidi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;
RT "Molecular cloning and expression of an il-6 signal transducer,
   gp130.";
RL Cell 63:1149-1157(1990).
RP [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
RX MEDLINE; 98169383.
RA Bravo J., Staunton D., Heath J.K., Jones E.Y.;
RT "Crystal structure of a cytokine-binding region of gp130.";
RL EMBO J. 17:1665-1674(1998).
CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
   IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
   SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
   RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
   AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
   EMBRYONIC DEVELOPMENT (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES
   EXAMINED. EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS.
CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- DATABASE: NMR-PRO; NOTE-CD guide CD130 entry;
   WWW="http://www.ncmi.nlm.nih.gov/prow/cd/cd130.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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   or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M57230; AAA59155.1; -.
DR PIR: A36337; A36337.
DR PDB: 1BQJ; 26-AUG-98.
DR MIM: 600694; -.
DR PRINTS: PR00014; FNTYPEIII.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
DR PFAM: PF00041; fn3; 3.
KM Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
   Repeat; 3D-structure.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT DOMAIN 23 619 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 620 641 POTENTIAL.
FT DOMAIN 642 918 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 120 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 124 222 FIBRONECTIN TYPE-III.
FT DOMAIN 223 324 FIBRONECTIN TYPE-III.
FT DOMAIN 325 423 FIBRONECTIN TYPE-III.
FT DOMAIN 424 517 FIBRONECTIN TYPE-III.
FT DOMAIN 518 613 FIBRONECTIN TYPE-III.
FT DOMAIN 725 755 SER-RICH.
FT DISULFID 134 144
FT DISULFID 172 182
FT CARBOHYD 43 43 POTENTIAL.
FT CARBOHYD 83 83 POTENTIAL.
FT CARBOHYD 131 131 POTENTIAL.
FT CARBOHYD 157 157 POTENTIAL.
FT CARBOHYD 227 227 POTENTIAL.
FT CARBOHYD 379 379 POTENTIAL.
FT CARBOHYD 383 383 POTENTIAL.
FT CARBOHYD 390 390 POTENTIAL.
FT CARBOHYD 553 553 POTENTIAL.
FT CARBOHYD 564 564 POTENTIAL.
SQ SEQUENCE 918 AA; 105522 MW; DB13F3672DD10D53 CRC64;
```


alignment_scores: Length: 152
 Quality: 76.50
 Ratio: 1.077
 Percent Similarity: 46.711
 Percent Identity: 21.711

alignment_block:
 US-09-240-675-1_COPY_27_427 x IL6B_HUMAN ..

Align seg 1/1 to: IL6B_HUMAN from: 1 to: 918

```

25  ACGACCGCTAGGCTGCTGCGCGCGCCATGGGTGTTCGCCGACGCC 74
    ::::::::::::::::::::|::|::|::|::|::|::|::|::|::|
187 SerthValIytrPheValaInIleGluValIytrValaGluInaInI 203
    75  ACGTGAAGA.....AATCTAAATCTCCCTCAAAAG 106
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
203 aleuGlyLysValIthrSerAspHisIleAsnPhesApsProValIytrLysV 220
    107 TAGAG.....CTGCACATCATAGATGACAACTTATC 138
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
220 allysProAsnProProHisAsnLeuSerValIleAsnSerGluGluLeu 236
    139 .....CTGAGGTG...AACAGACGATGAGTCTGTGG 170
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
237 SerSerIleLeuLysLeuThrItrPhrAsnProSerIleLysSerValI 253
    171 GAATGTGACTTTTCATTCATTCATTCATCAAAAGCTGGATGATATGGA 220
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
253 eileLeuLysTyraInIleGlnTyArgThrLysAspIleSerThrItrps 270
    221 TAAATGTCTGGGTGCAGATATCTACTACTACCAATGCAACTTTCT 270
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
270 ergInIleProPro...GluAspThrIleSerThrArgSerSerPheThr 285
    271 TCACCTCAAGCTGAATGTTATGAAGAATTAATTCCTATACAGACAGA 320
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
286 ValGlnAspLeuLysProPheThrGluTytrValPheArgIleAspGlySme 302
    321 AAAAGAAAAC..... 330
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
302 tlyGlnAspGlyLysGlyTytrPTrSerAspTrpSerGluGluIleAspG 319
    331 .....ACTTCTCATGCTATGAG 348
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
319 lylIleThrTyGluAspArgProSerLysAlaProSerPheThrIytrLys 335
    349 GTTGAC 354
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
336 IleAsp 337
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

seq_name: SwissProt_38:IL2R_HUMAN

seq_documentation_block:
 ID 112R_HUMAN STANDARD: PRT; 662 AA.
 AC PA2701:
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERLEUKIN-12 RECEPTOR BETA-1 CHAIN PRECURSOR (IL-12R).
 GN IL12RB1 OR IL12RB OR IL12R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94267217.
 RA Chua A.O., Chizzonite R., Desai B.B., Trullit T.P., Nunes P.,
 RA Minetti L.J., Warriner R.R., Presky D.H., Levine J.F., Gately M.K.,
 RA Gubler U.;
 RT *Expression cloning of a human IL-12 receptor component. A new member
 of the cytokine receptor superfamily with strong homology to gp130.*;

```

RL J. Immunol. 153:128-136(1994).
CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION.
CC -1- SUBUNIT: MAY FORM DIMERS OR OLIGOMERS. REQUIRES AN UNIDENTIFIED
CC SUBUNIT TO GENERATE A HIGH AFFINITY IL-12R COMPLEX.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: ALTERNATIVE SPLICING MAY GIVE RISE TO A
CC SECOND PROTEIN 2 AMINO ACIDS SHORTER.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: U03187; AAA21340.1; -.
CC DR MIM: 601604; -.
CC DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
CC DR PFM: PFM0041; fn3; 1.
CC KM Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;
CC Repeat.
CC FT SIGNAL 1 23 POTENTIAL.
CC FT CHAIN 24 662 INTERLEUKIN-12 RECEPTOR BETA-1 CHAIN.
CC FT DOMAIN 24 545 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 546 570 POTENTIAL.
CC FT DOMAIN 571 662 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 43 133 FIBRONECTIN TYPE-III.
CC FT DOMAIN 143 236 FIBRONECTIN TYPE-III.
CC FT DOMAIN 237 337 FIBRONECTIN TYPE-III.
CC FT DOMAIN 338 444 FIBRONECTIN TYPE-III.
CC FT DOMAIN 445 540 FIBRONECTIN TYPE-III.
CC FT DISULFD 52 62 BY SIMILARITY.
CC FT CARBOHYD 121 121 POTENTIAL.
CC FT CARBOHYD 329 329 POTENTIAL.
CC FT CARBOHYD 346 346 POTENTIAL.
CC FT CARBOHYD 352 352 POTENTIAL.
CC FT CARBOHYD 442 442 POTENTIAL.
CC FT CARBOHYD 456 456 POTENTIAL.
CC FT VARSPIC 659 662 KAKM -> DE (IN A SHORTER FORM).
CC SQ SEQUENCE 662 AA; 73108 MW; 541ADA60F62DA1EF CRC64;

```

alignment_scores: Length: 140
 Quality: 75.50
 Ratio: 1.020
 Percent Similarity: 52.857
 Percent Identity: 27.143

alignment_block:
 US-09-240-675-1_COPY_27_427 x IL2R_HUMAN ..

Align seg 1/1 to: IL2R_HUMAN from: 1 to: 662

```

34  GTGCTCGCGCGCGCGCCATGGGTGTTCGCCGACGCCAGTGGA 83
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
107 ValLeuTytrThrValIthrLeuTrpValGluSerTrpIleArg...AsnG 122
    84  AATCTAAATCTCCCTCA..... 102
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
122 nThrGluLysSerProGluValIthrLeuGlnLeuTyraSerValIytr 139
    103 .....AAGTAGAGTCGACATCATGATGACAACTT 135
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
139 yrgLupProProLeuGlyAspIleLysValSerLysLeuAlaGlyGlnLeu 155
    136 ATCTGTGAGTGGAACAGACGATGAGTCTGTGGG...AATGTACTT 182
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
156 ArgMetGluTrpGluTrpProAspAsnGlnValGlyIleAlaGlnIle 172
    183 TTCATTGCATTTATCAAAAAGCTGGATGATATGATATAAATCTG 232
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

```

172 earg.....HisArgThrProSerSerProTIP..LysLeuGIYA 185
233 GGTGT.....CAGAAATATTACTAGTACCAAAATGCAACTTTCTCTCACTC 276
    |||      |||:::      ::      |||      |||
185 spCysGIYProGInAspAspPThrGluSerCys..LeuCysProLeu 200
277 AACCTGAATGTTATGAGAAATTAATTGCGTATAGAGCAGAAAAAGA 326
    :::::|||||      ::|||:::|||||      |||
201 GluMetAsnValAlaGInGInLupheGInLeuValArgArgGInLeuGIYse 217
327 AACCACTTCTTCATGGTATGAGGTGACCTCATTTACACCATTCGCCAAAG 376
    :::::|||||      ::      |||      |||
217 rGInGIYSerSerTIPSerTIPSerSer.....ProValCysValP 232
377 CTCAGATTGGTCCCTCCAGAA 396
    ::|||      |||:::
232 roProGInAsnProProGIn 238

```


seq_documentation_block:
 ID 061190 PRELIMINARY; PRT: 349 AA.
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE CYTOKINE RECEPTOR FAMILY 2, MEMBER 4 (CLASS II CYTOKINE RECEPTOR 4).
 GN IL10RB OR CRFB4 OR CRF2-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 NC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP MEDLINE: 97199375.
 RA GIBBS V.C., PENNICA D.;
 RT "CRF2-4: Isolation of cDNA clones encoding the human and mouse
 proteins.";
 RL Gene 186:97-101(1997).
 DR EMBL: U53696; AAC53062.1;
 DR MGD: MGI:109380; I110rb.
 DR PIRAM: PF00041; fn3; 1.
 SO SEQUENCE 349 AA; 39774 MW; AAC1802A CRC32;

Alignment_scores:
 Quality: 127.00 Length: 121
 Ratio: 1.693 Gaps: 6
 Percent Similarity: 61.983 Percent Identity: 30.579

alignment_block:
 US-09-240-675-1_COPY_27_427 x 061190 ..

Align seg 1/1 to: 061190 from: 1 to: 349

```

46 GTGGGCCCATGGGTGTTCGCCGACGCCGACGAGAAAAATCTAAATC 95
   ::::: |||
9  LeuGlyAlaAlaIleSerProAspSerPheSerGlnLeuAlaIlePr 23
   ::::: |||
96 TCCTCAAAAGTAGAGTCGACATCATAGATGCACTTATCCCGAGGT 145
   |||::: |||
23 oProGluIysValArgMetAsnSerValAsnPheIysAsnIleLeuGln 40
   |||::: |||
146 GGAACAGCAGCAGATGAGTCTGTGCGAATGAGCTTTTCATCGATT 195
   ||::: |||
40 rProIuValProAlaPheProIysThrAsnLeuThrPheThrAlaGlnTy 56
   ::::: |||
196 CAA.....AAACTGGAGTGAATAATGGATMAAATTGTCTGGGTGCA 239
   ::::: |||
57 GluSerTyArgSerPheGlnAspHis.....CysIly 67
   ::::: |||
240 GAATATTACTACTACCAATGCAATTTCTTCTACTCAAGCTGAATGTT 289
   ::::: |||
67 sArgThrAlaSerThrGlnCysAspPheSer.....HisLeuSerIys 82
   ::::: |||
290 ATGAGAGAAATTAATTCGCTATAGACAGAA...AAGAGAAACACTTCT 336
   ||::: |||
82 yArgIysPryThrValArgValArgAlaGluLeuAlaAspGluHisSer 98
   ::::: |||
337 TCATGCTAGAGGTGAGCTATTACACATTTGCGAAAGCTCAGATTGG 386
   ::::: |||
99 GluTrpValAlaAsnVal...ThrPheCysProValGluAspThrIleIle 114
   ::::: |||
387 TCCTCCAGAGTA 399
   |||::: |||
114 yProProGluMet 118
   ::::: |||
seq_name: sp_rdent:063953
```

seq_documentation_block:
 ID 063953 PRELIMINARY; PRT: 332 AA.
 AC 063953;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA RECEPTOR BETA SUBUNIT).
 GN IFNGR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 NC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP MEDLINE: 94170381.
 RA HEMMI S., BOHNI R., STARK G., DI MARCO F., AGUET M.;
 RT "A novel member of the interferon receptor family complements
 RT the functionality of the murine interferon gamma receptor in human
 RT cells.";
 RL Cell 76:803-810(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129SV/J;
 RX MEDLINE: 97128072.
 RA EBENSBERGER C., RHEE S., MUTHUKUMARAN G., LEMBO D., DONNELLY R.,
 RA PESTKA S., DEMBIC Z.;
 RT "Genomic organization and promoter analysis of the gene Ifngr2
 RT encoding the second chain of the mouse interferon-gamma receptor.";
 RL Scand. J. Immunol. 44:599-606(1996).
 DR EMBL: U69599; AAC52938.1;
 DR EMBL: U69594; AAC52938.1; JOINED.
 DR EMBL: U69595; AAC52938.1; JOINED.
 DR EMBL: U69596; AAC52938.1; JOINED.
 DR EMBL: U69597; AAC52938.1; JOINED.
 DR EMBL: U69598; AAC52938.1; JOINED.
 DR EMBL: S69336; AAB30165.1;
 DR MGD: MGI:107654; Ifngr2.
 DR PIRAM: PF00041; fn3; 1.
 SO SEQUENCE 332 AA; 37471 MW; 0BF24E9E CRC32;

Alignment_scores:
 Quality: 120.00 Length: 130
 Ratio: 1.500 Gaps: 8
 Percent Similarity: 61.538 Percent Identity: 30.769

alignment_block:
 US-09-240-675-1_COPY_27_427 x 063953 ..

Align seg 1/1 to: 063953 from: 1 to: 332

```

61 TTGTCGCGAGCGGAGGTGA.....AAATCTAAATCTCC 98
   |||::: |||
16 LeuGlyAlaAlaIleSerProAspSerPheSerGlnLeuAlaIlePr 32
   ::::: |||
99 TCMAAAGTAGAGTCGACATCATAGATGACAACTTATCTCGAGTGA 148
   ||::: |||
32 oLeuAsnProArgLeuHisLeuTyAsnAspGlnIleLeuThrTrp 49
   ::::: |||
149 ACAGAGCGATGACT.....GTGGGAATGTGACT 180
   ::::: |||
49 lUpProSerProSerSerAsnAspProArgProValIleTyGluValGlu 65
   ||::: |||
181 TTTTCATCGATTATCAAAAACTGGATGAT...AATGATATAAATT 227
   ::::: |||
66 TySerPhe.....IleAspGlySerThrPheAspGly 76
   ::::: |||
228 G.....TCTGGTGTGCAATATTACTAGTACCAATGCAACTTTCTT 271
   ||::: |||
76 uLeuGluProAsnGlySerThrAspIleThrGluThrIleCysAspLeuThr 93
   ::::: |||
272 CA.....CTCAAGCTGAATGTTATGAA...GAATTAATATGGCT 309
   ::::: |||
93 lGlyGlyArgLeuIysLeuPheProHisProPheThrValAlaPheLeuArg 109
   ::::: |||
310 ATTAAGAGCAAAAGAAAGAAC...ACTCTTCAGCTGATGAGGTGATC 356
   ::::: |||
110 ValArgAlaIysArgGlyAsnLeuThrSerIlyStrIleGlyLeuGluPr 126
   ::::: |||
```



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99  tptvalaargvalysalaaargvalgylglnlysglu.....seralaty 113
342  GTATGAGGTGGACATCTATTACACCATTTCCGCAAAAGCTCAGATTGGTCTC 390
      :  ::  :::::||||:  |||  :::::|||||||
113  talalysserglnuphealaValcysaargaspolylysileglyprop 150
      :  ::  :::::||||:  |||  :::::|||||||
392  CAGAAAGTA 399
      ||:::||||:
130  rOlyslou 132

seq_name: sp_invertebrate:023020

```

```
seq_documentation_block:
ID      Q23020      PRELIMINARY;      PRT;      6048 AA.
```

DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE TWITCHIN.
GN UNC-22 OR ZK617.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
CC Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2.
RX MEDLINE: 90044042.
RA BENJAN G.M., KIFF J.E., NECKELMANN N., MOERMAN D.G., WATERSON R.H.,
RT "Sequence of an unusually large protein implicated in regulation of
RL myosin activity in C. elegans.",
RN Nature 342:45-50(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2.
RX MEDLINE: 93387664.
RA BENJAN G.M., L'HERNAULT S.W., MORRIS M.E.,
RT "Additional sequence complexity in the muscle gene, unc-22, and its
RL encoded protein twitchin, of Caenorhabditis elegans.",
RN Genetics 134:1097-1104(1993).

RP SEQUENCE FROM N.A.
RA HARRIS B.;
RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases
DR EMBL; J154423; CAA833463.1; -
DR EMBL; J738899; CAA88081.1; ALT=INT.
DR EMBL; J738897; CAA88081.1; JOINED.
DR HSSP; 063450; 1A06
DR PFAM; PF00041; In3; 31.
DR PFAM; PF00047; 1g; 13.
DR PFAM; PF00069; PKinase; 1.
DR PRINTS; PR00014; FNTYPEIII.
KM Myosin; kinase.
SQ SEQUENCE 6048 AA; 668449 MW; 1977C602 CRC32;

```

alignment_scores:
  Quality: 84.00      Length: 117
  Ratio: 1.151      Gaps: 8
Percent Similarity: 62.393      Percent Identity: 26.496

```

alignment_block:
US-09-240-675-1_COPY_27_427 x Q230200

Align seg 1/1 to: Q23020 from: 1 to: 6048

```

88 CTTAAATCTCCGCAAAA.....GTAGAGGTC...GAACATAT 122
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
1073 LeuAspArgProSerTyrProAsnGlyProLeuGluValSerAspValPh 1089
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
123 AGATGCAACATTATCTCTAGAGTGCACAGACGCATGATCTGTCCGGA 172
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
1089 eGluAspAsnLeuAsnLeuSerTyrProAspAspArgGlyGly 1106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

173  AAGTCACTTTTCATTCGATTTCAAAA.....ACGGGATGATAT 216
      ::      ::      ::      ::      ::      ::
1106  IuProIIeGIuTyrrYrGIuValGIuLysLeuAspThAlaIthGIaYr 1122Z
      ::      ::      ::      ::      ::      ::
217  TGGATMAATTTCTCGGGTCAGAAATTTACTAGTACCAATGCAACT 266
      ||||:      |||      ::      ::      ::      ::
1123  TrpValPro.....CysAlaLysValLysAspThrLysAlaHisI 1136Z
      ::      ::      ::      ::      ::      ::
267  TTCTTCACTCAAGCTGAAATGTTATGAGAAATTAATTAATGGGTATMAG 316
      ::      ::      ::      ::      ::      ::
1136  eaSpGIuLeuLysLysGI.....GIuThTyGIuInPheArYValLysA 1151Z
      ::      ::      ::      ::      ::      ::
317  CA...GAAAGAGAAACACTTCTTCATGATGATAGCTGACTCATTTCA 363
      ||||:      ||||:      ||||:      ||||:      ||||:
1151  IeValAsnLysGIuGIuLysAlaSerPaLaLeuSerThAspLysAspThr 1167Z
      ::      ::      ::      ::      ::      ::
364  .....CCATT...CGCAAGCTCAGATTGGCTCCGCAAGT 398
      ||||:      ::      ::      ::      ::      ::
1168  LysAlaLysAsnProTyAspGIuProGIuLysTrnGIuThrProAspVa 1184Z
      ::      ::      ::      ::      ::      ::
399  A 399
      |
1184  I 1184

```

seq_name: sp_invertebrate:Q23550

seq_documentation_block:			
ID	Q23550	PRELIMINARY;	PRT; 6831 AA.
AC	Q23550;		
DT	01-NOV-1996 (TrEMBLrel. 01, Created)		
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)		
DT	01-NOV-1999 (TrEMBLrel. 12, Last annotation update)		
DE	UNC-22 PROTEIN.		
GN	UNC-22.		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae; Rhabditina; Rhabditioidea; Rhabditidae; Peloderiinae; Caenorhabditis		
CC	[1]		
RN	SEQUENCE FROM N.A.		
RA	WRITE S.;		
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; Z73897; CAA98064.1; -		
DR	EMBL; Z73899; CAA98064.1; JOINED.		
DR	HSSP; P02751; IFFA.		
DR	PFAM; PF00041; fn3. 31.		
DR	PFAM; PF00047; 1g. 17.		
DR	PFAM; PF00069; pkInase. 1.		
DR	PRINTS; PR00014; ENTTYPEIT.		
SQ	SEQUENCE 6831 AA; 75257er MW: 0A66C338 CRC32:		

[illegible]

alignment_block:
US-09-240-675-1_COPY_27_427 x Q23550

Align seg 1/1 to: Q23550 from: 1 to: 6831

```

88 CTAAATCTCCCTCAAAA.....GTAGAGGTC..GACATCAT 122
      |||||
1856 LeuAspAaPProSerIysProAsnIyProLeuGluValSerAspValP 1872
      |||||
123 AGATGACAACCTTAAOCTAGAGTGGAACAGACGATAGTGTCCGGGA 172
      |||||
1872 eGluAspAsnLeuAsnLeuSerTTrpLysProProAspAspGlyGly 1888
      |||||
173 ATGTGACTTTTCATTCGATTCATCAAAA.....ACTGGGATGATTAAT 216
      |||||
1889 IurolleGIuTyTrpGluValGIuLysLeuAspThrAlaThcIyAr 1905
      |||||

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217 TCGATAAAATGCTGGGTGTCAGATATTTACTGACCAATGCAACTT 266
|||||
1906 TnpAlPro.....CysAlaLysValLysAspThrLysAlaHisI1 1919
267 TTCTTCACTCAAGCTGAATGTTATGAAGAATTAATTCGCTTAAGAG 316
|||||
1919 eaSPGlyLeuLysLysGly.....GlnThrTyrGlnPheArgValLysA 1934
317 CA...GAAAAAGAAACACTTCTTCATGATGATGAGTGTGACTCAATTACA 363
|||
1934 laValAsnLysGluGlyAlaSerAspAlaLeuSerThrAspLysAspThr 1950
364 .....CCATTT...CGCAAGCTCAGATTGGTCTCTCCAGAAAGT 398
|||||
1951 LysAlaLysAsnProTyrAspGluProGlyLysThrGlyThrProAspVa 1967
399 A 399
1967 1 1967
seq_name: sp_invertebrate:Q23551

```

```

seq_documentation_block:
ID Q23551 PRELIMINARY; PRT: 7160 AA.
AC Q23551;
DT 01-NOV-1996 (TEMBUREL. 01, Created)
DT 01-NOV-1998 (TEMBUREL. 08, Last sequence update)
DT 01-NOV-1999 (TEMBUREL. 12, Last annotation update)
DE ZK617.1B PROTEIN.
GN ZK617.1B.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA HARRIS B.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RX MEDLINE: 94150718.
RP SEQUENCE FROM N.A.
RX WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BOFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans".
RL Nature 368:32-38(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA WHITE S.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RX EMBL: Z73897; CA98082.1; -.
RX EMBL: Z73897; CA98082.1; JOINED.
RX EMBL: Z73897; CA98085.1; -.
RX EMBL: Z73899; CA98065.1; JOINED.
DR HSSP: P02751; 1FNA.
DR PFAM: PF00041; fn3. 31.
DR PFAM: PF00047; 1g. 17.
DR PFAM: PF00068; Pkinase. 1.
DR PRINTS: PR00014; ENTPERT11.
SO SEQUENCE 7160 AA; 789211 MW; EDD567FE CRC32;

```

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alignment_scores:
Quality: 84.00 Length: 117
Ratio: 1.151 Gaps: 8
Percent Similarity: 62.393 Percent Identity: 26.496

```

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alignment_block:
us-09-240-675-1_COPY_27_427 x Q23551 ..
Align seg 1/1 to: Q23551 from: 1 to: 7160

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```

88 CTAAATCTCTCAAAA.....GTAGAGTC...GACATCAT 122
|||||
2185 LeuAspArgProSerLysProAsnGlyProLeuGluValSerAspAlpH 2201
123 AGATGACAACTTTATCCTGAGTGCAGACAGAGATGATGCTGCGGA 172
|||||
2201 eGluAspAsnLeuAsnLeuSerThrLysProProAspAspAspGlyG 2218
173 ATGTGACTTTTTCATTCGATTATCAAAA.....ACTGGAGATGATAT 216
|||||
2218 TnpAlPro.....CysAlaLysValLysAspThrLysAlaHisI1 2248
217 TCGATAAAATGCTGGGTGTCAGATATTTACTGACCAATGCAACTT 266
|||||
2235 TnpAlPro.....CysAlaLysValLysAspThrLysAlaHisI1 2248
267 TTCTTCACTCAAGCTGAATGTTATGAAGAATTAATTCGCTTAAGAG 316
|||||
2248 eaSPGlyLeuLysLysGly.....GlnThrTyrGlnPheArgValLysA 2263
317 CA...GAAAAAGAAACACTTCTTCATGATGATGAGTGTGACTCAATTACA 363
|||
2263 laValAsnLysGluGlyAlaSerAspAlaLeuSerThrAspLysAspThr 2279
364 .....CCATTT...CGCAAGCTCAGATTGGTCTCTCCAGAAAGT 398
|||||
2280 LysAlaLysAsnProTyrAspGluProGlyLysThrGlyThrProAspVa 2296
399 A 399
2296 1 2296
seq_name: sp_vertebrate:O13048

```

```

seq_documentation_block:
ID O13048 PRELIMINARY; PRT: 402 AA.
AC O13048;
DT 01-JUL-1997 (TEMBUREL. 04, Created)
DT 01-JUL-1997 (TEMBUREL. 04, Last sequence update)
DT 01-NOV-1999 (TEMBUREL. 12, Last annotation update)
DE XNR-4.
GN XNR4.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae;
Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92728865.
RA JOSEPH E.M., MELTON D.A.;
RT "Xnr4, a Xenopus nodal-related gene expressed in the Spemann
organizer".
RL Dev. Biol. 184:367-372(1997).
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL: U79162; AAC60127.1; -.
DR HSSP: P18075; 1BWP.
DR PROSITE: PS00250; TGF-BETA. 1.
DR PFAM: PF00019; TGF-beta. 1.
DR PRINTS: PR00438; GFCYSKNOT.
KW Glycoprotein.
SO SEQUENCE 402 AA; 46271 MW; 039E7186 CRC32;

```

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alignment_scores:
Quality: 80.00 Length: 112
Ratio: 1.404 Gaps: 5
Percent Similarity: 50.893 Percent Identity: 23.214

```

alignment_block:

US-09-240-675-1_COPY_27_427 x 013048 ..

Align seg 1/1 to: 013048 from: 1 to: 402

```

48 GGGCCCATGGGTGTTCGCCGACCGCGGTGGAATAAATCTAATCTC 97
   |||  ::  ::::::::::::::|||  ::::::::::|||  |||
266 GlyIleGlnThrIleAlaHisThrArgArgHisArgSerHisIlePn 282
   98 CTCAAAAAGT..AGAGTCGACATCATAGATGACAACTTATCCGAGG 144
      :::::  |||  :::::  |||  :::::  |||  :::::  |||
282 elysGlnHisValMetCylMetLysHis.....ValProPro 295
   :::::  |||  :::::  |||  :::::  |||  :::::  |||
145 TGCAACGAGGAGCGATGAGTGTGCGGAATGCTTTTCATTCGTTA 194
   ::::::::::::::|||  ::::::::::::::|||  ::::::::::::::|||
295 laaspserserAlaGlnThrLeuGlnArgArgAlaAspPheVal 311
   :::::  |||  :::::  |||  :::::  |||  :::::  |||
195 TCAAAAAAAGTGGATGATGATTAATGATTAATGATGATGATGATG 244
   :::::  |||  :::::  |||  :::::  |||  :::::  |||
311 elysGlnIleGlyTrpAspSerTrpIle..... 320
   :::::  |||  :::::  |||  :::::  |||  :::::  |||
245 TTACTAGTACCAATGCACTTTCTTCTCACTCAAGCTGATTTAT... 291
   :::::  |||  :::::  |||  :::::  |||  :::::  |||
321 ..... 330
   :::::  |||  :::::  |||  :::::  |||  :::::  |||
292 ..... 311
   :::::  |||  :::::  |||  :::::  |||  :::::  |||
331 CysGlnGlyGlyLucyProSerProValAlaGlnSerValLysProAsnAs 347
   :::::  |||  :::::  |||  :::::  |||  :::::  |||
312 AAGAGCAGAAAAAGAAACACTTCTTCATGATGAT 345
   :::::  |||  :::::  |||  :::::  |||  :::::  |||
347 nHisAlaTrpMetGlnSerLeuLeuAlaGlnTyTrp 358
   :::::  |||  :::::  |||  :::::  |||  :::::  |||
seq_name: sp_human:Q10466

seq_documentation_block:
ID Q10466 PRELIMINARY: PRT: 26926 AA.
AC Q10466:
DT 01-NOV-1996 (TRENDBLREL. 01, Created)
DT 01-NOV-1996 (TRENDBLREL. 01, Last sequence update)
DT 01-NOV-1999 (TRENDBLREL. 12, Last annotation update)
DE TITIN, HEART ISOFORM N2-B (EC 2.7.1.-) (CONNECTIN).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
   Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RX LABELT S., KOLMER B.:
RX MEDLINE: 96026330.
RT "titins: giant proteins in charge of muscle ultrastructure and
   elasticity.";
RL Science 270:293-296(1995).
RN [2]
RP SEQUENCE OF 22277-25376 FROM N.A.
RX MEDLINE: 92258380.
RX LABELT S., GAUTEL M., LAKEY A., TRINICK J.:
RT "Towards a molecular understanding of titin.";
RL EMBO J. 11:1711-1716(1992).
RN [3]
RP SEQUENCE OF 1976-2014 FROM N.A.
RX LABELT S.:
RX SUBMITTED (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CHARACTERIZATION.
RX MEDLINE: 9531314.
RX GAUTEL M., CASTIGLIONE-MORELLI M.A., PFUHL M., MOTTA A., PASTORE A.:
RT "A calmodulin-binding sequence in the C-terminus of human cardiac
   titin kinase.";
RL Eur. J. Biochem. 230:752-759(1995).
CC -1- FUNCTION: THIS GIANT MUSCLE PROTEIN MAY BE INVOLVED IN MUSCLE
   ASSEMBLY AND IN MAINTAINING THE STRUCTURAL INTEGRITY OF

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CC SARCOMERES. MAY HAVE PROTEIN KINASE ACTIVITY.
CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF FORMS OF THIS PROTEIN ARE
CC PRODUCED BY ALTERNATIVE SPLICING WHICH DIFFER IN TISSUE
CC DISTRIBUTION. DIFFERENT SIZE TRANSCRIPTS MAY ALSO EXIST WITHIN ANY
CC ONE TISSUE. THE SEQUENCE SHOWN HERE IS THAT OF THE HEART ISOFORM
CC N2-B.
CC -1- TISSUE SPECIFICITY: MUSCLE-SPECIFIC.
CC -1- SIMILARITY: TO THE CATALYTIC DOMAINS OF OTHER SERINE/THREONINE
CC KINASES.
CC -1- SIMILARITY: BELONGS TO IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 112
CC IMMUNOGLOBULIN C2-LIKE DOMAINS AND 132 FIBRONECTIN TYPE III-LIKE
CC DOMAINS.
CC EMBL: X64598; CAA45939.1; -.
CC EMBL: X83270; CAA58243.1; -.
CC EMBL: X64697; CAA45938.1; -.
CC EMBL: X90568; CAA62188.1; -.
CC EMBL: X64699; CAA45940.1; -.
CC HSSP: P56276; ITLK.
CC PFAM: PF00041; fn3; 132.
CC PFAM: PF00047; IQ; 59.
CC PFAM: PF00069; PKinase; 1.
CC PRINTS: PR00014; FMYPRIT.
CC PRINTS: PR00726; LEXASERPTASE.
CC Muscle protein; Cytoskeleton; Structural protein; Calmodulin-binding;
   Serine/threonine-protein kinase; Alternative splicing; Repeat;
   Immunoglobulin domain; Phosphorylation.
CC DOMAIN 1370 1389
   4 X 5 AA TANDEM REPEATS OF R-W-S-P-A.
   GLU/LYS/PRO/VAL-RICH.
CC DOMAIN 24731 25070
   CATALYTIC.
CC DOMAIN 25030 25056
   CALMODULIN-BINDING.
CC MOD_RES 1372 1372
   PHOSPHORYLATION (BY PDKR) (POTENTIAL).
CC MOD_RES 1377 1377
   PHOSPHORYLATION (BY PDKR) (POTENTIAL).
CC MOD_RES 1382 1382
   PHOSPHORYLATION (BY PDKR) (POTENTIAL).
CC MOD_RES 1387 1387
   PHOSPHORYLATION (BY PDKR) (POTENTIAL).
CC MOD_RES 26171 26171
   PHOSPHORYLATION (POTENTIAL).
CC MOD_RES 26178 26178
   PHOSPHORYLATION (POTENTIAL).
CC MOD_RES 26184 26184
   PHOSPHORYLATION (POTENTIAL).
CC MOD_RES 26190 26190
   PHOSPHORYLATION (POTENTIAL).
CC CONFLICT 22277 22277
   T -> P (IN REF. 2).
CC CONFLICT 22449 22449
   E -> G (IN REF. 2).
CC CONFLICT 22454 22454
   T -> Q (IN REF. 2).
CC CONFLICT 23324 23324
   S -> L (IN REF. 2).
CC SO SEQUENCE 26926 AA; 2993428 MW; 0214E3A3 CRC32;

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alignment_scores:

Quality:	80.00	Length:	99
Ratio:	1.379	Gaps:	4
Percent Similarity:	58.586	Percent Identity:	25.253

alignment_block:

US-09-240-675-1_COPY_27_427 x Q10466 ..

Align seg 1/1 to: 010466 from: 1 to: 26926

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112 CTCGACATCATAGATGATGACAACTTATCTGAGTGGAGCAAGAGCAGGAGA 161
   |||||  ::  ::  |||  |||||  ::  |||
10922 ValAspValAspLysThrGlnValSerLeuValTrpAsnLysProAspAr 10958
   :::::  |||  :::::  |||  :::::  |||  :::::  |||
162 GTCGTGGGGAAT.....GTGACTTTTCATTCGATTAATCAAAAACATG 205
   :::::  |||  :::::  |||  :::::  |||  :::::  |||
10938 gaspGlyGlySerProIleThrGlyTrpLeuValGluTrpGlnGluGluG 10955
   :::::  |||  :::::  |||  :::::  |||  :::::  |||
206 GGATGATATGATGATTAATGCTGCTGGGTGCAATATTAATGATGATGAC 255
   ||  :::::  |||||  :::::  |||  :::::  |||  :::::  |||
10955 lYThrGlnAspTrpIleLysPhe.....LysThrValThrAsnLeu 10968
   :::::  |||  :::::  |||  :::::  |||  :::::  |||
256 AATGCAACTTTCTTCACCTCAAGCTGAATGATTTATGAAGAATTAATTT 305
   ::|||  :::::  |||  :::::  |||  :::::  |||  :::::  |||
10969 GlucyValValThrGlyLeuGln.....GlnGlyLysThrThy 10981
   ::|||  :::::  |||  :::::  |||  :::::  |||  :::::  |||
306 GCGTATTAAGACGAGAAAAAGAAACACTTCTTCATGATGATGATGATGATG 355
   |||||  :::::  |||  :::::  |||  :::::  |||  :::::  |||

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49 GGGCCATGGGTGTGTCGCCAGCCGACGATGCAAAA..... 84
113 GYARGTfPmetAlaserGlyglyserGlyGlnleuleutrpas 149
85 .....AATCTAAATCTGCT...CAAAAGTAGGCGACATCATG 124
149 pCysAlaAsnleuLysThrProheserProGlySerProAsnPhetpA 166
125 ATGCAACACTTATCCGTAGTGACAGACGATGATCTGTC..... 168
166 spClnValLysleuLeuArgTfPAsnleuLysAsnGlnSerValPheAla 182
169 .....GGCAATGTGACTTTTTCATTCGATTCATCAAAAAACTGG 206
183 SerIleSerSerArgValSerPhe...TfPAsnleuArgValGAsnG 198
207 GATGGAT.....AATGGATAAATGTCGTGGGTCTCAGAAATATCA 250
198 ySerProValleuGlnPheAlaGlnleuProGly..... 209
251 GTACCAATGCAACTTTTCTTCACGACGATGATTTATGAAAGAAAT 300
210 .....CysAspTrpSerSerLeuSerTrpAsnProSerAsnPalaser 223
301 AATTCGCTATAGACGACGAAAAAACAACCTCT.....TCATG 341
224 GlnleuIleValSerSerGlnSerGlnHisAlaSerValIleGlnLysTr 240
342 GTATGAGTTGACTCATTTACACCATTTGCGCAA 375
240 pAspSerArgPheThrSerThrProValLysGln 251
seq_name: sp_virus:065525

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seq_documentation_block:
ID Q06525 PRELIMINARY: PRT: 733 AA.
AC Q06525:
DT 01-NOV-1996 (TfREMBLrel. 01, Created)
DT 01-NOV-1996 (TfREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TfREMBLrel. 08, Last annotation update)
DE ROTAVIRUS C VP4.
OS Bovine group C rotavirus.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SHINTOKU:
RA JIANG B., GENTSCH J.R., TSUNEMITSU H., SAIF L.J., GLASS R.I.:
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U26551; AAB01672.1; -.
DR PFIAM; PF00426; VP4; 1.
SQ SEQUENCE 733 AA; 82494 MW; 93174D55 CRC32;

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alignment_scores:
Quality: 77.50 Length: 168
Ratio: 0.934 Gaps: 8
Percent Similarity: 49.405 Percent Identity: 23.810

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alignment_block:

US-09-240-675-1_COPY_27_427 x Q06525 ..

Align seg 1/1 to: Q065525 from: 1 to: 733

```

25 ACCAGCCCTAGCTGCTGCGCCGTCGCGCCA.....TGGGTGT 62
93 SerThrValLysleuLeuLysAsnGlyProGlnSerTrpSerTrpAsnle 109
63 GTCCGCGACGCCGA.....GCTGAAAAAAT..... 87
109 uAlaAlaPheGlnleuLeuTrpTfPArgLysAlaAsnThrThrValThrSera 126
88 .....CTAAATCTGCTCAAAAGTAGGCGACATC 120

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126 sPtyTrpSerGlyMetThrAsnSerGlyLysSerValGlnValAsp... 141
121 ATAGATGCAACTTATCCGTAGGTGGAACGAGCGATGATCTGTCGG 170
142 ...HisAspSerLeuValleuPheTrpAsnGlnGlySerThrAlaLeuSe 157
171 GAATGTGACTTTTTCATTCGATTCATCAAAAACTGGATGATAATTGCA 220
157 rAsnLysValIleAsnPheserTrpAsnValGlyGlyAla.....LeuI 172
221 TAAATTC.....TCGTGGTGTGAG 240
172 IeLysleuThrSerAsnThrArgIleAspIleCysMetAlaAsnMetAsp 188
241 AATATTACTAGTACCAATGCAACTTCT..... 270
169 AsnPheThrSerAspSerPheAsnTrpGlnLutTrpThrHisAsnPhetp 205
271 ...TCACTCAAGCTGAATGTTATGAAAGAAATTAATG..... 306
205 cArgSerAlaSerMetAlaSerIleTfPThrAspTfPTrpLeuAlaSerVal 222
307 .....CGTATAGACGACGAAAAAACAACCTCTTCATGCTAT 345
222 sPProTfPSerGlnIleArgAlaLeuGlnGlnProIleIleThrVal 238
346 GAGGTGACTCATTTACACCATTTGCAAGCTGATGATGCTTCGACA 395
239 GlnMetLysMetValLysValLysArgGlnGlySerIleAsnValAspGl 255
396 AGTA 399
255 uVal 256
seq_name: sp_fungi:Q08773

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seq_documentation_block:
ID Q08773 PRELIMINARY: PRT: 1120 AA.
AC Q08773:
DT 01-NOV-1996 (TfREMBLrel. 01, Created)
DT 01-NOV-1996 (TfREMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TfREMBLrel. 10, Last annotation update)
DE CHROMOSOME XV READING FRAME ORF YOR304M.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RA CZIEPLUCH C., JAUNTAUX J.C., KORDES E., POIREY R., PUJOL A.,
RA TOBIASCH E.:
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS:
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z75212; CAA9622.1; -.
DR PFIAM; PF00176; SNF2_N; 1.
SQ SEQUENCE 1120 AA; 130326 MW; 51FC7F47 CRC32;

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alignment_scores:
Quality: 77.50 Length: 125
Ratio: 1.123 Gaps: 4
Percent Similarity: 55.200 Percent Identity: 23.200

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alignment_block:

US-09-240-675-1_COPY_27_427 x Q08773 ..

Align seg 1/1 to: Q08773 from: 1 to: 1120

```

76 GGTGAAAAATCTA.....AATCTGCTCAAAAGTAGGCGACAT 119

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664 G1yAlAlAlAsmMetPheGluLysLysAlaSerLysValThrValAspAl 660
120 CATAGATGACAACTTATCTGAGTGCAGACAGAGAGATGCTGCTG 169
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
680 AspIleAspAlaPheLysLysGluGluGluLysThrGluGluLeu. 696
170 GCATATGACTTTTCATTGATATCAAAAACCTGGATGATTAATGG 219
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
697 .....AsnAlaLysTyrGlnSerLeuGlyLeuAspAlaPhe 708
220 ATAAATGTCGTGCTGATATTAAGTACCAATGCAACTTTC 269
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
709 GlnLysPheAsnGlyIleGluAsnGlnSerAlaTyrGluTrpAsnGly 725
270 TTCACGCAAGCTGAATGTTATGAGAAATTAATGCGTATA..... 312
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
725 sSerPheGlnLysLysSerAsnAspLysValValGluTrpIleAsnPro 742
313 ..AGACGACAAAAAAGAAACACTTCTTCATGATGATGAGTTCATTT 360
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
742 eTrArgTgGluArgArgGluGlnThrThrTyrSerValAspAspTyr 758
361 .....ACACG 365
759 TyrLysGluIleIleGlyGlySerLysSerAlaSerLysGlnThrPr 775
366 ATTCGCAAGCTCAGATTGCTCT 390
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
775 GlnProLysAlaProArgAlaPro 783

```

seq_name: sp_invertebrate:Q20930

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seq_documentation_block:
ID Q20930 PRELIMINARY: PRT: 508 AA.
AC Q20930:
DT 01-NOV-1996 (TREMBLER. 01, Created)
DT 01-NOV-1996 (TREMBLER. 01, Last sequence update)
DT 01-MAY-1999 (TREMBLER. 10, Last annotation update)
DE F5787.4 PROTEIN.
GN Caenorhabditis elegans.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditi; Rhabditida;
OC Rhabditi; Rhabditi; Rhabditi; Rhabditi; Rhabditi; Rhabditi;
RN [1]
RP SEQUENCE FROM N.A.
RA LENNARD N.:
RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA WILSON R., AINSWORTH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERY-MING J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPOAT J., WOHLDMAN P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
DR EMBL: Z74037; CAA98493.1;
DR PFAM: PF01421; ReproLysIn: 1.
SO SEQUENCE 508 AA; 57789 MW; B49E91AE CRC32;

```

Alignment_scores:
Quality: 75.50 Length: 148
Ratio: 1.079 Gaps: 5
Percent Similarity: 47.297 Percent Identity: 22.297

alignment_block:
US-09-240-675-1_COPY_27_427 x Q20930 ..

Align seg 1/1 to: Q20930 from: 1 to: 508

```

10 GTCTCTCTGCGCGGCGAGACAGACCTAGTGCCTGCGCGCGGCGCCATGGGT 59
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
118 ILeSerPheGlyAsnGluThrLeuHisMetValPheAlaGlyThrTrpI 134
60 GTTGTCCCGCCGCCGAGT..... 78
134 eAlaThrGlnGluArgAspCysProLeuTrpIleSerTrpAlaGluGlu 151
79 .....GGAATAAATCTAAATCTCCCTCAAAAGTAGAG 111
151 LuGluGluArgValLeuAsnGluGluIleArgArgLeuGluGluLysGlu 167
112 CTCGACATC.....ATAGATGCAACTTATCTGAGTGGAA 149
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
168 ArgAspLeuAsnSerThrPheValAspAspThrPhePheMetAsnSerTh 184
150 CAGAGCGATGAGTCTGTCGGAATGTCATTTTCATTCGATATCAAA 199
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
184 rAspSerAspAsnSerSerThrAspAlaLeuIleSerSerAspMetPro 201
200 AAACGTGGATGATTAATGATTAATGCTGCGGTGTCAGAAATTAAT 249
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
201 ys.....LysLeuArgLysPheValAspIleThr 210
250 AGTACCAATGCAACTTCTTCACCTCAGCTGATGTTTATGAGAAAT 299
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
211 .....LeuGluGluMetGlnGluAsnAsnSerThrGluLe 222
300 TAAATGCGTATTAAGACAGAAAAAGAAACACTTCTCATGATGATGAG 349
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
222 tThrLeuLysIleAspSerLysLys.....AlaI 232
350 TTGACTCATTTACACCATTTCCCAAGCTCAGATTGCTCTCA 393
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
232 leAspLysPheThrIleTrpLeuLysGluGlnThrGlyLeuPro 246

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227 A 227
67 s 67

seq_name: A_Geneseq_36:R14487

seq_documentation_block:

ID R14487 standard; Protein: 436 AA.
AC R14487;
DT 16-JAN-1992 (first entry)
DE Soluble Interferon-alpha/beta receptor.
KM IFN autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
PN FR2657881-A.
PD 09-AUG-1991.
PF 05-FEB-1990; FR-001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE.
PT Toyey MG, Uze G;
DR WPI: 91-319778/44.
DR N-PSDB: 014239.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Bence's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Claim 2; Page 45; 52pp; French.
CC The transmembrane and cytoplasmic domains of the native IFN receptor have been deleted to obtain a soluble, circulating form of the receptor. Potentially immunogenic epitopes have thus been eliminated. CC derivatives obtained by substitution or deletion of this sequence are also claimed as are hybrid molecules comprising the soluble CC receptor (or deriv.) and an immunoglobulin such as IgG1.
CC See also Q14240.
SO Sequence 436 AA;

Alignment_scores:

Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

Alignment_block:

US-09-240-675-1_COPY_1_229 x R14487 ..

Align seg 1/1 to: R14487 from: 1 to: 436

27 ATGATGCTGCTCTCTGGCGCGAGACCCCTAGTCTGCTGCGCCGTGGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAla 17
77 CCCATGGTGTGTCGCCAGCCGACAGTGGAAAAATCTAAATCTCCTC 126
|||||
17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
127 AAAAACTAGAGCTGCACATCATAGACAACTTATCTCTGAGGTGAAC 176
|||||
34 InLysValGluValAspIleIleAspAspAsnPhelLeuArgTrpAsn 50
177 AGGAGCGATGAGTCTGTCGGGAATGCACTTTTTCATTCGATTATCAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLys 67
227 A 227
67 s 67

seq_name: A_Geneseq_36:R28495

seq_documentation_block:

ID R28495 standard; Protein: 436 AA.
AC R28495;
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the Interferon (IFN) receptor

DE With a high affinity for IFN-alpha and -beta.
KM Interferon receptor; alpha-Interferon; beta-Interferon.
OS Synthetic.
PN W09218626-A.
PD 29-OCT-1992.
PF 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PT Toyey M, Uze G;
DR WPI: 92-382110/46.
DR N-PSDB: Q30532.
PT Water soluble polypeptide(s) strongly bind Interferon(s) alpha and beta - useful as immunosuppressants, for treating auto-immune diseases and transplant rejection
PS Claim 2; Fig 1; 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, CC bacteriophage lambda ZAP, containing the entire coding sequence of CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos Q30534 and Q30535. R28496 represents the complete receptor. R28495 CC lacks the transmembrane and cytoplasmic domains. Both forms bind CC IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the CC toxic side-effects of known immunosuppressants such as steroids.

Sequence 436 AA;

Alignment_scores:

Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

Alignment_block:

US-09-240-675-1_COPY_1_229 x R28495 ..

Align seg 1/1 to: R28495 from: 1 to: 436

27 ATGATGCTGCTCTCTGGCGCGAGACCCCTAGTCTGCTGCGCCGTGGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAla 17
77 CCCATGGTGTGTCGCCAGCCGACAGTGGAAAAATCTAAATCTCCTC 126
|||||
17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
127 AAAAACTAGAGCTGCACATCATAGACAACTTATCTCTGAGGTGAAC 176
|||||
34 InLysValGluValAspIleIleAspAspAsnPhelLeuArgTrpAsn 50
177 AGGAGCGATGAGTCTGTCGGGAATGCACTTTTTCATTCGATTATCAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLys 67
227 A 227
67 s 67

seq_name: A_Geneseq_36:R71723

seq_documentation_block:

ID R71723 standard; Protein: 436 AA.
AC R71723;
DT 16-OCT-1995 (first entry)
DE IFN receptor extracellular domain.
KM IFN receptor; Interferon receptor; Interferon-alpha;
KW Interferon-beta; monoclonal antibody; immunomodulator; AIDS.
OS Homo sapiens.
PN W09507716-A.
PD 23-MAR-1995.
PF 16-SEP-1994; E03114.
PR 17-SEP-1993; EP-402279.

PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benizri EJ, Tovey MG;
 DR WPI: 95-11187/17.
 DR N-PSDB: 086457.
 PT Compn. of monoclonal antibodies against Interferon receptor -
 PT useful as immuno-modulator, eg. for treating AIDS
 PS Disclosure: Fig. 2A-2B; 105pp; English.
 CC A recombinant soluble form of the human interferon class I receptor
 CC protein extracellular domain, given in R71723, was expressed in
 CC either E. coli or COS cell hosts. The protein was used to raise
 CC immunomodulatory monoclonal antibodies.
 SO Sequence 436 AA;

alignment_scores:
 Quality: 340.00 Length: 67
 Ratio: 5.075 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-240-675-1_COPY_1_229 x R71723

Align seg 1/1 to: R71723 from: 1 to: 436

```

27 ATGATGTCGTCCTCCTGGGCGGAGACCCCTAGTGTCTGCGCCGCTGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
77 CCCATGGGTGTGTCCGACGCCGAGTGGAATAATCTAAATCTCTC 126
|||||
17 yProTPrValLeuSerAlaAlaIaGlyGlyLysAsnLeuLysSerPro 34
127 AAAAAGTAGAGTCGACATCATGATGACAACTTATCTGAGGTGGAAC 176
|||||
34 InlysvAlaInuValAspIleIleAspAspAsnPhelLeuValArgTTPAsn 50
177 AGGAGCGATGAGTCTGTGCGGAATGTGACTTTTCATTCGATATCAAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
227 A 227
67 s 67

```

seq_name: A_Geneseq_36:W21806

seq_documentation_block:

ID W21806 standard; Protein: 496 AA.
 AC W21806;
 DR 23-SEP-1997 (first entry)
 DE Spliced-deleted Interferon alpha-receptor form 2.
 KW Interferon alpha-receptor; IFNAR.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 1..419
 FT /label= Extracellular domain
 FT /note= "comprises amino acid residues 1-413 and
 FT 422-427 of transmembrane IFNAR"
 FT domain 420..496
 FT /label= Intracellular domain
 FT /note= "comprises amino acids 481-557 of
 FT transmembrane IFNAR"
 PN AU9475977-A.
 PD 11-MAY-1995.
 PF 20-OCT-1994; 075977.
 PR 24-OCT-1993; IL-107378.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (ABRA/) ABRAMOVICH C.
 PI Abramovich C, Ratovitski E, Revel M;
 DR WPI: 95-200634/27.
 PT New mammalian soluble Interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Example 3; Fig 7; 46pp; English.

CC Novel splice-deleted Interferon alpha-receptor (IFNAR) form 2
 CC (W21806) is characterised by a double deletion when compared to
 CC transmembrane IFNAR (W21804). The extracellular domain is
 CC shortened by 6 amino acid residues and is followed by a truncated
 CC intracellular domain. There is no transmembrane region. The amino
 CC acid sequence is predicted from a cDNA clone (see also T73521) obtd.
 CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
 CC splice-deleted forms 1 (see also W21805) and 2 may regulate the
 CC response of human cells to IFNs, either by acting as IFN
 CC antagonists or by regulating IFN activities. They can be expressed
 CC in host cells and used to inhibit, modulate or modify the
 CC activities of IFNs alpha and beta in cells, tissues and organisms,
 CC or for diagnostic purposes.
 SO Sequence 496 AA;

alignment_scores:
 Quality: 340.00 Length: 67
 Ratio: 5.075 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-240-675-1_COPY_1_229 x W21806

Align seg 1/1 to: W21806 from: 1 to: 496

```

27 ATGATGTCGTCCTCCTGGGCGGAGACCCCTAGTGTCTGCGCCGCTGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
77 CCCATGGGTGTGTCCGACGCCGAGTGGAATAATCTAAATCTCTC 126
|||||
17 yProTPrValLeuSerAlaAlaIaGlyGlyLysAsnLeuLysSerPro 34
127 AAAAATAGAGTCGACATCATGATGACAACTTATCTGAGGTGGAAC 176
|||||
34 InlysvAlaInuValAspIleIleAspAspAsnPhelLeuValArgTTPAsn 50
177 AGGAGCGATGAGTCTGTGCGGAATGTGACTTTTCATTCGATATCAAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
227 A 227
67 s 67

```

seq_name: A_Geneseq_36:R11958

seq_documentation_block:

ID R11958 standard; Protein: 557 AA.
 AC R11958;
 DR 18-JUL-1991 (first entry)
 DE Human alpha-Interferon receptor protein.
 KW Human alpha IFN; IFN agonists; antiviral; anti tumour agent;
 KW drug targeting.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT peptide 1..27
 FT /label= signal peptide
 PN WO9105862-A.
 PD 02-MAY-1991.
 PF 19-OCT-1990; F00758.
 PR 20-OCT-1989; FR-013770.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PA (Mogens) KE, Uze G, Lutfalla G, Gresser I;
 DR WPI: 91-148740/20.
 DR N-PSDB: Q11701.
 PT New human alpha-Interferon receptor protein - useful for testing
 PT Interferon agonists and in treatment or diagnosis
 PS Disclosure: fig 4; 30pp; French.
 CC This recombinant human alpha Interferon (IFN) receptor protein is
 CC useful for the testing of IFN agonists and for treatment and diag-
 CC nosis of viral diseases and tumours. Antibodies raised against

CC this protein can be used for blocking the receptor when required,
 CC eg where overexpression of alpha-IFN is harmful. The Abs are
 CC also useful for eg drug targeting. Variants of the Abs are
 CC having residue 164 (Thr) replaced by Arg and an Asp inserted
 CC between residues 479 and 480, are also useful.
 CC Sequence 557 AA;

alignment_scores:
 Quality: 340.00 Length: 67
 Ratio: 5.075 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_1_229 x R11958

Align seg 1/1 to: R11958 from: 1 to: 557

```

27 ATGATGTCGTCCTCGGGCGGCGACGACCTAGTCGTCGCGCCGTGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
77 CCCATGGGTGTTCGCCGACGCCGACGAGTGAATAAATCTCCTC 126
|||||
17 YPOTIPValLeuSerAlaAlaGlyGlyAsnLeuYsserProg 34
127 AAAAAGTAGAGTCGACATCATAGTACACTTATCCTGAGGTGAC 176
|||||
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
177 AGGAGCGATGAGTCGCGGAATGTGACTTTTCATTCGATTATCAAA 226
|||||
51 ArgSerAspGlnSerValGlyAsnValThrPheSerPheAspTyrGlnLys 67

```

227 A 227

67 s 67

seq_name: A_Geneseq_36:R14488

seq_documentation_block:

ID R14488 standard; Protein: 557 AA.
 AC R14488;
 DT 16-JAN-1992 (first entry)
 DE Complete interferon-alpha/beta receptor.
 KM IFN; autoimmune disease; graft rejection; histocompatibility.
 OS Homo sapiens.
 FT Key Location/Qualifiers
 FT domain 437..457
 FT /label= transmembrane
 FT 458..557
 FT /label= cytoplasmic
 FT FR2657881-A.
 PN 09-FEB-1991.
 PD 05-FEB-1990; 001298.
 PR 05-FEB-1990; FR-001298.
 PA (EUBR-) LAB EURO BIOTECHNO.
 PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
 PI Tovey MG, Uze G;
 PI WPI: 91-319778/44.
 DR N-PSDB: Q14240.
 PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
 PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
 PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
 PS Disclosure: Page 47: 52pp; French.
 CC The invention covers derivatives of the interferon-alpha and/or beta
 CC receptor obtained by deleting the transmembrane and cytoplasmic domains
 CC of the native receptor or by substitution. Potentially immunogenic
 CC epitopes are eliminated and the deriv. can be secreted from
 CC transformed cells. Soluble deriv.s block the activity of IFN alpha/beta
 CC and can be used to treat autoimmune diseases or to inhibit graft
 CC rejection. See also Q14239.
 SO Sequence 557 AA;

alignment_scores:
 Quality: 340.00 Length: 67
 Ratio: 5.075 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_1_229 x R14488

Align seg 1/1 to: R14488 from: 1 to: 557

```

27 ATGATGTCGTCCTCGGGCGGCGACGACCTAGTCGTCGCGCCGTGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
77 CCCATGGGTGTTCGCCGACGCCGACGAGTGAATAAATCTCCTC 126
|||||
17 YPOTIPValLeuSerAlaAlaGlyGlyAsnLeuYsserProg 34
127 AAAAAGTAGAGTCGACATCATAGTACACTTATCCTGAGGTGAC 176
|||||
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
177 AGGAGCGATGAGTCGCGGAATGTGACTTTTCATTCGATTATCAAA 226
|||||
51 ArgSerAspGlnSerValGlyAsnValThrPheSerPheAspTyrGlnLys 67

```

227 A 227

67 s 67

seq_name: A_Geneseq_36:R28496

seq_documentation_block:

ID R28496 standard; Protein: 557 AA.
 AC R28496;
 DT 31-MAR-1993 (first entry)
 DE Sequence of a soluble form of the interferon (IFN) receptor
 DE with a high affinity for IFN-alpha and -beta.
 OS Interferon receptor; alpha-interferon; beta-interferon.
 KM Synthetic.
 OS Synthetic.
 PN WO9218626-A.
 PD 29-OCT-1992.
 PF 17-APR-1991; F00318.
 PR 17-APR-1991; WO-F00318.
 PA (EUBR-) LAB EURO BIOTECHNOLOGIE.
 PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
 PI Tovey M, Uze G;
 PI WPI: 92-382110/46.
 DR N-PSDB: Q30533.
 PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
 PT and beta - useful as immunosuppressants, for treating auto-immune
 PT diseases and transplant rejection
 PS Claim 3; Fig 2; 58pp; English.
 CC DNA encoding the water-soluble polypeptide with a high affinity for
 CC IFN-alpha and -beta is isolated by PCR, using appropriate
 CC oligonucleotides as primers and cloned cDNA as template.
 CC bacteriophage lambda ZAP, containing the entire coding sequence of
 CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
 CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
 CC lacks the transmembrane and cytoplasmic domains. Both forms bind
 CC IFN in the same way as antibodies so are immunosuppressants e.g. for
 CC treating autoimmune diseases and graft rejection. They lack the
 CC toxic side-effects of known immunosuppressants such as steroids.
 SO Sequence 557 AA;

alignment_scores:
 Quality: 340.00 Length: 67
 Ratio: 5.075 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_1_229 x R28496 ..

Align seg 1/1 to: R28496 from: 1 to: 557

```

27 ATGATGCTGCTCTCTCGGCGCGAGACCCCTAGTCTGCTGCGCGTGGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValAlaValAlaG1 17
77 CCCATGGGTGTGTCGCGAGCCGAGGTGGAATAATCTAAATCTCCTC 126
|||||
17 yProtrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
127 AAAAAAGTAGAGTCGACATCATAGATGACACTTATCTGAGGTGGAAC 176
|||||
34 InlyValAlaGlyValAlaAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
177 AGGAGCGATGAGTCTGCGGGAATGTGACTTTTTCATTGATTATCAAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
227 A 227
67 s 67

```

seq_name: A_Geneseq_36:R42635

seq_documentation_block:

```

ID R42635 standard; Protein; 557 AA.
AC R42635;
DT 20-APR-1994 (first entry)
DE Human interferon receptor.
KW IFN-R; extracellular domain; monoclonal antibody; viral infection;
KW cell proliferation; allograft rejection; systemic lupus erythematosus;
KW psoriasis; multiple sclerosis; Behcet's disease; aplastic anaemia;
KW immunodeficiency; measles virus; interferon alpha-beta.
OS Homo sapiens.
FT domain 1..436
FT key /label= extracellular domain
FT /note= "soluble, immunogenic form of IFN-R"
PN EP-563487-A.
PD 06-OCT-1993.
PE 31-MAR-1992; 400902.
PR 31-MAR-1992; EP-400902.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG;
DR WPI: 93-312951/40.
DR P-PSDB: R42635.
PT Monoclonal antibody to human interferon type-I receptor - having
PT neutralising activity against human type I interferon, used for
PT therapy and diagnosis
PS Disclosure: Fig.3; 21pp; English.
CC Monoclonal antibodies produced against soluble forms of the human
CC interferon alpha-beta receptor based on the full-length human IFN-R
CC sequence are claimed. The antibodies are useful for treatment and
CC prophylaxis of disorders involving cell proliferation and/or viral
CC infection.
SQ Sequence 557 AA:

```

alignment_scores:

Quality:	340.00	Length:	67
Ratio:	5.075	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment_block:

US-09-240-675-1_COPY_1_229 x R42635 ..

Align seg 1/1 to: R42635 from: 1 to: 557

```

27 ATGATGCTGCTCTCTCGGCGCGAGACCCCTAGTCTGCTGCGCGTGGG 76
|||||

```

```

1 MetMetValValLeuLeuGlyAlaThrThrLeuValAlaValAlaG1 17
77 CCCATGGGTGTGTCGCGAGCCGAGGTGGAATAATCTAAATCTCCTC 126
|||||
17 yProtrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
127 AAAAAAGTAGAGTCGACATCATAGATGACACTTATCTGAGGTGGAAC 176
|||||
34 InlyValAlaGlyValAlaAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
177 AGGAGCGATGAGTCTGCGGGAATGTGACTTTTTCATTGATTATCAAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
227 A 227
67 s 67

```

seq_name: A_Geneseq_36:R75356

seq_documentation_block:

```

ID R75356 standard; Protein; 557 AA.
AC R75356;
DT 16-OCT-1995 (first entry)
DE Human IFN receptor.
KW IFN receptor; interferon receptor; interferon-alpha;
KW interferon-beta; monoclonal antibody; immunomodulator; AIDS.
OS Homo sapiens.
FT domain 1..436
FT key /label= Extracellular domain
FT /note= "soluble, immunogenic form of IFN-R"
PN WO9507716-A.
PD 23-MAR-1995.
PE 16-SEP-1994; E03114.
PR 17-SEP-1993; EP-402279.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benizri EJ, Tovey MG;
DR WPI: 95-131187/17.
DR N-PSDB: Q86458.
PT Compsn. of monoclonal antibodies against interferon receptor -
PT useful as immunomodulator, eg. for treating AIDS
PS Disclosure: Fig.3A-2B; 105pp; English.
CC The amino acid sequence of human interferon class I receptor is
CC given in R75356. A recombinant soluble form of the extracellular
CC domain of this receptor (R71723) has been used to raise
CC immunomodulatory monoclonal antibodies.
SQ Sequence 557 AA:

```

alignment_scores:

Quality:	340.00	Length:	67
Ratio:	5.075	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment_block:

US-09-240-675-1_COPY_1_229 x R75356 ..

Align seg 1/1 to: R75356 from: 1 to: 557

```

27 ATGATGCTGCTCTCTCGGCGCGAGACCCCTAGTCTGCTGCGCGTGGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValAlaValAlaG1 17
77 CCCATGGGTGTGTCGCGAGCCGAGGTGGAATAATCTAAATCTCCTC 126
|||||
17 yProtrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
127 AAAAAAGTAGAGTCGACATCATAGATGACACTTATCTGAGGTGGAAC 176
|||||
34 InlyValAlaGlyValAlaAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
177 AGGAGCGATGAGTCTGCGGGAATGTGACTTTTTCATTGATTATCAAAA 226
|||||

```

51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnIly 67

227 A 227

67 s 67

seq_name: A_Geneseq_36:W21804

seq_documentation_block:

ID W21804 standard; Protein: 557 AA.

AC W21804;

DE 23-SEP-1997 (first entry)

DE Transmembranal interferon alpha-receptor.

KM Interferon alpha-receptor; IFNAR.

OS Homo sapiens.

FN Key Location/Qualifiers

FT domain 1..436

FT domain /label= Extracellular_domain

FT domain /label= Transmembrane_domain

FT domain 458..557

FT domain /label= Intracellular_domain

PN AU9475977-A.

PD 11-MAY-1995.

PF 20-OCT-1994; 075977.

PR 24-OCT-1993; IL-107378.

PA (YEDA) YEDA RES & DEV CO LTD.

PA (ABRA/) ABRAMOVICH C.

PI Abramovich C, Ratovitski E, Revel M;

DR WPI: 95-200634/27.

PT New mammalian soluble interferon alpha-receptor forms - used for

PS inhibiting, modulating or modifying the activities of interferon(s)

CC Human transmembranal interferon alpha receptor (IFNAR) (W21804)

CC includes a 21-amino acid transmembrane region. Novel, splice-

CC deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected

CC that lack this transmembrane domain. These, soluble non-membrane

CC bound polypeptides can be expressed in host cells and used to

CC inhibit, modulate or modify the activities of interferons alpha

CC and beta in cells, tissues and organisms, or for diagnostic

CC purposes.

CC Sequence 557 AA;

SQ

alignment_scores:

Quality: 340.00

Ratio: 5.075

Percent Similarity: 100.000

Percent Identity: 100.000

Length: 67

Gaps: 0

Align seg 1/1 to: W21804 from: 1 to: 557

US-09-240-675-1_COPY_1_229 x W21804

27 ATGATGTCCTCTCTGCGCGCAGCAGCCTAGTCTCTGCGCGG 76

1 MethetvalValLeuLeuGlyAlaThrThrLeuValLeuAlaValG 17

77 CCGATGGGTGTTCGCCGCGCAGCGAGTGAATAAATCTCTCTC 126

17 yPOTrPValLeuSerAlaAlaGlyGlyAsnLeuLysSerProg 34

127 AAAAGTGGAGTGGAGCATCATAGTGAACAATTATCTGAGTGAAC 176

34 InLysValGluValAspLeuLeuLeuLeuLeuLeuLeuLeuArgTrpAsn 50

177 AGGAGCGATGAGTCTGTCGGAATGACTTTTCATTCGATTCAAA 226

51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnIly 67

227 A 227

67 s 67

seq_name: A_Geneseq_36:W93941

seq_documentation_block:

ID W93941 standard; Protein: 1429 AA.

AC W93941;

DE 30-JUN-1999 (first entry)

DE Human brx protein.

KM Brx protein; breast cancer; nuclear receptor-binding auxiliary protein;

KM anti-cancer; anti-proliferative; mitogen; transcription factor; human;

KM tumour suppressor; ovarian cancer; proliferative disorder; treatment;

KM immune tissue; prevention; reproductive tissue.

OS Homo sapiens.

FN MO9915544-A1.

PD 01-APR-1999.

PF 23-SEP-1998; U19782.

PR 23-SEP-1997; US-059621.

PA (DRIG/) DRIGGERS P H.

PA (RUBI/) RUBINO D M.

PA (SEGE/) SEGERS J.

PI Driggers PH, Rubino DM, Segers J;

DR WPI: 99-254688/21.

DR N-PSDB: X24044.

PT Breast cancer gene encoding a nuclear receptor-binding auxiliary

PS protein, brx

CC Claim 1b: Page 58-62: 69pp: English.

CC This invention describes a novel human breast cancer gene encoding a

CC nuclear receptor-binding auxiliary protein, brx. The brx encoded protein

CC has anti-cancer, anti-proliferative and mitogenic activity and acts as a

CC transcription factor and tumour suppressor. Levels of expression of brx

CC can be detected using the primers, probes and antibodies (contained in

CC the kit) to determine a predisposition to breast and ovarian cancer and

CC other proliferative disorders of immune tissues. Vectors containing the

CC brx gene can be used for prevention and treatment of cancers and

CC proliferative diseases of mammalian reproductive and immune tissues.

CC Sequence 1429 AA;

SQ

alignment_scores:

Quality: 79.00

Ratio: 1.837

Percent Similarity: 52.439

Percent Identity: 41.463

Length: 82

Gaps: 6

Align seg 1/1 to: W93941 from: 1 to: 1429

US-09-240-675-1_COPY_1_229 x W93941

5 AGGATCTGCGCGCGCTCCAGATGATGCTGCTCTGCGCGCAGCA 54

1226 ArgGluLeuArg.....AspGlyArgProSerTrp..... 1235

55 CCTAGTCTGCTGCGCGCGCTCCAGATGATGCTGCTCTGCGCGCAGCA 104

1236 .ProSerAlaArgArgArgCysSerArgGly.....SerArgThrT 1249

105 GGAATAAATAAATCTCTCAAAAGTAGAGCTGCACATCATATATA 154

1249 rPyIsArgSerGlyArgSerSerArgArgArgAlaHisSerGlnTyr 1265

155 CAACCTT.....TATCTGAGGTGAGACAGA 180

1266 AspLeuGluArgLeuArgAlaAlaGlnLysGlnLeuGluArgGluInd 1282

181 GCCATGAGTCTGCGGGAATGACTTTTCATTCGATTATCAAA 226

1282 uHis...ValArgArgGluAlaGlu.....ArgLeuSerGln 1293

seq_name: A_Geneseq_36:W31867

seq_documentation_block:

ID W31867 standard; Protein: 1382 AA.

AC W31867;

34 IntysValGIuValAspIleIleAspAspAsnPhelIleuArgTrpAsn 50

177 AGGAGCATGAGTCTCGGAAATGACTTTTTCATTTCATTAACAAA 226

51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnIly 67

227 A 227

67 s 67

seq_name: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:US-08-307-588-2

seq_documentation_block:

; Sequence 2, Application US/08307588

; Patent No. 5919453

; GENERAL INFORMATION:

; APPLICANT: BENOIT, Patrick

; APPLICANT: MEYER, Francois

; APPLICANT: MAGUIRE, Deborah

; APPLICANT: PLAVEC, Ivan

; APPLICANT: TOVEY, Michael G.

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/307,588

; FILING DATE: 05-DEC-1994

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP93/00770

; FILING DATE: 30-MAR-1993

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: EP 92400902.0

; FILING DATE: 31-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Saxe, Bernhard D.

; REGISTRATION NUMBER: 28,665

; REFERENCE/DOCKET NUMBER: 17283/117/GUPL

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 436 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-307-588-2

; alignment_scores:

Quality: 340.00 Length: 67

Ratio: 5.075 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_1_229 x US-08-307-588-2 ..

Align seg 1/1 to: US-08-307-588-2 from: 1 to: 436

27 ATGATGCTCCTCCTCGGCGGACACCCCTAGTCTGCGCGGTGG 76

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1 MetMetValValIleuLeuClAlaThrThrLeuValIleuValAlaValAl 17

77 CCCATGGGTGTTGTCGCCAGCCGACAGTGGAAAAAATCTAAATCTCTC 126

17 yPcOTpValIleuSerAlaAlaIleGlyLysAsnLeuLysSerProG 34

127 AAAAAGTAGAGTCCGACATCATGATGACAACTTATCTGAGGTGAGC 176

34 IntysValGIuValAspIleIleAspAspAsnPhelIleuArgTrpAsn 50

177 AGGAGCATGAGTCTCGGAAATGACTTTTTCATTTCATTAACAAA 226

51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnIly 67

227 A 227

67 s 67

seq_name: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:US-08-328-256-12

seq_documentation_block:

; Sequence 12, Application US/08328256

; Patent No. 5643749

; GENERAL INFORMATION:

; APPLICANT: REVEL, Michel

; APPLICANT: ABRAMOVICH, Carolina

; APPLICANT: RATOVIJSKI, Edward

; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/328,256

; FILING DATE: 24-OCT-1994

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: IL 107378

; FILING DATE: 24-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, Roger L.

; REGISTRATION NUMBER: REVEL-13

; REFERENCE/DOCKET NUMBER: 25,618

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 496 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-328-256-12

; alignment_scores:

Quality: 340.00 Length: 67

Ratio: 5.075 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_1_229 x US-08-328-256-12 ..

27 ATGATGCTCCTCCTCGGCGGACACCCCTAGTCTGCGCGGTGG 76

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Align seg 1/1 to: US-08-328-256-12 from: 1 to: 496

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27 ATATGATGCTCTCTCCGCGCGGACACCTAGTCTGCTCCGCGG 76
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1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
77 CCATGAGGTGTGTCCGACCGCGAGGTGAAAAAATCTAAATCTCTC 126
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17 yProTPValLeuSerAlaAlaIaGlyGlyLysAsnLeuLysSerProG 34
34 InlySValGIuValAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
177 AGAGCGATAGCTCTCGGAATGTGACTTTTCATTCGATTCATAAA 226
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51 ArgSerAspGluSerValGIyAsnValThrPheserPheAspTyrGlnLy 67
227 A 227
67 s 67
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seq_name: /cgn2.6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-10

seq_documentation_block:

Sequence 10, Application US/08328256

Patent No. 5643749

GENERAL INFORMATION:

APPLICANT: REVEL, Michel

APPLICANT: ABRAMOVICH, Carolina

APPLICANT: RATOVIJSKI, Edward

TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS

TITLE OF INVENTION: PREPARATION AND USE

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/328,256

FILING DATE: 24-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 11,107,378

FILING DATE: 24-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: REVEL-13

REFERENCE/DOCKET NUMBER: 25,618

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-328-256-10

alignment_scores: Quality: 340.00 Length: 67

Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_1_229 x US-08-328-256-10 ..

Align seg 1/1 to: US-08-328-256-10 from: 1 to: 557

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27 ATGATGATGCTCTCTCCGCGCGGACACCTAGTCTGCTCCGCGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
77 CCATGAGGTGTGTCCGACCGCGAGGTGAAAAAATCTAAATCTCTC 126
|||||
17 yProTPValLeuSerAlaAlaIaGlyGlyLysAsnLeuLysSerProG 34
34 InlySValGIuValAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
177 AGAGCGATAGCTCTCGGAATGTGACTTTTCATTCGATTCATAAA 226
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51 ArgSerAspGluSerValGIyAsnValThrPheserPheAspTyrGlnLy 67
227 A 227
67 s 67
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seq_name: /cgn2.6/ptodata/1/1aa/5A_COMB.pep:US-08-471-454-2

seq_documentation_block:

Sequence 2, Application US/08471454

Patent No. 5731169

GENERAL INFORMATION:

APPLICANT: MOGENSEN, Knud E.

APPLICANT: UZE, Gilles

APPLICANT: LUTFALLA, Georges

APPLICANT: GRESSER, Ion

TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,454

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/900,642

FILING DATE: 15-JUN-1992

APPLICATION NUMBER: FR 89/13770

FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 960-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-454-2

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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Align seg 1/1 to: US-08-471-454-2 from: 1 to: 557

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27 ATGATGTCCTCTCTGCGCGCAGACCTAGTCCTGCGCGG 76
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1 MetMetValValLeuLeuGlyAlaThrThrLeuValAlaValAlG 17
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17 yProTrrValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
127 AAAAGTAGAGTCGACATCATAGATGACACTTATCTGAGGTG 176
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34 InLysValGluValAlaSpIleIleAspAspAsnPhelLeuArgTrpAsn 50
177 AGGAGCGATGAGTCGTGCGGGAATGTGACTTTTCATTCGATTATCAAAA 226
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51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrgInLys 67
227 A 227
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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-466-974-2

seq_documentation_block:

Sequence 2, Application US/08466974
Patent No. 5861258
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,974
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-974-2

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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Align seg 1/1 to: US-08-466-974-2 from: 1 to: 557

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77 CCATGGGTGTGTCGCCGCGCAGCGAGTGAATAAATCTAAATCTCC 126
|||||
17 yProTrrValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
127 AAAAGTAGAGTCGACATCATAGATGACACTTATCTGAGGTGGAAC 176
|||||
34 InLysValGluValAlaSpIleIleAspAspAsnPhelLeuArgTrpAsn 50
177 AGGAGCGATGAGTCGTGCGGGAATGTGACTTTTCATTCGATTATCAAAA 226
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51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrgInLys 67
227 A 227
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67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-471-453-2

seq_documentation_block:

Sequence 2, Application US/08471453
Patent No. 586153
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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: SOFTWARE: Patent In Release #1.0, Version #1.25
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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/471,453
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 536
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/900,642
: FILING DATE: 15-JUN-1992
: APPLICATION NUMBER: FR 89/13770
: FILING DATE: 20-OCT-1989
: ATTORNEY/AGENT INFORMATION:
:
: NAME: BYRNE, THOMAS E.
: REGISTRATION NUMBER: 32,205
: REFERENCE/DOCKET NUMBER: 960-7
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 816-4000
: TELEFAX: (703) 816-4100
:
: TELEX: 200797 NIXN UR
: INFORMATION FOR SEQ ID NO: 2:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 557 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: OS-08-471-453-2

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alignment_scores:
  Quality: 340.00
  Ratio: 5.075
  Percent Similarity: 100.000
  Length: 67
  Gaps: 0
  Percent Identity: 100.0000
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1 MeMeVValValLeuLeuLysValAlaThrThrLeuValLeuValAlaValG 17
77 CCCATGGGTGTTCCTCGCAGCCGAGTGGGAAAAATATAATCTCTC 136
17 yProTIPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
127 AAAAGTACAGGTGCAATCATAGATGACAACTTATCTCGAGTGGAC 176
34 InLysValGluValAlaSpIleIleIleAspAspAsnPhleIleLeuAlaGTrPAsn 50
177 AGAGAGGATGAGCTGCTGGGAATGTGACTTTTCATCGAATTCAAA 226
51 ArgSerAspLysSerValLysAsnValThrPheSerPheAspTrpGlnGly 67

227 A 227
67 s 67

seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-307-588-4

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seq_documentation_block:
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Patent No. 5919453

APPLICANT: BENOIT, Patrick
MEYER, Francois

APPLICANT: MAGUIRE, Deborah
PLAYEC: IVAN

APPLICANT: IVEI, MICHAEL G.
TITLE OF INVENTION: MONOCLONAL

TITLE OF INVENTION: INTERFERON

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835
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839
840
84

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO),
Copyright 1997 PatentIn, Inc.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992

ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids
TYPE: amino acid
TOPOLOGY: 1; near

MOLECULE TYPE: protein
8-307-588-4

alignment_scores:	
Quality:	340.00
Ratio:	5.075
Percent Similarity:	100.000
	Length: 67
	Gaps: 0
Percent Identity:	100.000

alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-307-588-4 . .

Align seg 1/1 to: US-08-307-588-4 from: 1 to: 557

27 ATATGTCCTCCTCCTGGGCGCCGACGACCCAGTGCCTGCGCCGTTGG 76
1 MetheValValIleuLeuLylalathrThrIleuValIleuValAlaValGl 17
77 CCATGGGCTTTCTCCGACCGCCAGTCGTGAAAAATCATTAATCTCTC 136
17 yProTrrValIleuSerAlaAlaAlaGlyGlyAsnIleuIlySerProG 34
127 AAAAGATGAGCTGCACATCATAGATGACAACTTATCTCTAGGTGAAC 176
34 InlyValAlGluValAspIleIleAspAspAspPheIleLeuAlaTrpAsn 50
177 AGGAGCAGTACGCTCTCGGAGATGTGACTTTTCATTCGATTTATCAAAA 226
51 ArgSerAspGluSerValAlGlyAsnValIlnrPheSerPheAspTrpGlnly 67
227 A 227
↓
67 s 67

name: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:PCT-US94-14277-3

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documentation_block:
sequence 3, Application PC/TUS9414277
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APPLICANT: Aguet, Michel
APPLICANT: Bohn1, Ruth

APPLICANT: Hemml, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-3

alignment_scores:
Quality: 112.00 Length: 39
Ratio: 3.613 Gaps: 0
Percent Similarity: 79.487 Percent Identity: 48.718

alignment_block:
US-09-240-675-1_COPY_1_229 x PCT-US94-14277-3 ..

Align seg 1/1 to: PCT-US94-14277-3 from: 1 to: 202

108 AAAATCTAAATCTCTCAAAAGTAGAGTGCATCATGATGACAA 157
:::||||| |:::||||| |:::||||| |:::||||| |
1 GUAAnbLulysProProGluAnbLleAsp**YrIlelleAspAspAs 17
158 CTTTCTCTGAGGTGGAACAGACGAGTCTGTCTGGGAATGTGACT 207
:::||||| |:::||||| |:::||||| |:::||||| |
17 nYrThrLeuLysTrpSerSerHisGlyGluSerMetGlySerValThrP 34
208 TTTCATGATATCA 224
||||| :::|||||:::
34 hSeSerAlaGluTrpArg 39

seq_name: /cgn2.6/ptodata/1/1aa/5B_COMB.pcp:US-08-469-412A-7

seq_documentation_block:
; Sequence 7, Application US/08469412A
; Patent No. 5856125
; GENERAL INFORMATION:
; APPLICANT: Mavrothalassitis, George J.
; APPLICANT: Blair, Donald G.
; APPLICANT: Fisher, Robert J.
; APPLICANT: Beal Jr., Gregory J.
; APPLICANT: Athanasiou, Meropi A.
; APPLICANT: Sgouras, Dionysios N.
; TITLE OF INVENTION: The ERF Genetic Locus and Its Products

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,412A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 015280-229000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/REV: Protein
LOCATION: 1..543
OTHER INFORMATION:
OTHER INFORMATION: (first 8 amino acids from first exon not included)
US-08-469-412A-7

alignment_scores:
Quality: 65.00 Length: 32
Ratio: 2.826 Gaps: 1
Percent Similarity: 71.875 Percent Identity: 43.750

alignment_block:
US-09-240-675-1_COPY_1_229/rev x US-08-469-412A-7 ..

Align seg 1/1 to: US-08-469-412A-7 from: 1 to: 543

108 TTTCACCTGCGGCTCGGAGACACACCCATGGGCCGCGGAGAGACT 59
||| :::||||| |:::||||| |:::||||| |:::||||| |
367 PheLysPheLysLeuGlnProProLeuGlyArgArgGlnArgAlaAl 383
58 AGGCTGCTCGCGCCAGAGAGA.....CGACCATCATCTGGGAGC 19
||:::||||| |:::||||| |:::||||| |:::||||| |
383 aGlyGluLysAlaProGlyGlyThrAspLysSerSerGlyGlySer 398

seq_name: /cgn2.6/ptodata/1/1aa/5B_COMB.pcp:US-08-317-310A-64

seq_documentation_block:
; Sequence 64, Application US/08317310A
; Patent No. 5858701
; GENERAL INFORMATION:
; APPLICANT: WHITE, Morris F.
; APPLICANT: SUN, Xiao Jian
; APPLICANT: PIERCE, Jacalyn H.
; TITLE OF INVENTION: THE IRS FAMILY OF GENES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston

STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,310A
FILING DATE: 03-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,865
REFERENCE/DOCKET NUMBER: JDP-022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 1321 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-317-310A-64

alignment_scores:
Quality: 63.50 Length: 72
Ratio: 1.984 Gaps: 2
Percent Similarity: 44.444 Percent Identity: 29.167

alignment_block:
US-09-240-675-1_COPY_1_229/rev x US-08-317-310A-64 ..

Align seg 1/1 to: US-08-317-310A-64 from: 1 to: 1321

124 GGAGATTAGATTTCACACCTCGCGGCGGCAACACCCAGGCGC 75
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1029 GYASPLEUTYRARGLEUPROGLASERALAATHRSERGLNGLYR 1045
74 CACGCGAGAGACTAGGTCGTCGCCGCCAGGA..... 40
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1045 OTHRALACYSERSETMET.SERSETGLUPROGLASPARSNGLYSPYR 1061
40 40
1062 ThrGIuMetAlaPheGLyValAlaAlaThrProProGIuPheValAl 1078
39 GGAGAGCATCATCTGGAGCC 18
1078 APROProLysPROGIuGLyAlaArgValAlaSerProThrSerGLyLeuL 1095
17 GCCGCGAGATCCCTG 4
::|||:|||||
1095 YSARGLEUSERLEU 1099

seq.name: /cgn2_6/ptodata/1/laa/5B_COMB.pep:US-08-683-743-4

seq_documentation_block:

Sequence 4, Application US/08683743
Patent No. 5843697
GENERAL INFORMATION:
APPLICANT: Pestka, Sidney
APPLICANT: Kolenko, Serguei
TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
TITLE OF INVENTION: CHAIN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor

CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,743
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
US-08-683-743-4

alignment_scores:
Quality: 61.50 Length: 54
Ratio: 1.922 Gaps: 1
Percent Similarity: 59.259 Percent Identity: 29.630

alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-683-743-4 ..

Align seg 1/1 to: US-08-683-743-4 from: 1 to: 325

81 TGGGTGTTCGCCGAGCGCGAGTGAATAATCTAAATCT..... 122
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
3 TRPserLeuGLysERTripLeuGLyGLyCysLeuLeuValSerAlaLeuGL 19
123CTCAAAAAGTAGAGTCGACATCATGACAACT 159
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
19 YMETValProProGIuSValArgMETAsnSerValAsnPheLysA 36
160 TTATCTCGAGGTGAGACAGCGATGAGTCTGCGGGAATGTGACTTT 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
36 snlLeuGLnTRPGLysERProAlaPheAlaLysGLyAsnLeuThrPhe 52
210 TCATTCGATTAT 221
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53 ThrAlaGLnTYR 56

seq.name: /cgn2_6/ptodata/1/laa/5A_COMB.pep:US-08-323-170B-2

seq_documentation_block:

Sequence 2, Application US/08323170B
Patent No. 5733772
GENERAL INFORMATION:
APPLICANT: Williamson, Kim C.
APPLICANT: Kaslow, David C.
TITLE OF INVENTION: Cloning and Expression of Plasmodium
TITLE OF INVENTION: falciParum Transmission-Blocking Target Antigen, Pf5230
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco

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STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,170B
FILING DATE: 13-OCT-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010,409
FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ouline, Jonathan A.
REGISTRATION NUMBER: P-41,261
REFERENCE/DOCKET NUMBER: 015280-113100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-323-170B-2
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alignment_scores:
Quality: 59.00      Length: 51
Ratio: 1.844        Gaps: 3
Percent Similarity: 62.745      Percent Identity: 37.255
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alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-323-170B-2
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Align seg 1/1 to: US-08-323-170B-2 from: 1 to: 3135
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90 TCCGACGCCGAGGTGA.....AAAAATCTAAATCTCTCA 127
||||| ||||| ||||| |||||
787 serglaspilleglylileleupheprolysasnileysstrpth 803
128 AAAAGTACGATCGACATGATGACACTTATCTGTGAGGAGCA 177
||||| ||||| ||||| |||||
803 rcyspheglu...glumetileprotyrAsnLysgluileysstrpAsnL 819
178 GGAGCATGAGCTGTGCGGAAAT...GTGACTTTTCATTCGATTATCAA 224
||||| ||||| ||||| |||||
819 ysgluAsnLysSerleuclYasnleuValaAsnSerValValtyrAsn 835
225 AAA 227
|||
836 Lys 836
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seq_name: /cgn2_6/ptodata/1/laa/5A_COMB.pep:US-08-469-427A-7
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seq_documentation_block:
; Sequence 7, Application US/08469427A
; Patent No. 5607918
; GENERAL INFORMATION:
; APPLICANT: Eriksson, Ulf
; APPLICANT: Olofsson, Birgitta
; APPLICANT: Alltalo, Kari
; APPLICANT: Pajusola, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
```

```
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,427A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 41979cp2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-469-427A-7
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alignment_scores:
Quality: 58.00      Length: 70
Ratio: 1.611        Gaps: 2
Percent Similarity: 51.429      Percent Identity: 24.286
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alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-469-427A-7
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Align seg 1/1 to: US-08-469-427A-7 from: 1 to: 195
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23 CCGATGATGTCGT.....CCTCTGGCGCGAGACCCCTGTGTC 63
||||| ||||| ||||| |||||
83 ProAspAspIleuGlucysValProthnglyglInhisglInvalArgme 99
64 TCGGCGCCGCGGCGCCATGGGTGTGTCGCGACGCCGAGGTGGA 113
||||| ||||| ||||| |||||
99 tglInValProglYProMetclYglInleuMetlleglInYrProSerS 116
114 CTAATCTCTCTCAAAAAGTAGAGTGCATCATGATGACACTTAT 163
||||| ||||| ||||| |||||
116 erglInleuGlYgluMetSerleuGlInHisSerGlncysglYsArg 132
164 CCGAGGTGGAACAGAG.....CGATGATCTG 192
||||| ||||| ||||| |||||
133 ProLysLysLysgluSerAlaValLysProAspSerProArgtlleuclY 149
193 TCGGGAATG 202
|||
149 sProProCys 152
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seq_name: /cgn2_6/ptodata/1/laa/5B_COMB.pep:US-08-609-443B-7
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seq_documentation_block:
; Sequence 7, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, ULF
; APPLICANT: OLOFSSON, Birgitta
```

APPLICANT: ALITALO, Karl
 APPLICANT: PAJUSOLA, Katri
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
 TITLE OF INVENTION: DNA CODING THEREFOR
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
 STREET: 1200 G Street, N.W., Suite 700
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/609,443B
 FILING DATE: 01-MAR-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/397,651
 FILING DATE: 01-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/469,427
 FILING DATE: 06-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/569,063
 FILING DATE: 06-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: EVANS, Joseph D
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 1064/41979CP4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 195 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 TISSUE TYPE: adult mouse heart
 US-08-609-443B-7

alignment_scores:
 Quality: 58.00 Length: 70
 Ratio: 1.611 Gaps: 2
 Percent Similarity: 51.429 Percent Identity: 24.286

alignment_block:

US-09-240-675-1_COPY_1_229 x US-08-609-443B-7 ..

Align seg 1/1 to: US-08-609-443B-7 from: 1 to: 195

23 CCAGATGATGCTCT.....CCTCTGGCGCGCGACGCCCTAGTGC 63
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 83 ProAspAspIlyLeuGIucysValProThrgIyGlnHisGlnValArgme 99
 64 TCCTCGCGCGTGGCCATGGCTGTTCGCCGACGCCGAGGTGAAAAAT 113

 99 tGlnValProGIyPrometGIyGlnIleuMetIleGlnIlyProserS 116
 114 CTAATACTCTCTCAAAAAGTAGAGTGCAGACATCATAGATGACAATTAT 163
 |||||
 116 erGlnLeuGIyGlnMetSerLeuGIuGlnHisSerGlnGlnGlnGlnGln 132
 164 CTTGAGGTGAGACAGGAG.....CGATGAGTCTG 192

|||||
 133 ProLysLysLysGlnSerAlaValLysProAspSerProArgIleLeuGly 149
 193 TCGGGAATGT 202
 |||||
 149 sProProCys 152

Mon Jun 5 12:51:10 2000

us-09-240-675-1_copy_1_229.modif.rai


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C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S27387; S33770
R:Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
A:Title: Specific antiviral activities of the human alpha interferons are determined at
A:Reference number: S27387; MUID:93076908
A:Accession: S27387
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-560 <MOU>
A:Cross-references: EMBL:X68443; NID:9431; PIDN:CAA48484.1; PID:9432
R:Experimental source: MDBK cells
R:Lim, J.K.; Langer, J.A.
Biochim. Biophys. Acta 1173, 314-349, 1993
A:Title: Cloning and characterization of a bovine alpha interferon receptor.
A:Reference number: S33770; MUID:93305725
A:Accession: S33770
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-421, 'V', 423-560 <LIM>
A:Cross-references: EMBL:L06320; NID:9163187; PIDN:AAA02571.1; PID:9163188
A:Experimental source: Lung
C:Keywords: antiviral; cytokine receptor; transmembrane protein
F:1.24/Domain: signal sequence #status predicted <SIG>
F:2.560/Product: Interferon alpha receptor type 1 #status predicted <MAT>

alignment_scores:
Quality: 209.00 Length: 65
Ratio: 3.800 Gaps: 2
Percent Similarity: 84.615 Percent Identity: 69.231

alignment_block:
US-09-240-675-1_COPY_1_229 x S27387
Align seg 1/1 to: S27387 from: 1 to: 560

30 ATGGTCGCTCCTCGGCGGCGAGCAGCCTAGTGTCTGCGCGCCGCGGCC 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MetLeuAlaLeuLeuGlyAlaIleThrIleuMetLeuValAla...GlyAr 16
80 ATGGGTGTTGTCGCCAGCCGCGAGGTGGAATAATCTAAATCTCTCTCAA 129
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
16 gtrPvalLeuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA 32
130 AAGTAGAGTCGACATCATAGACAACTTATCTGAGGTGGAACAGG 179
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
32 snValGluIleHisIleIleAspAsnPhenLeuLysTirpAsnSer 48
180 AGCGATGAGTGTCTGCGGAATGTGACTTTTCATTCGATTATCAA 224
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
49 SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGln 63

seq_name: p1r2:AA5283

seq_documentation_block:
Interferon alpha/beta receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429
R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudmon, D.; Mogensen, K.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
A:Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homospere
A:Reference number: A45283; MUID:92262522
A:Accession: A45283
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-550 <UZE>
A:Cross-references: GB:M89641; NID:9194111; PIDN:AAA37890.1; PID:9194112
A:Note: sequence extracted from NCBI backbone (NCBIN:102354, NCBI:P:102357)
R:Lutfalla, G.; Uze, G.
Gene 148, 343-346, 1994

A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-1
A:Reference number: I48423; MUID:95047447
A:Accession: I48423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 118-125 <RES>
A:Cross-references: EMBL:U06237; NID:9497103; PIDN:AAA65003.1; PID:9755810
A:Accession: I48424
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 127-224 <RE2>
A:Cross-references: EMBL:U06238; NID:9497104; PIDN:AA01749.1; PID:9755811
A:Accession: I48425
A:Molecule type: DNA
A:Residues: 243-264 <RE3>
A:Cross-references: EMBL:U06239; NID:9497106; PIDN:AAA65004.1; PID:97510261
A:Accession: I48426
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 365-375 <RE4>
A:Cross-references: EMBL:U06240; NID:9497108; PIDN:AAA65005.1; PID:97510262
A:Accession: I48427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 397-424 <RE5>
A:Cross-references: EMBL:U06241; NID:9497110; PIDN:AAA65006.1; PID:9755812
A:Accession: I48428
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 426-445 <RE6>
A:Cross-references: EMBL:U06242; NID:9497112; PIDN:AAA65007.1; PID:9755813
A:Accession: I48429
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 473-590 <RE7>
A:Cross-references: EMBL:U06244; NID:9497114; PIDN:AAA65008.1; PID:97510265
C:Genetics:
A:Gene: IFNAR
A:Introns: 177/3; 331/1
C:Keywords: cytokine receptor; transmembrane protein

alignment_scores:
Quality: 198.00 Length: 65
Ratio: 3.536 Gaps: 0
Percent Similarity: 86.154 Percent Identity: 55.385

alignment_block:
US-09-240-675-1_COPY_1_229 x A45283
Align seg 1/1 to: A45283 from: 1 to: 590

30 ATGGTCGCTCCTCGGCGGCGAGCAGCCTAGTGTCTGCGCGCCGCGGCC 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MetLeuAlaValValGlyAlaAlaIleLeuValIleValAlaGlyAla 17
80 ATGGGTGTTGTCGCCAGCCGCGAGGTGGAATAATCTAAATCTCTCTCAA 129
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 oTrpValLeuProSerAlaIleGlyGluAlaAsnLeuLysProProGluA 34
130 AAGTAGAGTCGACATCATAGACAACTTATCTGAGGTGGAACAGG 179
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 snIleAspValTyrIleIleAspAsnTyrThrLeuLysTirpSerSer 50
180 AGCGATGAGTGTCTGCGGAATGTGACTTTTCATTCGATTATCAA 224
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 HisGlyGluSerMetGlySerValThrPheSerAlaGluTyrArg 65

seq_name: p1r2:SI13141

seq_documentation_block:
hypothetical protein (ribosomal RNA repeat region) - Giardia lamblia
```


seq_name: pir2:S42718

seq_documentation_block:

nuclear pore complex protein nup153 - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S42718; S37477
R:McMorrow, I.; Bastos, R.; Horton, H.; Burke, B.
Biochim. Biophys. Acta 1217, 219-223, 1994
A:Title: Sequence analysis of a cDNA encoding a human nuclear pore complex protein, hnup153
A:Reference number: S42718; MUID:94154002
A:Accession: S42718
A:Molecule type: mRNA
A:Residues: 1-1475 <MCM>
A:Cross-references: EMBL:Z25535; NID:g406224; PIDN:CAAB0982.1; PID:g406225

alignment_scores:

Quality:	69.00	Length:	77
Ratio:	1.683	Gaps:	3
Percent Similarity:	53.247	Percent Identity:	33.766

alignment_block:

US-09-240-675-1_COPY_1_229/rev x S42718 ..

Align seg 1/1 to: S42718 from: 1 to: 1475

```
193 ACAGCTCATTCGCTCTCCACCCAGATTAAGTTCATCATATGAT 144
|||||
1248 ThSerGlnSerLeuLeuPheSerGlnAspSerLysLeuAlaThrThrSer 1264
143 GTTCGACCTTACTTTTGGAGATTTTGAATTTTCCACCTGCGGCTG 94
|||||
1264 rSerThrGlyThrAlaValThrProPheValPheGlyProGlyAlaSerS 1281
93 CGGACACACAC.....CATGGCCCGGCGGCGGACG 62
|||||
1281 eRAsnAsnThrThrThrSerGlyPheGlyAlaThrThrThrThrSer 1297
61 .....ACTAGGCTGCTCGGCGGCGGACG 42
|||||
1298 SerSerAlaGlySerSerPheValPheGlyThr.GlyProSerAlaProS 1314
41 GAGGAGCAGCATCATCTGGAGCGGCGGCGC 13
|||||
1314 eRAlaSerProAlaPheGlyAlaAsnGln 1323
```

seq_name: pir2:T26391

seq_documentation_block:

hypothetical protein Y105C5B.o - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T26391
R:McMurray, A.
Submitted to the EMBL Data Library, September 1999
A:Reference number: Z20208
A:Accession: T26391
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-194 <WIL>
A:Cross-references: EMBL:AL110479; NID:e1542153; PIDN:CAB54363.1; CESP:Y105C5B.o
A:Experimental source: clone Y105C5B
C:Genetics:
A:Gene: CESP:Y105C5B.o
A:introns: 13/1: 56/3: 155/2

alignment_scores:

Quality:	68.50	Length:	56
Ratio:	1.756	Gaps:	2
Percent Similarity:	69.643	Percent Identity:	32.143

alignment_block:

US-09-240-675-1_COPY_1_229 x T26391 ..

Align seg 1/1 to: T26391 from: 1 to: 194

```
36 GTCTCTCTGGGCGGAGACCTAGTGTCTGCTCCGCTGGGCGGCGGATGGT 85
|||||
1 MetLeuLeuArgAlaAlaLeuLeuIlePheIleSer...AlaProTyrPva 16
86 GTTCTCCGACCGGCGGATGGGAAAAATCTAAATCTTCTCTCAAAAAGTAG 135
|||||
16 IleuSerValThrValLysArgAsnMetThrGlyTyrGlnLysIleH 33
136 AGGTGACATCATATGATGACAACTTATCTGAGGTGAGACGAGCGAT 185
|||||
33 IStIleAsnLeuLeu.....AsnGlyIleArgGlnLysAsnAlaIleAsp 47
186 GAGTCTGTGGGGAATGTG 203
|||||
48 GluGlnValAlaAlaAsnMet 53
```

seq_name: pir2:J00405

seq_documentation_block:

hypothetical 119.5K protein (uvra region) - Micrococcus luteus
N:Alternate names: ORF 1 protein
C:Species: Micrococcus luteus, Micrococcus lysodeikticus
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1993
R:Shiota, S.; Nakayama, H.
Mol. Gen. Genet. 217, 332-340, 1989
A:Title: Micrococcus luteus homolog of the Escherichia coli uvra gene: identification
A:Reference number: J00405
A:Accession: J00405
A:Molecule type: DNA
A:Residues: 1-1106 <SHI>
A:Cross-references: EMBL:X15867
A:Note: all the codons between two in-frame stop codons are translated; the translat:
A:Note: the gene encoding this protein overlaps uvra gene

alignment_scores:

Quality:	67.50	Length:	78
Ratio:	1.875	Gaps:	3
Percent Similarity:	46.154	Percent Identity:	30.769

alignment_block:

US-09-240-675-1_COPY_1_229/rev x J00405 ..

Align seg 1/1 to: J00405 from: 1 to: 1106

```
204 TCACATTCGCCGACGACATCGCTCTGTCACACCTCAGATTAAGTTG 155
|||||
36 SerProInnGlyGlnThrProValSerCysPro..... 46
154 TCATCTATGATGTGCGACCTTACTTTTGGAGAGATTTTACATTTTTC 105
|||||
47 .....CysProPheLeuCysTyrProArgAlaGlnGlnLeuLeuH 60
104 ACCTCGGCTG.....CGACAAACCCATGGGC 76
|||||
60 IShIAsrGlnLeuLeuArgArgArgGlyProArgArgArgProArgLeuArg 76
75 CCAGCGCAGCAGCAGCTAGGTGCGGCGGCGCA.....GGAGAGC 35
|||||
77 ProArgArgArgAlaLeuGlyArgAlaGlyProHisArgArgProGlyArg 93
34 ACCATCATCTGGGAGCGCGCCAGATCCCTGAC 1
|||||
93 gProArgAlaGlnProGlnGlyArgGlyCysGln 104
```

seq_name: pir2:T08930


```

117 rHsValGluProThrLeuArgaspAlaProSerLeuLeuSerLeuAla 133
78 CCATGG.....GTGTGTCCGCA.....95
134 ProTrpTyrGlyLysLysHsArgaspAsnThrLeuSerMetLysArgPh 150
96 .....GCCCGAGGTGGAAAAAATCTAAATCTC 123
150 eHrAsnGlyArgGlyPheTrpCysLeuGlyLysAlaAlaLysAsn 167
124 CTCMAAAGTAGAGTCGACATCATAGATGACAACTTATCTGAGAGTG 173
167 yArgGluLysSerValAspValValGlyTyrAspGluLeuAlaAlaPh 183
174 MACAGAGCGCATGATCTGCGGAATGACCTTTTCATTCAT 218
184 AspAlaAspLeuGluLysGluGlySerProThrPheLeuGlyAsp 198

```

seq_name: p1r2:A45731

seq_documentation_block:

```

comC: alpha protein - phage T4
N: Alternate names: gp comC alpha
C: Species: phage T4
A: Note: host Escherichia coli
C: Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Oct-1999
C: Accession: A45731
R: Sanson, B.; Uzan, M.
J. Bacteriol. 174, 6539-6547, 1992
A: Title: Sequence and characterization of the bacteriophage T4 comCalpha gene product, a
A: Reference number: A45731; MUID:93015705
A: Accession: A45731
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-141 <SAN>
A: Cross-references: GB:M89919; NID:9215829; PIDN:AAA32485.1; PID:9215832
C: Genetics:
A: Gene: comC alpha
A: Map position: 5.848-6.274
C: Superfamily: phage T4 comC-alpha protein
C: Keywords: transcription regulation

```

alignment_scores:

```

Quality: 62.50 Length: 50
Ratio: 2.155 Gaps: 3
Percent Similarity: 58.000 Percent Identity: 34.000

```

alignment_block:

US-09-240-675-1_COPY1_1_229 x A45731 ..

Align seg 1/1 to: A45731 from: 1 to: 141

```

42 CTGGGCGCGAGCCCTAGTCTGCTGCGCGCCGATGGTGTGTC 91
||||| ||| :|||||:|||||:
49 LeuGlyArgProThrLysIleMetThrSerIleGly.....ValLeuLys 63
92 CGCAGCCGCGAGGTGGAAAAATCTAAATCTCTCAAAAAAGTAGAGTCG 141
: :|||||:|||||:
63 sArgCysAlaGlyGly.....A 69
142 ACATCATAGATGACACTTATCTGATGAGGAGACAGAGAGATGACTCT 191
|||||:|||||:|||||:
69 sPheLeuAspGluAsnPhelle.....TTrpLeuSerThrAsnGluAla 83

```

seq_name: p1r2:B42701

seq_documentation_block:

```

PR264 protein - chicken
C: Species: Gallus gallus (chicken)
C: Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 24-Sep-1999
C: Accession: B42701; S17327

```

```

Rivellard, M.; Sureau, A.; Soret, J.; Martinerie, C.; Perbal, B.
Proc. Natl. Acad. Sci. U.S.A. 89, 2511-2515, 1992
A: Title: A potential splicing factor is encoded by the opposite strand of the trans-
A: Reference number: A42701; MUID:92212859
A: Accession: B42701
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-221 <VEL>
A: Cross-references: EMBL:X62446; NID:963751; PIDN:CAA44306.1; PID:963752
C: Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleopri
F:15-82/Domain: ribonucleoprotein repeat homology <RRM2>

```

alignment_scores:

```

Quality: 62.50 Length: 55
Ratio: 2.083 Gaps: 3
Percent Similarity: 54.345 Percent Identity: 38.182

```

alignment_block:

US-09-240-675-1_COPY1_1_229 x B42701 ...

Align seg 1/1 to: B42701 from: 1 to: 221

```

5 AGGATCTGCGG...CGGCTCCAGATGATGTCGTCCT.....43
|||||:|||||:
83 ArgGluLeuArgValGlnMetAlaArgTyrGlyArgProAspSerH1 99
44 ....GGCGCGCGACCTAGTCTGCTGCGCGCGCGCCATGGTGTG 89
99 sHsSerArgArgGlyProProProArgArgArgTyrGlySerGlyTyrG 116
90 TCGCG.....AGCGCAGGTGGAAAAATCTAAATCTCCCA 127
116 lYArgArgSerArgSerProArgArgArgArgArgSerArgSerArg 132
128 AAAAGTAGAGTCGA 142
133 ArgSerArgSerArg 137

```

seq_name: p1r2:T02841

seq_documentation_block:

```

probable membrane protein MTCC - Leishmania major
C: Species: Leishmania major
C: Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 10-Dec-1999
C: Accession: T02841
R: Myler, P.J.
submitted to the EMBL Data Library, May 1998
A: Description: The nucleotide sequence of Leishmania major Friedlin chromosome 1.
A: Reference number: 214740
A: Accession: T02841
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-326 <MYL>
A: Cross-references: EMBL:AE001274; NID:93264850; PID:91617564
C: Genetics:
A: Gene: MTCC
A: Map position: 1
C: Superfamily: Saccharomyces probable membrane protein YOR271c

```

alignment_scores:

```

Quality: 62.50 Length: 66
Ratio: 1.645 Gaps: 3
Percent Similarity: 57.576 Percent Identity: 30.303

```

alignment_block:

US-09-240-675-1_COPY1_1_229 x T02841 ..

Align seg 1/1 to: T02841 from: 1 to: 326

```

12 TGGCGGCGCTCCAGATGATGTCGTCCTCCTG.....CG 46
|||||:|||||:

```


OM of: US-09-240-675-1_COPY_1_229 to: SwissProt_38.* out-format: pfs

Date: Jun 1, 2000 12:37 AM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=frame+2zp.model -DEV=xlp
-O=/gen2_1/USPRO.spool/US09240675/runat_30052000.16413.24686/app-query.fasta.1
-DB=SwissProt_38 -OFT=fastan -SUFFIX=modif.rsp -GAPOP=12.000
-GAPERT=0.000 -MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -GAPERT=0.050 -XGAPOP=10.000 -XGAPERT=0.500
-GAPOP=6.000 -GAPERT=7.000 -YGAPOP=10.000 -YGAPERT=0.500
-DELDP=6.000 -DELXT=7.000 -STARF=1 -MATRIX=blonsum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR_SCORE=pcr
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US09240675 -NCPU=6 -ICPU=3 -NO_XLPRY -MATT
-THREADS=1

Search information block:

Query: US-09-240-675-1_COPY_1_229
Query length: 229
Database: SwissProt_38.*
Database sequences: 83857
Database length: 30454973
Search time (sec): 45.030000

score_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
SwissProt_38:INRI_HUMAN	340.00	695.87	6.5e-32	557	P17181 homo sapiens (human)
SwissProt_38:INRI_BOVIN	209.00	421.06	1.3e-16	560	Q04790 bos taurus (bovine)
SwissProt_38:INRI_SHEEP	204.00	410.57	5.0e-15	560	Q28589 ovis aries (sheep)
SwissProt_38:INRI_MOUSE	198.00	397.55	2.5e-15	590	P33896 mus musculus (mouse)
SwissProt_38:INRI_HUMAN	69.00	119.30	3.20	1475	P45790 homo sapiens (human)
SwissProt_38:IDDP_RATRA	68.00	121.79	4.02	854	Q34971 ratthayabacter ratthay
SwissProt_38:IF3A_HUMAN	67.00	115.66	5.45	1382	Q14152 homo sapiens (human)
SwissProt_38:IF3A_HUMAN	65.50	121.32	7.54	483	Q70569 homo sapiens (human)
SwissProt_38:IF3A_MOUSE	65.00	119.17	8.71	551	P70459 mus musculus (mouse)
SwissProt_38:IF3A_MOUSE	63.50	122.58	12.29	252	P24728 autographa californica
SwissProt_38:IF3A_MOUSE	63.50	108.69	13.93	1321	P81122 mus musculus (mouse)
SwissProt_38:IF3A_MOUSE	63.00	107.50	15.95	1344	P23116 mus musculus (mouse)
SwissProt_38:IF3A_MOUSE	62.50	125.35	15.40	141	Q01438 bacteriophage t4. com
SwissProt_38:IF3A_MOUSE	62.50	121.59	15.93	221	P30352 gallus gallus (chick)
SwissProt_38:IF3A_MOUSE	62.00	110.52	19.94	730	P06300 pseudomonas aerugin
SwissProt_38:IF3A_MOUSE	61.50	119.49	20.84	221	Q01130 homo sapiens (human)
SwissProt_38:IF3A_MOUSE	61.50	116.26	21.46	325	Q08334 homo sapiens (human)
SwissProt_38:IF3A_MOUSE	61.50	111.40	22.41	580	P13365 saccharomyces cerev
SwissProt_38:IF3A_MOUSE	61.50	106.98	23.32	982	P13365 saccharomyces cerev
SwissProt_38:IF3A_MOUSE	60.50	113.80	28.17	339	P72404 streptomyces coelic
SwissProt_38:IF3A_MOUSE	60.00	111.05	32.72	415	P37745 streptococcus coli
SwissProt_38:IF3A_MOUSE	60.00	107.76	33.70	615	P16362 bacillus p33 (therm
SwissProt_38:IF3A_MOUSE	60.00	96.26	37.57	2424	P27884 oryctolagus cunicul
SwissProt_38:IF3A_MOUSE	59.00	118.07	39.45	140	P23152 homo sapiens (human)
SwissProt_38:IF3A_MOUSE	59.00	116.75	39.93	164	P23152 homo sapiens (human)
SwissProt_38:IF3A_MOUSE	59.00	108.45	43.02	441	Q080910 human papillomavir
SwissProt_38:IF3A_MOUSE	59.00	107.47	43.40	496	P31360 homo sapiens (human)
SwissProt_38:IF3A_MOUSE	59.00	94.23	48.88	2405	Q33610 chlamydomonas reinh
SwissProt_38:IF3A_MOUSE	59.00	92.01	49.87	3135	Q08372 plasmidium falci
SwissProt_38:IF3A_MOUSE	58.50	98.87	53.13	1220	Q14562 homo sapiens (human)
SwissProt_38:IF3A_MOUSE	58.00	113.96	52.57	178	Q57136 methanococcus jann
SwissProt_38:IF3A_MOUSE	58.00	111.46	53.77	247	P19664 lotus tetragonolob
SwissProt_38:IF3A_MOUSE	58.00	106.61	55.16	337	P15893 spiroplasma virus
SwissProt_38:IF3A_MOUSE	58.00	107.47	55.73	386	P20599 triticum aestivum (w
SwissProt_38:IF3A_MOUSE	58.00	106.47	56.24	435	P22533 brassica oleracea var
SwissProt_38:IF3A_MOUSE	58.00	106.22	56.36	448	P46936 gallus gallus (chick
SwissProt_38:IF3A_MOUSE	58.00	106.11	56.42	454	Q080903 human papillomavir
SwissProt_38:IF3A_MOUSE	58.00	105.75	56.60	474	Q53305 mycobacterium tuberc
SwissProt_38:IF3A_MOUSE	58.00	103.19	57.92	643	P06440 vaccinia virus (str
SwissProt_38:IF3A_MOUSE	58.00	96.40	61.56	1446	P133479 pseudorabies virus
SwissProt_38:IF3A_MOUSE	58.00	96.31	61.61	1461	P11675 pseudorabies virus

SwissProt_38:YAO2_SCHPO + 57.50 110.41 61.51 240 | Q08675 schizosaccharomy
SwissProt_38:SRA_MOUSE + 57.50 109.03 62.28 283 | Q06701 mus musculus (mo
SwissProt_38:MMS3_MYCTU + 57.50 108.57 62.54 299 | Q10390 mycobacterium tu
SwissProt_38:TAP_DROME + 57.50 106.17 63.90 398 | Q16867 drosophila melano

seq.name: SwissProt_38:INRI_HUMAN

seq-documentation_block:

ID	INRI_HUMAN	STANDARD:	PRT:	557 AA.
AC	P17181			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	15-FEB-2000 (Rel. 39, Last annotation update)			
DE	INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).			
GN	IFNARI OR IFNAR.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Homnidae; Homo.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 90124632.			
RA	Uze G., Lutfalla G., Gresser I.;			
RT	"Genetic transfer of a functional human interferon alpha receptor			
RL	into mouse cells: cloning and expression of its cDNA.";			
RL	Cell 60:225-234 (1990).			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 92129376.			
RA	Lutfalla G., Gardiner K., Proudman D., Vielh E., Uze G.;			
RT	"The structure of the human interferon alpha/beta receptor gene.";			
RL	J Biol. Chem. 267:2802-2809 (1992).			
RN	(3)			
RP	PHOSPHORYLATION BY TYR2.			
RX	MEDLINE: 95059042.			
RA	Colaninici O., Yan H., Domanski P., Handa R., Smalley D.,			
RT	Mullerman J., Witte M., Krishnan K., Krolewski J.;			
RL	Direct binding to and tyrosine phosphorylation of the alpha subunit			
RL	of the type I interferon receptor by p135tyk2 tyrosine kinase.";			
RL	Mol. Cell. Biol. 14:8133-8142 (1994).			
CC	- FUNCTION: RECEPTOR FOR INTERFERON ALPHA AND BETA. BINDING TO TYPE			
CC	I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS			
CC	INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-			
CC	SUBUNIT THEMSELVES.			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND			
CC	EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.			
CC	- PTM: PHOSPHORYLATION ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.			
CC	- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.			
CC	- THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: J03171; AAA52730.1; -			
DR	EMBL: X60459; CAA42992.1; -			
DR	PIR: A32694; A32694.			
DR	PIR: S17112; S17112.			
DR	MIM: 107450; -			
KW	Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;			
KW	Phosphorylation.			
FT	SIGNAL	1	27	POTENTIAL.
FT	CHAIN	28	557	INTERFERON-ALPHA/BETA RECEPTOR ALPHA
FT	DOMAIN	28	436	CHAIN.
FT	DOMAIN	437	457	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	458	557	POTENTIAL.
FT	DISULFID	79	87	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	199	220	BY SIMILARITY.

KW Receptor: Transmembrane: Glycoprotein: Signal.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 590 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 FT
 FT DOMAIN 27 429 CHAIN.
 FT TRANSMEM 430 449 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 450 590 POTENTIAL.
 FT DISULFID 78 86 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 199 220 BY SIMILARITY.
 FT CARBOHYD 43 43 POTENTIAL.
 FT CARBOHYD 109 109 POTENTIAL.
 FT CARBOHYD 181 181 POTENTIAL.
 FT CARBOHYD 214 214 POTENTIAL.
 FT CARBOHYD 314 314 POTENTIAL.
 FT CARBOHYD 370 370 POTENTIAL.
 FT CARBOHYD 409 409 POTENTIAL.
 FT CARBOHYD 413 413 POTENTIAL.
 SQ SEQUENCE 590 AA; 65776 MW; 7EC6DF370185D3A CRC64;

alignment_scores:
 Quality: 198.00 Length: 65
 Ratio: 3.536 Gaps: 0
 Percent Similarity: 86.154 Percent Identity: 55.385

alignment_block:

US-09-240-675-1_COPY_1_229 x INR1_MOUSE ..

Align seg 1/1 to: INR1_MOUSE from: 1 to: 590

```

30 ATGTCGTCCTCTGCGCGGAGACCTAGTCGTCGCGCGGCGCC 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MetLeuAlaValAlaValAlaAlaAlaValAlaAlaGlyAlaLeu 17
80 ANGCGTGTGTCGCGAGCCGAGGTGGAATAATCTAAATCTCTCAA 129
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 CrrpAlleupProserAlaAlaGlyGlyAlaLeuLysProGluAla 34
130 AAGTAGAGTCGACATGACATGACATCTTATCTGAGGTGAACAGG 179
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 snilespAllyrIlelleaspAspAspTyrThrLeuLysTrpSer 50
180 AGCGATGCTGTCGGAATGCTATTCATTCGATTATCA 224
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 H1SGlyGlySerMetClySerValThrPheSerAlaGlyTyrArg 65

```

seq_name: SwissProt_38:N153_HUMAN

seq_documentation_block:

ID N153_HUMAN STANDARD; PRT; 1475 AA.
 AC P49790;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUP153).
 GN NUP153.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RX MEDLINE; 94154002.
 RA McMorris I., Bastos R., Horton H., Burke B.;
 RT "Sequence analysis of a cDNA encoding a human nuclear pore complex protein, hnup153.";
 RL Biochem. Biophys. Acta 1217:219-223(1994).
 CC -1- FUNCTION: POSSIBLE DNA-BINDING SUBUNIT OF THE NUCLEAR PORE COMPLEX (NPC). THE REPEAT-CONTAINING DOMAIN MAY BE INVOLVED IN ANCHORING COMPONENTS OF THE PORE COMPLEX TO THE PORE MEMBRANE.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX. LOCATED TO THE TERMINAL RING STRUCTURE OF THE NUCLEOPLASMIC CAGE.
 CC -1- DOMAIN: CONTAINS X-F-X-F-G REPEATS.

CC -1- SIMILARITY: THE REPEAT REGION COMPOSED OF PENTAPEPTIDE REPEATS
 CC SEPARATED BY SER/THR-RICH DOMAINS IS SIMILAR TO THAT OF YEAST
 CC NUP1, NSP1, POM 121 AND MAMMALIAN P62.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: Z25535; CA80982.1; -
 DR MIM: 603948; -
 DR PIR: P00061; zf-RanBP; 4.
 KW Nuclear protein; Transport; Repeat; Zinc-finger; DNA-binding.
 FT DOMAIN 4 14 GLY-RICH.
 FT DOMAIN 443 447 POLY-GLY.
 FT ZN_FING 662 681 C4-TYPE.
 FT ZN_FING 726 745 C4-TYPE.
 FT ZN_FING 797 816 C4-TYPE.
 FT ZN_FING 855 874 C4-TYPE.
 SQ SEQUENCE 1475 AA; 153889 MW; 3CB415A6909DF80E CRC64;

alignment_scores:
 Quality: 69.00 Length: 77
 Ratio: 1.683 Gaps: 3
 Percent Similarity: 53.247 Percent Identity: 33.766

alignment_block:

US-09-240-675-1_COPY_1_229/rev x N153_HUMAN ..

Align seg 1/1 to: N153_HUMAN from: 1 to: 1475

```

193 ACAGATCATGCTCTCTGTCACCTGAGTAAGTGTCTATGAT 144
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1248 ThrSerGlnSerLeuLeuPheSerGlnAspSerLysLeuAlaThrThr 1264
143 CTCGACCTCTACTTTTTCAGAGATTTTATGATTTTTCACCTCGGCTG 94
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1264 rSerThrGlyThrAlaValAlaThrProPheValPheGlyProGlyAlaSer 1281
93 CGGACCAACACC.....CATGGCCACGCGGACGAGC 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1281 eRasAsnThrThrThrSerGlyPheGlyAlaThrThrThrSer 1297
61 .....ACTAGGTCGTCGCGCCGAG 42
1298 SerSerAlaGlySerSerPheValPheGlyThrGlyProSerAlaPro 1314
41 GAGGACGACCATCATCTGGAGCGCGCCG 13
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1314 eAlaSerProAlaPheGlyAlaAsnGln 1323

```

seq_name: SwissProt_38:KDPD_RATRA

seq_documentation_block:

ID KDPD_RATRA STANDARD; PRT; 854 AA.
 AC O34971;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE SENSOR PROTEIN KDPD (EC 2.7.3.-).
 GN KDPD.
 OS Rathayibacter rathayi (Corynebacterium rathayi).
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Micrococciaceae; Microbacteriaceae; Rathayibacter.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-25;
 RA Labadie J.C.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM KDPD/KDPE
CC INVOLVED IN THE REGULATION OF THE KDP OPERON. KDPD MAY FUNCTION
CC AS A MEMBRANE-ASSOCIATED PROTEIN KINASE THAT PHOSPHORYLATES KDPE
CC IN RESPONSE TO ENVIRONMENTAL SIGNALS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC -1- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
CC KINASES.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AJ002069; CAA05169.1; -
CC DR EMBL: AF030293; AAB84261.1; -
CC DR PFM: PFM0512; signal; 1.
CC KW Sensory transduction; transferase; kinase; phosphorylation;
CC Transmembrane.
CC FT TRANSMEM 35 55 POTENTIAL.
CC FT TRANSMEM 158 178 POTENTIAL.
CC FT TRANSMEM 374 394 POTENTIAL.
CC FT TRANSMEM 409 429 POTENTIAL.
CC FT TRANSMEM 450 470 POTENTIAL.
CC FT DOMAIN 605 854 TRANSMITTER DOMAIN (POTENTIAL).
CC FT MOD_RES 628 628 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
CC SO SEQUENCE 854 AA; 90670 MW; 201867CAFDDB865 CRC64;

alignment_scores:
Quality: 68.00 Length: 45
Ratio: 2.519 Gaps: 2
Percent Similarity: 60.000 Percent Identity: 44.444

alignment_block:

US-09-240-675-1_COPY_1_229 x KDPD_RATRA ..

Align seg 1/1 to: KDPD_RATRA from: 1 to: 854

8 GATCTCGCGCGCTCCAGATGATGTCGCTCCCTCGG..... 46
|||||
629 ASPLenUAIARgPrOpheAspGlyGlnGlnLysGlyGlyTrpLeuA1 645
47CGGACGACCTAGTGCCTGCGCGCTGGCCCGCAGGTG 89
|||||
645 AleuHISArgAspAspProValLysArg.....ProGlyGlyAlaA 660
90 TCCGACGCCGACGAGTGGAAAAATCTAAATCTCC 124
:::|||||
660 laArgspArgArgArgLysProAlaHISLeuSer 671

seq_name: SwissProt_38:IF3A_HUMAN

seq_documentation_block:

ID IF3A_HUMAN STANDARD: PRT: 1382 AA.

AC Q14152; 000653;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE EUKARYOTIC TRANSDUCTION INITIATION FACTOR 3 SUBUNIT 10 (EIF-3 THETA)
DE (EIF3 P167) (EIF3 P180) (EIF3 P185) (KIAA0139).
GN EIF3S10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euteria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BONE MARROW;
RX MEDLINE: 96127530.
RA Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. IV.

RT The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by
RT analysis of cDNA clones from human cell line KG-1.";
RT DNA Res. 2:167-174(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97294683.

RA Scholler J.K., Kanner S.B.;
RT "The human p167 gene encodes a unique structural protein that contains
RT centrosomin A homology and associates with a multicomponent complex.";
RT DNA Cell Biol. 16:515-531(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97207269.

RA Johnson K.R., Merrick W.C., Zoll W.L., Zhu Y.;
RT "Identification of cDNA clones for the large subunit of eukaryotic
RT translation initiation factor 3. Comparison of homologues from human,
RT Nicotiana tabacum, Caenorhabditis elegans, and Saccharomyces
RT cerevisiae.";
RT J. Biol. Chem. 272:7106-7113(1997).

CC -1- FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING OF
CC METHIONYL-TRNAI AND MRNA.
CC -1- SUBUNIT: EIF-3 IS COMPOSED OF AT LEAST 10 DIFFERENT SUBUNITS.
CC -1- SUBCELLULAR LOCATION: CYTOSOLASMIC.

CC -1- PTM: PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO THE EIF3S10 FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: D50929; BAA09488.1; -
CC DR EMBL: U58046; AAB41584.1; -
CC DR EMBL: U78311; AAB80695.1; -
CC DR MIM: 602039; -
CC KW Initiation factor; Protein biosynthesis; Repeat; Phosphorylation.
CC FT DOMAIN 925 1172 25 X 10 AA TANDEN REPEAT OF D-(DE)-D-R-
CC (GP)-(PS)-(RW)-R-(GN)-(AM).
CC SO SEQUENCE 1382 AA; 166568 MW; 485C01B28D67EBBA CRC64;

alignment_scores:
Quality: 67.00 Length: 87
Ratio: 1.634 Gaps: 6
Percent Similarity: 47.126 Percent Identity: 32.184

alignment_block:

US-09-240-675-1_COPY_1_229 x IF3A_HUMAN ..

Align seg 1/1 to: IF3A_HUMAN from: 1 to: 1382

23 CCAGATGATGTCGCTCTCTCT.....GGCGCGACGACCTAGTCTCG 66
|||||
952 ProAspAspAspArgValProArgArgGlyMetAspAspAspArgGlyPr 968
67 TCGCCGTGGCCCATGGGTGTGTCGCGACCGCGAG..... 103
|||||
968 cArgArgGlyProGlnGlnAspArgPheSerArgArgGlyAlaAspAspA 985
104TGAAAAAATCT.....AAATC 121
|||||
985 spArgProSerTyrArgAsnThrAspAspAspArgProProArgArgIle 1001
122 TCCCTCAAAAAGTAGAGT.....CGACATCATAGATGACACTTATCC 165
|||||
1002 AlaAspGlnAspArgGlyAsnTyrArgHis AlaAspAspAspArgProp 1018
166 TGAGC.....TGAAACAGACGACATAG 188
|||||
1018 roArgArgGlyLeuAspGlnAspArgGlySerTyrArgTThrAlaAspGln 1034

189 TCTGTCGCG 197
::: |||
1035 Asparagly 1037

seq_name: SwissProt_38:Y481_HUMAN

seq_documentation_block:

ID Y481_HUMAN STANDARD: PRT: 483 AA.

AC 075069:

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE HYPOPHYSAL PROTEIN KIAA0481 (H1480).

GN KIAA0481.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homnidae; Homo.

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN.

RX MEDLINE: 98116662.

RA Seki N., Ohira M., Nagase T., Ishikawa K.-I., Miyajima N.,

RA Nakajima D., Nomura N., Ohara O.;

RT "Characterization of cDNA clones in size-fractionated cDNA libraries

RT from human brain.";

RL DNA Res. 4:345-349(1997).

CC -1 SIMILARITY: SOME, TO HUMAN TEX28.

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CC -----

DR EMBL: AB007950; BAA32326.1; -

KM Hypothetical protein.

FT DOMAIN 28 34 POLY-GLN.

SO SEQUENCE 483 AA: 52462 MW: A9EB8EPD793D866 CRC64;

Alignment_scores:

Quality: 65.50 Length: 71

Ratio: 1.598 Gaps: 3

Percent Similarity: 57.746 Percent Identity: 33.803

Alignment_block:

US-09-240-675-1_COPY_1_229/rev x Y481_HUMAN ..

Align seg 1/1 to: Y481_HUMAN from: 1 to: 483

222 GATTAATCGAATAAGTCAATTCGCGAGCACTGCTGCTGCTTC 173

||||| :|||:||||| :||| :|||

40 ASPTSPKASDPLULYSGIUNRSGRPRGLUMETHLSARVALSERLY 56

||||| :|||:||||| :||| :|||

172 CACCTCAGATTAAGTGTGAT...CTATGATGCGACTGCTGCTGCTTTC 126

||||| :|||:||||| :||| :|||

56 RLALNET.....SERLEUHLISAPLEUPROALATGPROTHRALAPHEA 71

||||| :|||:||||| :||| :|||

125 AGGAGATTTTACATTTTTCACACTGCGGCTCGGAGCAACACCCATGGGC 76

||||| :|||:||||| :||| :|||

71 SNAIRVALLEUEN.....GLNILEARGSERARGPROSERILE 83

||||| :|||:||||| :||| :|||

75 CCACGCGCGAGCAGCTAGGTCGTCGCGCCGAGAGAGAGCAGCATCATC 26

||||| :|||:||||| :||| :|||

84 LYSARGGLYALASERLEHISSEISERISERISERISERISERISERIS 100

||||| :|||:||||| :||| :|||

25 TGGAGACCGCGCG 13

||||| :|||:||||| :||| :|||

100 ISEISERISERIS 104

seq_name: SwissProt_38:ERF_MOUSE

seq_documentation_block:

ID ERF_MOUSE STANDARD: PRT: 551 AA.

AC P70459:

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE ETS-DOMAIN TRANSCRIPTION FACTOR ERF.

GN ERF.

OS Mus musculus (mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN-129/SVJ.

RX MEDLINE: 97282708.

RA Liu D., Pavlopoulos E., Modi N., Moschonas N., Mayrochalisitis G.J.;

RT "ERF: genomic organization, chromosomal localization and promoter

RT analysis of the human and mouse genes.";

RL Oncogene 14:1445-1451(1997).

CC -1 FUNCTION: POTENT TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE H1

CC ELEMENT OF THE ERS2 PROMOTER. MAY REGULATE OTHER GENES INVOLVED

CC IN CELLULAR PROLIFERATION (BY SIMILARITY).

CC -1 SUBCELLULAR LOCATION: NUCLEAR.

CC -1 PTM: PHOSPHORYLATED BY MULTIPLE KINASES INCLUDING PROBABLY ERK2.

CC PHOSPHORYLATION REGULATES THE ACTIVITY OF ERF (BY SIMILARITY).

CC -1 SIMILARITY: BELONGS TO THE ETS FAMILY.

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CC -----

DR EMBL: U58533; AAC09474.1; -

DR EMBL: U58534; AAC09474.1; JOINED.

DR HSSP: 001543; 1FTI.

DR MGD: MGI:109637; ERF.

DR PRINTS: PR00454; ETSDOMAIN.

DR PROSITE: PS00345; ETS_DOMAIN_1; 1.

DR PROSITE: PS00346; ETS_DOMAIN_2; 1.

DR PROSITE: PS50061; ETS_DOMAIN_3; 1.

DR PFM: PF00178; Ets; 1.

KM Transcription regulation. Repressor; DNA-binding; Nuclear protein;

KM Phosphorylation.

FT DNA_BIND 27 107 ETS-DOMAIN.

FT DOMAIN 166 171 POLY-SER.

FT DOMAIN 290 293 POLY-GLY.

FT DOMAIN 362 373 POLY-SER.

FT DOMAIN 420 425 POLY-PRO.

FT MOD_RES 529 529 PHOSPHORYLATION (BY ERK2) (BY

FT SIMILARITY).

SO SEQUENCE 551 AA: 59050 MW: SACL1B72FEB243FES CRC64;

Alignment_scores:

Quality: 65.00 Length: 32

Ratio: 2.826 Gaps: 1

Percent Similarity: 71.875 Percent Identity: 43.750

Alignment_block:

US-09-240-675-1_COPY_1_229/rev x ERF_MOUSE ..

Align seg 1/1 to: ERF_MOUSE from: 1 to: 551

108 TTCCACCTGCGGCTGCGAGAACCCATGAGCCGAGGAGAGAGACT 59

||||| :|||:||||| :||| :|||

375 PhelysphenylsleuGlnProProProluGlyArgArgGlnalGalaal 391

||||| :|||:||||| :||| :|||

58 AGGTCGTCGCGCGCCGAGAGGA.....CGACCATCATCTGGGAGC 19

```

Seq_name: SwissProt_38::VPHE_NPVAC
          |||.....|||...::|||...|||...
391 aclygiulLysAlaProGlyGlyThrAspLysSerSerGlyGlySer 406

```

```
seq_documentation_block:
ID      VPHE_NPVAC      STANDARD;      PRT;      252 AA
AC      P34738.
```

DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE POLYHEDRAL ENVELOPE PROTEIN (PE) (POLYHEDRAL CALYX PROTEIN)
 GN P34.
 OS Autographa californica nuclear polyhedrosis virus (ACNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 NC Nucleopolyhedrovirus.
 CC full

RP SEQUENCE FROM N.A.
RX MEDLINE: 87311863.
RA Oelling C., Happ B., Mueller T., Doerfler W.;
RT "Overlapping sets of viral RNAs reflect the array of polypeptides in
RT the EcoRI J and N fragments (map positions 81.2 to 85.0) of the
RT Autographa californica nuclear polyhedrosis virus genome.";
RL J. Virol. 61:3048-3057(1987).

RE SEQUENCE FROM N.R.
RC STRAIN-C6;
RX MEDLINE; 94303173.
RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.,
RT "The complete DNA sequence of Autographa californica nuclear
polyhedrosis virus.";
RL Virology 202:586-605(1994).
CC -1- FUNCTION: MAJOR COMPONENT OF THE POLYHEDRA ENVELOPE.
CC -1- SIMILARITY: TO PE FROM OTHER BACULOVIRUSES.

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DR	EMBL:	M17548:	AAA66805.1:	-
DR	EMBL:	L28258:	AAA66761.1:	-
DR	PIR:	C43679:	C43679.	-
KW	Envelope protein, Viral occlusion body.			
FT	DOMAIN	98	140	ARG/SER-RICH.
SO	SEQUENCE	252 AA:	29079 MW:	3322B0C8E195A15D CRC64

```
alignment_scores:      Quality:    63.50      Length:    73
                       Ratio:       1.924          Gaps:      2
Percent Similarity:   45.205      Percent Identity: 31.507
```

alignment_block:
US-09-240-675-1_COPY_1_229/rev x VPHE_NPVAC

Align seg 1/1 to: VPHE_NPVAC from: 1 to: 252

[illegible]

128 TTGAGGAGATTTAGATTTTTTCACCTGCGGCTGCGGACACACCATG 79
120ArgSerArgSerProHisCys 126

78 GGGCCAGGCGGAGACACACACATGGGTCTGCGCCGCCAGAGACACACATC 29
 ||||| ||||| ::||| ||||| ::|||
 127 ArgProArgSerArgSerArgSerArgSerArgSerArgSerArgSerArgSer 14
 28 ATCTGGAGGCCGCCGACAGA 10
 ||||| |||||
 143 TSePProArgArgGlyArg 149

```
seq_name: SwissProt_38:IRS2_MOUSE
seq_documentation_block:
ID   IRS2_MOUSE    STANDARD;          PRT;   1321 AA
```

DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS).
 GN IRS2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia.
 OC Eutheria; Rodentia; Sclurognathii; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.

RX MEDLINE: 95405472.
 RA Sun X.-J., Wang L.-M., Zhang Y., Yenush L., Myers M.G., Jr.,
 RA Glasheen E., Lane W.S., Pierce J.H., White M.F.:
 "Role of IRS-2 in insulin and cytokine signalling.".
 RT Nature 377:173-177(1995).
 RL

CC -1- FUNCTION: MAY MEDiate THE CONTROL OF VARIOUS CELLULAR PROCESSES
CC BY INSULIN.
CC -1- TISSUE SPECIFICITY: SKELETAL MUSCLE, LUNG, BRAIN, LIVER, KIDNEY
CC HEART AND SPLEEN.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 PTB DOMAIN.

```
DR HSSP; P35568; 1IRS.  
DR MGD; MGI:109334; IRS2.  
DR PRINTS; PRO0628; INSULINRSI.  
DR PROSITE; PS50003; PH_DOMAIN; 1.
```

DR	PFAM; PF00169; PH; 1.	
KW	Phosphorylation.	
FT	16	144
FT	DOMAIN	300
FT	187	PTB.
FT	336	PHOSPHORYLATION (BY INSR
FT	MOD_RSS	536

FT		(BY SIMILARITY).
FT	MOD_RES	649
FT		PHOSPHORYLATION (BY INSR (BY SIMILARITY)).
FT	MOD_RES	671
FT		PHOSPHORYLATION (BY INSR

FT		(BY SIMILARITY).
FT	MOD_RES	911
FT		PHOSPHORYLATION (BY INSR
FT		(BY SIMILARITY).
FT	MOD_RES	970
		PHOSPHORYLATION (BY INSR

FT		(BY SIMILARITY).
FT	MOD_RES	1242
FT		PHOSPHORYLATION (BY INSR
FT		(BY SIMILARITY).
FT	MOD_RES	1303
FT		PHOSPHORYLATION (BY INSR
FT		(BY SIMILARITY).

FT	19	28	(BY SIMILAKITI).
FT	444	449	POLY-ASN.
FT	638	641	POLY-SER.

SQ SEQUENCE 1321 AA; 136526 MW; 5069CE9D614960C7 CRC64;

```

alignment_scores:
  Quality: 63.50
  Ratio: 1.984
  Percent Similarity: 44.444
  Length: 72
  Gaps: 2
  Percent Identity: 29.167

```

```
alignment_block:
US-09-240-675-1_COPY_1_229/rev x IRS2_MOUSE
..
```

Align seg 1/1 to: IRS2_MOUSE from: 1 to: 1321

RT "Nucleotide sequence and expression of a phosphate-regulated gene
RT encoding a secreted hemolysin of Pseudomonas aeruginosa."
RL J. Bacteriol. 167:291-296(1986).
RN [2]

RP REVISIONS.

RA Pritchard A.E.;
RL Submitted (AUG-1986) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: HYDROLYSES SPHINGOMYELIN IN ADDITION TO
CC PHOSPHATIDYLCHOLINE.

CC -1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O = 1,2-
CC DIACYLGLYCEROL + CHOLINE PHOSPHATE.

CC -1- SIMILARITY: 40% IDENTITY TO NON-HEMOLYTIC PHOSPHOLIPASE C.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL: M3047; AA25966.1; -
DR PIR; A26391; A26391.

KW Hemolysis: Toxin; Hydrolase; Signal.

FT SIGNAL 1 38
FT CHAIN 39 730 HEMOLYTIC PHOSPHOLIPASE C.
SQ SEQUENCE 730 AA; 82655 MW; F1D3695824445F8F CRC64;

alignment_scores:

Quality: 62.00 Length: 69
Ratio: 1.824 Gaps: 4
Percent Similarity: 49.275 Percent Identity: 26.087

alignment_block:

US-09-240-675-1_COPY_1_229 x PHLC_PSEAE ..

Align seg 1/1 to: PHLC_PSEAE from: 1 to: 730

```

63 CTCGCGCGCGGCGCATGGGTGTGTCGCGCGCGCGAGTGGAAAAA 112
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
404 LeuIleAlaIleSerProIrp.....SerLysGlyGly..... 414
113 TCTAAATCTCCTCAAAAAGTAGAGTCGACATCATAGACAACTTTA 162
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
415 .....LysValSerAlaGluValPheAspHisThrSerV 426
163 TCCTGAGG..... 170
   |||:|||||
426 allLeuArgPheLeuGluArgArgPheGlyLeuValGluGluAsnIleSer 442
171 ...TGGACAGGAGGAGATGAGCTCTCGGGAATGAGACTTTTCATTGCA 217
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
443 ProIrpArgArgAla.....ValCysGlyAspLeuThrSerLeuPheAs 457
218 TTATCAA 224
   |||:|||||
457 ppheGln 459

```


OM of: US-09-240-675-1_COPY_1_229 to: SPTRMBL_12.* out_format: pfs

Date: Jun 1, 2000 12:39 AM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODE=frame+zip.model -DEV=xlp
-O/cgcn2.1/USPTO.spool/US09240675/runat.30052000.164313.24664/app-query.fasta.1
-DB=SPTRMBL_12 -QFMT=fastan -SUFFIX=modif.rspt -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -DOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -STRAP=1 -MATRIX=blomsu62
-RANS=human.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US09240675 -NCPV=6 -ICPV=3 -NO_XLPHY -WAIT
-THREDS=1

Search information block:

Query: US-09-240-675-1_COPY_1_229
Query length: 229
Database: SPTRMBL_12.*
Database sequences: 225878
Database length: 69334122
Search time (sec): 89.940000

seq_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
SP_vertbrate:09YHW0	+	113.50	225.40	2.3e-05	569 09YHW0 gallus gallus (chicken).
SP_human:09Y576	+	79.00	144.87	0.2831	1429 09Y576 homo sapiens (human).
SP_invertebrate:09XZV7	-	77.00	152.39	0.5389	286 09XZV7 giardia lamblia (giard
SP_human:015178	+	67.00	127.43	8.13	466 015178 homo sapiens (human).
SP_human:015152	+	67.00	119.45	7.62	1382 015152 caenorhabditis elegans
SP_invertebrate:076514	+	66.00	127.08	10.85	365 076514 caenorhabditis elegans
SP_mhc:030849	+	63.50	121.88	21.56	358 030849 oryctolagus cuniculus (r
SP_invertebrate:088970	+	63.50	116.61	20.67	734 088970 mus musculus (mouse).
SP_invertebrate:084317	+	63.00	118.55	23.90	640 084317 bacteriophage n15 (termi
SP_human:013507	+	63.00	118.48	23.50	848 013507 homo sapiens (human).
SP_invertebrate:060697	+	63.00	111.10	22.87	1344 060697 mus musculus (mouse).
SP_invertebrate:094603	+	62.50	120.43	28.52	326 094603 leishmania major. mtc
SP_plant:023212	+	62.00	116.28	27.59	573 023212 arabidopsis thaliana (mc
SP_mammal:077669	+	62.00	126.88	34.76	117 077669 bos taurus (bovine).
SP_human:095927	+	62.00	120.22	32.94	290 095927 homo sapiens (human).
SP_invertebrate:089019	+	62.00	110.69	30.51	1062 089019 mus musculus (mouse).
SP_bacteria:007239	-	61.50	113.57	36.13	620 007239 mycobacterium tuberculosis
SP_bacteria:054272	-	61.00	113.41	42.42	417 054272 streptomyces hygroscopic
SP_vertebrate:09W721	+	61.00	112.55	41.45	616 09W721 brachydanio rerio (zebra
SP_invertebrate:09W75	+	61.00	112.23	41.34	644 09W75 mus musculus (mouse).
SP_invertebrate:09W74	+	61.00	111.90	41.24	673 09W74 mus musculus (mouse).
SP_bacteria:09ZB87	-	60.50	122.95	52.15	129 09ZB87 streptomyces coelicolor
SP_human:09Y415	-	60.50	118.65	50.37	232 09Y415 homo sapiens (human).
SP_bacteria:086774	-	60.50	118.84	49.25	340 086774 streptomyces coelicolor
SP_bacteria:09X4V6	-	60.50	115.84	49.25	340 09X4V6 streptomyces griseoloid
SP_invertebrate:091232	+	60.50	115.84	49.25	340 091232 caenorhabditis elegans
SP_invertebrate:0920H1	+	60.50	111.41	47.52	622 0920H1 mus musculus (mouse).
SP_invertebrate:018465	-	60.50	103.30	44.51	1880 018465 hirtida medialis (m
SP_plant:064410	+	60.00	116.46	57.26	270 064410 zea mays (maize). cytoch
SP_invertebrate:002424	+	60.00	113.95	56.25	379 002424 caenorhabditis elegans
SP_invertebrate:023047	+	60.00	113.98	56.12	369 023047 caenorhabditis elegans
SP_invertebrate:050805	+	60.00	106.90	53.01	984 050805 mus musculus (mouse).
SP_human:09Y519	-	60.00	98.87	49.69	2871 09Y519 homo sapiens (human).
SP_virus:065088	-	60.00	98.41	49.51	3164 065088 human herpesvirus 1. vi
SP_human:014396	+	59.50	124.79	70.84	75 014396 homo sapiens (human).
SP_archaea:09Y86	+	59.50	122.12	69.33	108 09Y86 aeropyrum pernix. 108aa
SP_invertebrate:062143	+	59.50	118.21	67.18	184 062143 mus musculus (mouse).
SP_invertebrate:021784	+	59.50	113.92	64.90	330 021784 caenorhabditis elegans
SP_fungi:09Y775	+	59.00	112.72	64.27	389 09Y775 candida tropicalis (yeas
SP_mammal:079321	+	59.00	120.46	79.14	117 079321 sus scrofa (pig). beta c
SP_bacteria:088073	+	59.00	112.97	74.51	325 088073 streptomyces coelicolor

SP_bacteria:007452	+	59.00	112.68	74.33	338 007452 alcaligenes eutroph
SP_fungi:012405	-	59.00	111.68	73.74	387 012405 saccharomyces cerev
SP_plant:008700	+	59.00	110.66	73.14	445 008700 brassica napus (rap
SP_plant:09XFW6	+	59.00	110.66	73.14	445 09XFW6 brassica oleracea ('

seq_name: SP_vertbrate:09YHW0

seq_documentation_block:

AC 09YHW0 PRELIMINARY; PRT; 569 AA.
ID 09YHW0;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TEMBLrel. 10, Last annotation update)
DE INTERFERON ALPHA/BETA RECEPTOR 1.
GN IFNAR1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA REBOUL J., GARDINER K., MONNERON D., UZE G., LUTFALLA G.;
RT "Comparative genomic analysis of the interferon/interleukin-10
RL Receptor gene cluster."
DR EMBL; AF082664; AAD13669.1; -;
KM Receptor.
SO SEQUENCE 569 AA; 64055 MW; F99BC099 CRC32;

alignment_scores:

Quality: 113.50 Length: 71
Ratio: 2.365 Gaps: 3
Percent Similarity: 67.606 Percent Identity: 40.845

alignment_block:
US-09-240-675-1_COPY_1_229 x 09YHW0 ..

Align seg 1/1 to: 09YHW0 from: 1 to: 569

12	TGCGGCGGCTCCCATATGATGCTGCTGCGGCGGAGACCGCTAGT	61
6	CysAlaSerGlyArgLeuAlaValLeuLeu.....CysVal	18
62	GCCTGCTCCCGGCGGCGGCTGCTGCGGCGGAGACCGGAAAA	111
18	lleuValValValSer.....ArgCysValGlyGlnThr	31
112	ATCTAAATCTCTCTCAAAAGTAGAGTCGACATCATGACACACTT	161
31	snleuLysSerProGlnAspIleGlnValTyAlaValAsnThrAsn	47
162	ATCCGAGAGTGAACAGCAGCATGAGTCGCGGAGTACATTTC	211
48	ThrIleuMetTrpAsnTrpThrLysAspGlyThr...AsnValThr	Phese 63
212	ATTCGATTATCA	224
63	ValGlnTrpGln	67

seq_name: SP_human:09Y576

seq_documentation_block:
ID 09Y576 PRELIMINARY; PRT; 1429 AA.
AC 09Y576;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE BRAS1 CANCER NUCLEAR RECEPTOR-BINDING AUXILIARY PROTEIN.
GN BRX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.

RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RX MEDLINE: 9828806.
 RA RUBINO D., DRIGGERS P., ARBIT D., KEMP L., MILLER B., COSO O.,
 RA PAGLIAI K., GAY K., GUTKIND S., SEGARS J.;
 RT "Characterization of Bcr, a novel Dbl family member that modulates
 RT estrogen receptor action.";
 RL Oncogene 16:2513-2526(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RA RUBINO D.M., DRIGGERS P.H., MILLER B., SEGARS J.H.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF126008; AAD21311.1;
 KW Receptor.
 SO SEQUENCE 1429 AA; 161033 MW; 542B8C25 CRC32;

alignment_scores:

Quality: 79.00 Length: 82
 Ratio: 1.837 Gaps: 6
 Percent Similarity: 52.439 Percent Identity: 41.463

alignment_block:

US-09-240-675-1_COPY_1_229 x Q9Y5T6

Align seg 1/1 to: Q9Y5T6 from: 1 to: 1429

5 AGGAGATCTGGCGCGCTCCAGATGATGCTGCTCCCTGGCGGCGACGA 54
 |||||
 1226 ATGGLLLeuArg.....AspGlyArgProSerTrp..... 1235
 55 CCTAGTGTCTGCGCGCGCTCCAGATGATGCTGCTCCCTGGCGGCGACGA 104
 |||||
 1236 .ProSerAlaArgArgArgCysSerArgLy.....SerArgTrp 1249
 105 GGAAGAAATCTAAATCTCTCTCAAAAGTAGAGTCGACATCATGATGA 154
 |||||
 1249 rPySArgSerGlyArgSerSerArgArgArgAlaHisSerGlnTy 1265
 155 CAACCT.....TATCTGAGGTGGAACAGCA 180
 1266 AspLeuGluArgLeuArgAlaAlaGlnLysGlnLeuGlnArgGlnGln 1282
 |||||
 1282 uHis....ValArgArgGluAlaGlu.....ArgLeuSerGln 1293

seq_name: sp_invertebrate:Q9XZV7

seq_documentation_block:

ID Q9XZV7 PRELIMINARY; PRT; 286 AA.
 AC Q9XZV7;
 DT 01-NOV-1999 (TRENBLREL. 12, Created)
 DT 01-NOV-1999 (TRENBLREL. 12, Last sequence update)
 DT 01-NOV-1999 (TRENBLREL. 12, Last annotation update)
 DE DNA FOR RNA TANDEM REPEAT UNIT (FRAGMENT).
 OS Giardia lamblia (Giardia intestinalis).
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90326542.
 RA HEALEY A., MITCHELL R., UPCROFT J.A., BOREHAM P.F.L., UPCROFT P.;
 RT "Complete nucleotide sequence of the ribosomal RNA tandem repeat unit
 RT from Giardia intestinalis.";
 RL Nucleic Acids Res. 18:4006-4006(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91088287.
 RA UPCROFT J.A., HEALEY A., MITCHELL R., BOREHAM P.F.L., UPCROFT P.;
 RT "Antigen expression from the ribosomal DNA repeat unit of Giardia
 RT intestinalis.";

RL Nucleic Acids Res. 18:7077-7081(1990).
 DR EMBL: X52949; CAB44501.1;
 FT NON_TER 286
 SO SEQUENCE 286 AA; 28277 MW; 53B84096 CRC32;

alignment_scores:

Quality: 77.00 Length: 29
 Ratio: 3.500 Gaps: 0
 Percent Similarity: 75.862 Percent Identity: 51.724

alignment_block:

US-09-240-675-1_COPY_1_229/rev x Q9XZV7

Align seg 1/1 to: Q9XZV7 from: 1 to: 286

93 CGGACACACCCATGGCGCCGACGAGACACTAGGTCGCGGCC 44
 |||
 243 ArgArgSerAlaGlnGlyProArgAlaArgArgGlyAlaAlaArgPr 259
 43 AGCAGACAGACCATCATCTGGAGCCGCGCAGATCC 7
 |||||
 259 OGlySnaArgGlyAlaGlyGlyProArgArgArgSer 271

seq_name: sp_human:Q15778

seq_documentation_block:

ID Q15778 PRELIMINARY; PRT; 466 AA.
 AC Q15778;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)
 DE P167 (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90239007.
 RA KANNER S.B., REYNOLDS A.B., VINES R.R., PARSONS J.T.;
 RT "Monoclonal antibodies to individual tyrosine-phosphorylated protein
 RT substrates of oncogene-encoded tyrosine kinases.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3328-3332(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA SCHOLLER J.K., KANNER S.B.;
 RL DNA Cell Biol. 0:0-0(0).
 DR EMBL: U58047; AAB41586.1;
 FT NON_TER 1
 SO SEQUENCE 466 AA; 56657 MW; 08C47AAE CRC32;

alignment_scores:

Quality: 67.00 Length: 87
 Ratio: 1.634 Gaps: 6
 Percent Similarity: 47.126 Percent Identity: 32.184

alignment_block:

US-09-240-675-1_COPY_1_229 x Q15778

Align seg 1/1 to: Q15778 from: 1 to: 466

23 CCAGATGATGTCGCTCTCT.....GGCGCGACGACCTAGTCTCG 66
 |||||
 36 ProGAsPaPaPaPaPaValProArgArgGlyMetAsPaPaPaPaGlyPr 52
 67 TCGCGGTGGCCCATGGGTGTTCGCCGACGCGCAGG..... 103
 |||||
 52 CarGArgGlyProGluGluAsPaPaPheSerArgArgGlyAlaAsPaPa 69
 |||||
 104TCGAAAAAATCT.....AAATC 121
 |||||
 69 SPArgProSerTrpArgSnaThrAsPaPaPaPaPaPaPaArgArgArgGly 85

```

122 TCCTCAAAAGTAGAGT.....CGACATCATAGTACACTTATCC 165
      : : : : : : : : : : : : : : : : : : : : : : : :
86 AlaSpluAspArgGlyAsnTrpArgHis.AlaSpsAspArgProp 102
166 TGAG.....TGGAACAGAGCGATGAG 188
      : : : : : : : : : : : : : : : : : : : : : : : :
102 roArgArgGlyLeuAspGluAspArgGlySerTrpArgTrnAlaSpGlu 118
189 TCTGTGGG 197
      : : :
119 AspArgGly 121

```

seq_name: sp_human:014152

```

seq_documentation_block:
ID 014152 PRELIMINARY: PRT: 1382 AA.
AC 014152: 000653.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE KIAA0139 PROTEIN.
GN KIAA0139.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96127530.
RA NAGASE T., SEKI N., TANAKA A., ISHIKAWA K., NOMURA N.;
RT "Prediction of the coding sequences of unidentified human genes. IV.
RT The coding sequences of 40 new genes (KIA011-KIA0160) deduced by
RT analysis of cDNA clones from human cell line KG-1."
RL DNA Res. 2:167-174(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90239007.
RA KANNER S.B., REYNOLDS A.B., VINES R.R., PARSONS J.T.;
RT "Monoclonal antibodies to individual tyrosine-phosphorylated protein
RT substrates of oncogene-encoded tyrosine kinases."
RL Proc. Natl. Acad. Sci. U.S.A. 87:3328-3332(1990).
RN [3]
RP SEQUENCE FROM N.A.
RA SCHOLLER J.K., KANNER S.B.;
RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97207269.
RA JOHNSON K.R., MERRICK W.C., ZOLL W.L., ZHU Y.;
RT "Identification of cDNA clones for the large subunit of eukaryotic
RT translation initiation factor 3. Comparison of homologues from human,
RT Nicotiana tabacum, Caenorhabditis elegans, and Saccharomyces
RT cerevisiae."
RL J. Biol. Chem. 272:7106-7113(1997).
RN [5]
RP SEQUENCE FROM N.A.
RA ZHU Y., JOHNSON K.R.;
RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: D50929; BAA09488.1; -
DR EMBL: U58046; AAB41584.1; -
DR EMBL: U78311; AAB00695.1; -
KW Initiation factor.
SQ SEQUENCE 1382 AA: 165568 MW: AEF0846C CRC32:

```

alignment_scores:
Quality: 67.00 Length: 87
Ratio: 1.634 Gaps: 6
Percent Similarity: 47.126 Percent Identity: 32.184

alignment_block:
US-09-240-675-1_copy_1_229 x 014152

Align seg 1/1 to: 014152 from: 1 to: 1382

```

23 CCAGATGATGTCGCTCCT.....GGCGGAGACGACCCCTATGCTCG 66
      : : : : : : : : : : : : : : : : : : : : : : : :
952 ProSpsAspArgValProArgArgGlyMetAspAspArgGlyPr 968
67 TCGCCGTGGGCCCATGGGTGTGTCGACCGCAG..... 103
      : : : : : : : : : : : : : : : : : : : : : : : :
968 oArgArgGlyProGluGluAspArgPheSerArgArgGlyAlaAspAsp 985
104 .....TGCAAAAATCT.....AAATC 121
      : : : : : : : : : : : : : : : : : : : : : : : :
985 sPArgProSerTrpArgAsnTrnAspAspArgProproAlaArgGly 1001
122 TCCTCAAAAGTAGAGT.....CGACATCATAGTACACTTATCC 165
      : : : : : : : : : : : : : : : : : : : : : : : :
1002 AlaSpluAspArgGlyAsnTrpArgHis.AlaSpsAspArgProp 1018
166 TGAG.....TGGAACAGAGCGATGAG 188
      : : : : : : : : : : : : : : : : : : : : : : : :
1018 roArgArgGlyLeuAspGluAspArgGlySerTrpArgTrnAlaSpGlu 1034
189 TCTGTGGG 197
      : : :
1035 AspArgGly 1037

```

seq_name: sp_invertebrate:076514

```

seq_documentation_block:
ID 076514 PRELIMINARY: PRT: 365 AA.
AC 076514:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE CET-1.
GN CET-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabdita; Rhabditida;
OC Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-N2;
RA MORITA K., CHOW K.L., UENO N.;
RT "Body length and Male tail Ray Pattern Formation of C. elegans are
RT Regulated by a Member of TGFb Family."
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF074395; AAC26791.1; -
DR HSSP: P18075; 1BNP.
DR PFM: PF00019; TGF-beta: 1.
DR PRINTS: PR00438; GFCYSKNOT.
SQ SEQUENCE 365 AA: 41781 MW: 54051BBE CRC32:

```

alignment_scores:
Quality: 66.00 Length: 54
Ratio: 1.941 Gaps: 2
Percent Similarity: 62.963 Percent Identity: 31.481

alignment_block:
US-09-240-675-1_COPY_1_229 x 076514

Align seg 1/1 to: 076514 from: 1 to: 365

```

53 GACCCTAGTGTGTCGCGTGGGCCCATGGGTGTGTCGACGCCGAG 102
      : : : : : : : : : : : : : : : : : : : : : : : :
228 GiUpProSerSerValArgArg.....LysArgSerArgG1 239
103 GTGCAAAAATCTAAATCTCTCAAAAGTAGAGTCGACATCATGAT 152
      : : : : : : : : : : : : : : : : : : : : : : : :
239 nThrGlyAsnSerGluArgGlyAsnArgGlyGlyArgGlyHis 255
153 GACACTTTATCTCGAGAGTGAACAGAGCATGAGTCTCTGGGAATGT 202
      : : : : : : : : : : : : : : : : : : : : : : : :

```

266AsnThrGluAlaGluSerAsnLeuGlyArgThr 267
203 GACTTTTCATT 214
|||||:
268 AspheTyrVal 271

seq_name: sp_mhc:030849

seq_documentation_block:
ID 030849 PRELIMINARY; PRT: 358 AA.

AC 030849;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE MHC CLASS I ANTIGEN PRECURSOR
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B/J;
RX MEDLINE: 84290724.
RA TYKOCINSKI M.L., MARCHE P.N., MAX E.E., KINDT T.J.;
RT "Rabbit class I MHC genes: cDNA clones define full-length transcripts
of an expressed gene and a putative pseudogene."
RL J. Immunol. 133:2261-2269(1984).
DR EMBL: K02442; AAA98731.1; -
DR HSSP: P30460; 1AGE.
DR PRAM: PF00047; 1g; 1.
DR PRAM: PF00129; MHC_I; 1.
KW SIGNAL: MHC.
FT CHAIN 22 358 POTENTIAL.
SQ SEQUENCE 358 AA; 39828 MW; 86894130 CRC32.

alignment_scores:
Quality: 63.50 Length: 95
Ratio: 1.296 Gaps: 3
Percent Similarity: 51.579 Percent Identity: 23.158

alignment_block:

US-09-240-675-1_COPY_1_229 x 030849 ..

Align seg 1/1 to: 030849 from: 1 to: 358

12 TGCGGGGCTCCAGATGATGCTCCTCCGCGGAGACACCTAGT 61
|||||:
3 CysGlyAla.....LeuLeuLeuLeuAlaGlyAlaLeuThrLeuTh 17
62 GCTCGTCCGCGGCGCCATGGGTGTG.....TCCGAGCCGCGAG 102
: : : : :
17 rglurhrarghrghlyserhlsrleuargtyrphethrrhrlalvalS 34
103 GTGGAATAATCTCAAAATCTCTCAAAAGTAGAGGTGACATCTAAT 152
: : : : :
34 errargProGlyLeuProGluProArgPheMetSerValGlyTyrValasp 50
153 GACACTTATCTCTGAG..... 170
| : : : :
51 AsprhrghlnphevalargPheaspseraspalaalaserProArgAlaGl 67
171TGGAACAGA 180
67 uProArgAlaProTrpMetArgGlnValaspProGlyTyrTrpAspArgG 84
181 CGGATGAGTCTGTGCGAATGAGACTTTTTCATT 215
: : : : :
84 InThrGluArgAlaLysAsnThrAlaLeuSerPhe 95

seq_name: sp_rdent:088970

seq_documentation_block:

ID 088970 PRELIMINARY; PRT: 734 AA.
AC 088970;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE INSULIN RECEPTOR SUBSTRATE-2 (FRAGMENT).
GN IRS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA XU G., UIMER W.T., WOLF B.A.;
RT "Partial genomic DNA sequence of mouse beta-cell IRS-2."
RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF090738; AAC61743.1; -
FT NON-TER 1 1
SQ SEQUENCE 734 AA; 75251 MW; B3410CAF CRC32;

alignment_scores:
Quality: 63.50 Length: 72
Ratio: 1.984 Gaps: 2
Percent Similarity: 44.444 Percent Identity: 29.167

alignment_block:

US-09-240-675-1_COPY_1_229/rev x 088970 ..

Align seg 1/1 to: 088970 from: 1 to: 734

124 GGAGATTTAGATTTTTCACCTGCGCTGCGGACACACCCATGGGCC 75
|||||:
439 GlyaspLeuTyrArgLeuProProAlaSerAlaAlaThrSerGlnGlypr 455
74 CACGGCGACGACACTAGGCTGCGCGCCGACGA..... 40
| : : : :
455 OThrAlaGlySerSerMet.SerSerGluProGlyAspAsnGlyAspTyr 471
40 40
472 ThrGluMetAlaPheGlyValAlaAlaThrProProGlnProIleValAl 488
39GGACGACCATCATCTGGGAGCC 18
: : : : :
488 aProProLysProGluGluAlaArgValAlaSerProThrSerCylLeu 505
17 GCCCGACATCCCTG 4
: : : : :
505 ysaArgLeuSerLeu 509

seq_name: sp_phae:064317

seq_documentation_block:
ID 064317 PRELIMINARY; PRT: 640 AA.

AC 064317;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE TERMINASE LARGE SUBUNIT.
GN GENE 2.
OS Bacteriophage N15.
OC Viruses.
RN [1]
RP SEQUENCE FROM N.A.
RA HENDRIX R.W., RAVIN V.K., CASJENS S.R., FORD M.E., RAVIN N.V.,
RA SMIRNOV I.K.;
RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF064539; AAC19038.1; -
SQ SEQUENCE 640 AA; 73094 MW; E1B34267 CRC32;

alignment_scores:
Quality: 63.00 Length: 99

Ratio: 1.340 Gaps: 4
Percent Similarity: 47.475 Percent Identity: 26.263

alignment_block:

US-09-240-675-1_COPY_1_229 x 064317 ..

Align seg 1/1 to: 064317 from: 1 to: 640

```

8 GATTCGGCGGCGCTCCAGATGATGT..... 34
   ||||| ||||| |||||
101 GULeuLeuTrpLeuProThrAspValAlaAspAspMetLysS 117
   ||||| ||||| |||||
35 .....CGTCCTCTGGCGGAGCAGCCAGTCTGCTGCGCGGCG 77
   ||||| ||||| |||||
117 rHisValGluProThrIleArgAspValProSer.LeuLeuSerLeuAla 133
   ||||| ||||| |||||
78 CCATG.....GCTGTCTCCGCA..... 95
   ||||| ||||| |||||
134 ProTrpTyrGlyLysLysHisArgAspAsnThrLeuSerMetLysArgPh 150
   ||||| ||||| |||||
96 .....GCCGCGAGTGAATAAATCTAAATCTC 123
   ||||| ||||| |||||
150 eHrnsnGlyArgGlyPheTrpCysLeuGlyLysAlaAlaLysAsnT 167
   ||||| ||||| |||||
167 yArgGluLysSerValAspValAlaGlyTyrAspGluLeuAlaAlaPhe 183
   ||||| ||||| |||||
174 AACAGAGGAGTGTCTCTCGGAATGTACTTTTCTTGTGAT 218
   ||||| ||||| |||||
184 AspAlaAspIleGluLysGluLysSerProThrPheLeuGlyAsp 198

```

seq_name: sp_human:Q13507

seq_documentation_block:

```

ID Q13507 PRELIMINARY; PRT; 848 AA.
AC Q13507; 000593;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE TRANSIENT RECEPTOR POTENTIAL RELATED CHANNEL 3 PROTEIN.
GN TRPC3 OR HTRP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96234226.
RA ZHU X., JIANG M., PEYTON M., BOULAY G., HUNST R., STEFANI E.,
RA BIRNBAUMER L.;
RT "trp, a novel mammalian gene family essential for agonist-activated
RT capacitative Ca2+ entry.";
RL Cell 85:661-671(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97358541.
RA XU X.Z.S., LI H.S., GUGGINO W.B., MONTELL C.;
RT "Coassembly of TRP and TRPL produces a distinct store-operated
RT conductance.";
RL Cell 89:1155-1164(1997).
DR EMBL: 047050; AAC51653.1; -
DR EMBL: Y13758; CAA74083.1; -
DR PFMW: PF00023; ank; 2.
DR PRINTS: PR01097; TRNSRCEPTRP.
SQ SEQUENCE 848 AA: 97354 MW: 78kC2E9D CRC32:

```

alignment_scores:

Quality: 63.00 Length: 75
Ratio: 1.537 Gaps: 3
Percent Similarity: 54.667 Percent Identity: 33.333

alignment_block:

US-09-240-675-1_COPY_1_229 x Q13507 ..
Align seg 1/1 to: Q13507 from: 1 to: 848

```

30 ATGGTCGTCTCTCGGCGGCGAGCAGCCAGTCTGCTGCGCGGCGGCC 79
   ||||| ||||| |||||
351 LeuValValLeuValAlaLeuGlyLeuProPheLeuAlaIleGlyTyr 367
   ||||| ||||| |||||
80 ATGGGTCTTGTCCGAGCGCGAGGTGAAAAAATCTAAATCTCTCTCAA 129
   ||||| ||||| |||||
367 rTriPheLeuProCysSerArgLeuGlyLysIleLeuArgSerProPhe 384
   ||||| ||||| |||||
130 AAGTAGAGTC.....GACATCATAGATGACACTTATCTGTG 167
   ||||| ||||| |||||
384 eLysPheValAlaHisAlaLaserPheIleIlePheLeuGlyLeuLeu 400
   ||||| ||||| |||||
168 AGGTGAGACAGAGGAGTGTCTGTGCGG.....AATGT 202
   ||||| ||||| |||||
401 ValPheAsnAlaSerAspArgPheGluGlyIleThrThrLeuProAsnI 417
   ||||| ||||| |||||
203 GACTTTTCTTCGATTATCAAAA 227
   ||||| ||||| |||||
417 eHrValThr...AspTyrProLys 424

```

seq_name: sp_rodent:Q60697

seq_documentation_block:

```

ID Q60697 PRELIMINARY; PRT; 1344 AA.
AC Q60697;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE P162 PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-LYMPHOID TUMOR;
RA FISHER R., FILLMORE H., REYNOLDS A.B.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U14172; AAA90910.1; -
SQ SEQUENCE 1344 AA: 161949 MW: 86593FEF CRC32:

```

alignment_scores:

Quality: 63.00 Length: 103
Ratio: 1.432 Gaps: 7
Percent Similarity: 42.718 Percent Identity: 31.068

alignment_block:

US-09-240-675-1_COPY_1_229 x Q60697 ..

Align seg 1/1 to: Q60697 from: 1 to: 1344

```

11 CTGCGCGGCTC.....CC 24
   ||||| ||||| |||||
936 LeuArgArgLeuGlyGlyAspAspGluLArgGluSerLeuArgPr 952
   ||||| ||||| |||||
25 ACATGATGTCCTCTCTCT.....GGCGCGACACACCTAGTGTCTGTC 68
   ||||| ||||| |||||
952 oAspAspAspArgIleProArgArgGlyLeuAspAspArgGlyProA 969
   ||||| ||||| |||||
69 GCGGTGGCGCATGGGTGTCTCCGACCGCAGC..... 103
   ||||| ||||| |||||
969 rArgGlyProAspGluAspArgPheSerArgArgGlyThrAspAsp 985
   ||||| ||||| |||||
104 .....TGGAAAAAATCT.....AAATCTC 123
   ||||| ||||| |||||
986 ArgProSerTrpArgAsnAlaAspAspArgProArgArgIleG 1002
   ||||| ||||| |||||
124 CTCAAAAAGTAGAGT.....CGACATCATGATGACAACTTATCTCTG 167
   ||||| ||||| |||||

```

1002 yaspaspasparglysertparh1s.thraspaspargpropro 1018
 168 AGG.....TGAACAGAGGAGCATGATC 190
 1019 ArgArgGlyLeuaspaspGluArgGlySertParh1aspGluas 1035
 191 TGTCGGG 197
 1035 parggly 1037

seq_name: sp_invertebrate:Q94603

seq_documentation_block:
 ID Q94603 PRELIMINARY; PRT; 326 AA.
 AC Q94603;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
 DE MTCC.
 GN MTCC.
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

RA SISK E., SUNKIN S., SMARTZELL S., WESTLAKE T., MAGNESS C., BASTIEN P.,
 RA FU G., IVENS A., STUART K.,
 RA "Leishmania major Friedlin chromosome 1 has only two polyclistronic
 RT units of protein coding genes."
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RA MYLER P.J., AUDLEMAN L., HIXSON G., KISER P., LEMLEY C., RICKEL E.,
 RA SISK E., SUNKIN S., SMARTZELL S., WESTLAKE T., MAGNESS C., BASTIEN P.,
 RA FU G., IVENS A., STUART K.,
 RA "The nucleotide sequence of Leishmania major Friedlin chromosome 1."
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE001274; AAC24664.1;
 SO SEQUENCE 326 AA; 36141 MW; A629DA98 CRC32;

alignment_scores:
 Quality: 62.50 Length: 66
 Ratio: 1.645 Gaps: 3
 Percent Similarity: 57.576 Percent Identity: 30.303

alignment_block:
 US-09-240-675-1_COPY_1_229 x Q94603 ..

Align seg 1/1 to: Q94603 from: 1 to: 326

12 TGGGGGGGCGCCAGATGATGCTGCTCCTG.....GG 46
 156 CysGlyLeuSerLeuAlaThrMetTrpLeuLysArgLeProThrG 172
 47 CGCGAGACACCTAGTCTCTGTC...GCCGTGGCCCATGGGTGTGCG 93
 172 ythrtrhrthserthrleuLeuArgAlaThrValProPhelLeuAlaValS 189
 94 CAGCCGAGGTGGAAAAATCTAAATCTCTCAAAAAGTAGAG..... 137
 189 erCysAlaAlaThrValAsnLeuAlaSerMetArgLysAsnGluTrpLeu 205
 138GTGACATCATAGATGACACTTATCTGAGG 170
 206 SerSerGlyGlnGlyLeuArgValValaspaspGlyValThrArg 221

seq_name: sp_plant:O23212

seq_documentation_block:
 ID O23212 PRELIMINARY; PRT; 573 AA.
 AC O23212;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE SPLICING FACTOR-LIKE PROTEIN.
 GN C7A10.670.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 OC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BEVAN M., TERRY N., VOS P., HEIJNEN L., MEMES H.W., SCHUELLER C.,
 RA CHALMERS N.,
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z99708; CAB16828.1;
 DR HSSP; P19339; 2SXL.
 DR PFAM; PF00076; trm; 2.
 SO SEQUENCE 573 AA; 63551 MW; 07954A00 CRC32;

alignment_scores:
 Quality: 62.50 Length: 75
 Ratio: 1.645 Gaps: 3
 Percent Similarity: 50.667 Percent Identity: 33.333

alignment_block:
 US-09-240-675-1_COPY_1_229 x O23212 ..

Align seg 1/1 to: O23212 from: 1 to: 573

5 AGGAGTCTCGGCGGCTCCAGATGATGCTGCTCCTGGGCGGAG.. 52
 46 ArgGluThrSerArgSerLysAspArgGluArgGlyArgAspLys 62
 53GACCTAGTCTGCTGCGCGCGGCGCCAGGGGTGTG 89
 62 sasparGluArgAspSerGluValSerArgArgSer..... 74
 90 TCCGACGCCGCGAGGTGGAAAAATCTAAATCTCTCAAAAAGT..... 133
 75 ..ArgaspArgaspGlyGluLysSerLysGluArgSerArgAspLysasp 90
 134AGAGTGCATCATGATGACACAACTTATCTCGAGCGGA 174
 91 ArgaspHisArgGluArgHisHisArgSerSerArgHisArgAspHis 107
 107 fArgGluArgGlyGluArgArgGlu 115

seq_name: sp_mammal:O77699

seq_documentation_block:
 ID O77699 PRELIMINARY; PRT; 117 AA.
 AC O77699;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE TRP3 PROTEIN (FRAGMENT).
 GN TRP3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Bovine; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA WISSENBACH U., PHILIPP S., FLOCKERZ V.,
 RT "Cloning and analysis of TRP channels."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ006781; CA07246.1;
 FT NON_TER 1 1
 FT NON_TER 117 117
 SO SEQUENCE 117 AA; 13295 MW; B9F9B808 CRC32;

alignment_scores:

Quality: 62.00 Length: 75
Ratio: 1.512 Gaps: 3
Percent Similarity: 54.667 Percent Identity: 33.333

alignment_block:

US-09-240-675-1_COPY_1_229 x 077699 ..

Align seg 1/1 to: 077699 from: 1 to: 117

```
30 ATGTCGTCCTCGTCGGCGCGACGACCTAGTCGTGCGCCGCGGCC 79
   :::::::::::::: :::: :::::
25 LeuValValLeuValAlaLeuGlyLeuProPheLeuAlaIleGlyTY 41
80 ATGGGTGTTCGCCGACGCCGAGGTGAAAAATCTAAATCTCTCAAA 129
   ::::: ::::: ::::: :::::
41 rTTPLeuAlaProCysSerArgLeuGlyLysValLeuArgSerProPhe 58
   ::::: ::::: :::::
130 AAGTAGAGGTC.....GACATCATGATGACACATTATCTCTG 167
   :::::
58 eLysPheValAlaHisAlaAlaSerPheIleIlePheLeuGlyLeu 74
   :::::
168 AGGTGGAACAGGAGGATGATGTCGCGG.....AATGT 202
   :::::
75 ValPheAsnAlaSerAspArgPheGluGlyIleThrThrLeuProAsn 91
   :::::
203 GACCTTTTCATTCGATTATCAAAA 227
   :::::
91 eThrVal...IleAspTyrProLys 98
```

seq_name: sp_human:095927

seq_documentation_block:

ID 095927 PRELIMINARY: PRT: 290 AA.
AC 095927:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE D1465N24.2.1 (PUTATIVE NOVEL PROTEIN) (ISOFORM 1).
GN D1465N24.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA WILSON S.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL031432; CAB37992.1; ..
SQ SEQUENCE 290 AA; 33613 MM; B59E0C18 CRC32;

alignment_scores:

Quality: 62.00 Length: 62
Ratio: 2.296 Gaps: 1
Percent Similarity: 43.548 Percent Identity: 29.032

alignment_block:

US-09-240-675-1_COPY_1_229 x 095927 ..

Align seg 1/1 to: 095927 from: 1 to: 290

```
32 GGTGTCCTCGTCGGCGCGACGACCTAGTCGTGCGCCGCGGCCAT 81
   :::::
11 GlySerProGlnGluLysAspSerProSerThrSerArgSerGlyGlySe 27
82 GGGTGTTCGCCGACGCCG.....
   :::::
27 rSerArgLeuSerSerArgSerArgSerPheSerArgSerSerA 44
101 .....AGGTGAAAAAATCT 115
   :::::
```

```
44 rGSerHisSerArgValSerSerArgPheSerSerArgSerArgSer 60
116 AAATCTCTCAAAAAGTAGAGTGCACATCATAGA 151
   :::::
61 LysSerArgSerArgSerArgArgHisGlnArg 72
```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 00:40:12 ; Search time 42.08 Seconds

(Without alignments)
114.265 Million cell updates/sec

Title: US-09-240-675-2_COPY_27_229

Perfect score: 1072
Sequence: 1 GKNLSPQKVEVDIIDNFI.....WKIGYSPVHCIKITVENEL 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_35.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1072	100.0	436	1 R14487	Soluble Interferon
2	1072	100.0	436	1 R28495	Sequence of a soul
3	1072	100.0	436	1 R17723	IFN receptor extra
4	1072	100.0	557	1 R11958	Human alpha-interf
5	1072	100.0	557	1 R14488	Complete Interfero
6	1072	100.0	557	1 R28496	Sequence of a soul
7	1072	100.0	557	1 R42635	Human interferon r
8	1072	100.0	557	1 R75356	Human IFN receptor
9	1067	99.5	434	1 W21805	Spliced-deleted in
10	1067	99.5	496	1 W21806	Spliced-deleted in
11	1067	99.5	557	1 W21804	Transmembranal int
12	214	20.0	325	1 W52296	CRFB4 protein. New
13	199	18.6	332	1 R75782	IFN-gamma receptor
14	166.5	15.5	553	1 W79159	Zcytor7 cytokine r
15	144	13.4	337	1 R1035	Human IFN-gamma ac
16	142	13.2	317	1 R75783	IFN-gamma receptor
17	131.5	12.3	211	1 W97864	Human cytokine rec
18	131.5	12.3	574	1 W97861	Human cytokine rec
19	111	10.4	210	1 R14643	Gamma interferon r
20	111	10.4	227	1 R14642	Gamma interferon r
21	111	10.4	231	1 R14641	Gamma interferon r
22	111	10.4	473	1 R55749	Extracellular doma
23	111	10.4	489	1 R07469	Plasmaid PBABLU hu
24	111	10.4	942	1 R70113	Gamma-IFN-R-GBP 13
25	108	10.1	245	1 R62023	Soluble human inte
26	93.5	8.7	219	1 W17734	Human truncated ti
27	93.5	8.7	263	1 W17725	Human tissue facto
28	92	8.6	265	1 R80063	Human IFNAB-BPI en
29	90.5	8.4	219	1 W17749	Human truncated ti
30	90.5	8.4	219	1 W17750	Human truncated ti
31	90.5	8.4	263	1 W17742	Human tissue facto
32	90.5	8.4	263	1 W17743	Human tissue facto
33	90.5	8.4	553	1 W5856	Human CD45 for use
34	89.5	8.3	219	1 W17751	Human truncated ti

35	89.5	8.3	219	1	W17732	Human truncated ti
36	89.5	8.3	219	1	W17733	Human truncated ti
37	89.5	8.3	263	1	W17744	Human tissue facto
38	89.5	8.3	263	1	W17723	Human tissue facto
39	89.5	8.3	263	1	W17724	Human tissue facto
40	89.5	8.3	223	1	W26356	Rabbit LDL recepto
41	89	8.3	239	1	R80067	Human IFNAB-BPI
42	89	8.3	331	1	R80066	Human IFNAB-BPI. N
43	88.5	8.3	219	1	W69605	Human truncated ti
44	87.5	8.2	219	1	W17752	Human truncated ti
45	87.5	8.2	219	1	W17728	Human truncated ti

ALIGNMENTS

RESULT	1	
R14487		
ID	R14487 standard: Protein; 436 AA.	
AC	R14487	
DE	16-JAN-1992 (first entry)	
DR	Soluble Interferon-alpha/beta receptor.	
KW	IFN; autoimmune disease; graft rejection; histocompatibility.	
OS	Homo sapiens.	
PN	FR2657881-A.	
PD	09-AUG-1991.	
PF	05-FEB-1990; 001298.	
PR	05-FEB-1990; FR-001298.	
PA	(FBI-) LAB EURO BIOTECHNO.	
PI	Eid P, Gresser I, Lutalla G, Meyer F, Mogenssen KE;	
PI	Tovey MG, Uze G;	
DR	WPI; 91-31978/44.	
DR	N-PSDB; Q14239.	
PT	New water-soluble polypeptide(s) with affinity for IFN-alpha and	
PT	beta - used to treat e.g. lupus erythematosus, Behcet's disease,	
PS	aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.	
PS	Claim 2; Page 45; 52pp: French.	
CC	The transmembrane and cytoplasmic domains of the native IFN receptor	
CC	have been deleted to obtain a soluble, circulating form of the	
CC	receptor. Potentially immunogenic epitopes have thus been eliminated.	
CC	Derivatives obtained by substitution or deletion of this sequence	
CC	are also claimed as are hybrid molecules comprising the soluble	
CC	receptor (or deriv.) and an immunoglobulin such as IgG1.	
CC	See also Q14240.	
SO	Sequence 436 AA;	

Query Match 100.0%; Score 1072; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 1.1e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GKNLSPQKVEVDIIDNFIIRNRSDESVGNVTFSPDYORTGMDNMKLSGCONITSTK	60
DB	27	GKNLSPQKVEVDIIDNFIIRNRSDESVGNVTFSPDYORTGMDNMKLSGCONITSTK	86
QY	61	CNFSLLKLVYEELIKRIRAKENTSSWYEDSTPPKKAQIGPEVHLEDAIYIH	120
DB	87	CNFSLLKLVYEELIKRIRAKENTSSWYEDSTPPKKAQIGPEVHLEDAIYIH	146
QY	121	SPGKDSYMAALDGLSPFYSLIKNNSGVEERENIYSRKIKYKLSPEYTCIKVRAAL	180
DB	147	SPGKDSYMAALDGLSPFYSLIKNNSGVEERENIYSRKIKYKLSPEYTCIKVRAAL	206
QY	181	LTSWKIGYSPVHCIKITVENEL	203
DB	207	LTSWKIGYSPVHCIKITVENEL	229

RESULT 2
R28495
ID R28495 standard: Protein; 436 AA.
AC R28495:
DT 31-MAR-1993 (first entry)

DE Sequence of a soluble form of the interferon (IFN) receptor
 DE with a high affinity for IFN-alpha and -beta.
 KM Interferon receptor; alpha-interferon; beta-interferon.
 OS Synthetic.
 PN MO9218626-A.
 PD 29-OCT-1992.
 PF 17-APR-1991; F00318.
 PF 17-APR-1991; MO-F00318.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
 PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
 PI Tovey M, Uze G.
 DR N-PSDB: Q30532.
 DR WPI: 92-38210/46.
 PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
 PT and beta - useful as immunosuppressants, for treating auto-immune
 PT diseases and transplant rejection
 PS Claim 2: Fig 1: 58pp: English.
 CC DNA encoding the water-soluble polypeptide with a high affinity for
 CC IFN-alpha and -beta is isolated by PCR, using appropriate
 CC oligonucleotides as primers and cloned cDNA as template. For example,
 CC bacteriophage lambda ZAP, containing the entire coding sequence of
 CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
 CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
 CC lacks the transmembrane and cytoplasmic domains. Both forms bind
 CC IFN in the same way as antibodies so are immunosuppressants e.g. for
 CC treating autoimmune diseases and graft rejection. They lack the
 CC toxic side-effects of known immunosuppressants such as steroids.
 SO Sequence 436 AA.

Query Match 100.0%; Score 1072; DB 1; Length 436;
 Best Local Similarity 100.0%; Pred. No. 1.1e-101;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GKNLSPKQVEVDIIDDNFILRNRSDESGVNTFSFDYQKTMGMWIKLSGCCNITSTK 60
 DB 27 GKNLSPKQVEVDIIDDNFILRNRSDESGVNTFSFDYQKTMGMWIKLSGCCNITSTK 86
 OY 61 CNFSSLKLVYEEIKLRIRAKENTSSWYEDSFTPFRAKQIGPPEVHLEADKAIVYHI 120
 DB 87 CNFSSLKLVYEEIKLRIRAKENTSSWYEDSFTPFRAKQIGPPEVHLEADKAIVYHI 146
 OY 121 SPGTDSVMMALDGLSFTYSLILWKNSSGVEERIEINYSRHKIKYKLSPTTYCLKVKAAL 180
 DB 147 SPGTDSVMMALDGLSFTYSLILWKNSSGVEERIEINYSRHKIKYKLSPTTYCLKVKAAL 206
 OY 181 LTSMKIGVSPVHCITKTVENEL 203
 DB 207 LTSMKIGVSPVHCITKTVENEL 229

RESULT 3
 R71723

ID R71723 standard; Protein: 436 AA.
 AC R71723;
 DT 16-OCT-1995 (first entry).
 KM IFN receptor extracellular domain.
 KM IFN receptor; interferon receptor; interferon-alpha;
 KM interferon-beta; monoclonal antibody; immunomodulator; AIDS.
 OS Homo sapiens.
 PN MO9507716-A.
 PD 23-MAR-1995.
 PF 16-SEP-1994; E03114.
 PF 17-SEP-1993; EP-402279.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benizri EJ, Tovey MG.
 DR WPI: 95-131187/17.
 DR N-PSDB: Q86457.
 PT Compos. of monoclonal antibodies against interferon receptor -
 PT useful as immunomodulator, eg. for treating AIDS
 PS Disclosure: Fig.2A-2B: 105pp: English.
 CC A recombinant soluble form of the human interferon class I receptor
 CC protein extracellular domain, given in R71723, was expressed in

CC either E. coli or COS cell hosts. The protein was used to raise
 CC immunomodulatory monoclonal antibodies.
 SO Sequence 436 AA.

Query Match 100.0%; Score 1072; DB 1; Length 436;
 Best Local Similarity 100.0%; Pred. No. 1.1e-101;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GKNLSPKQVEVDIIDDNFILRNRSDESGVNTFSFDYQKTMGMWIKLSGCCNITSTK 60
 DB 27 GKNLSPKQVEVDIIDDNFILRNRSDESGVNTFSFDYQKTMGMWIKLSGCCNITSTK 86
 OY 61 CNFSSLKLVYEEIKLRIRAKENTSSWYEDSFTPFRAKQIGPPEVHLEADKAIVYHI 120
 DB 87 CNFSSLKLVYEEIKLRIRAKENTSSWYEDSFTPFRAKQIGPPEVHLEADKAIVYHI 146
 OY 121 SPGTDSVMMALDGLSFTYSLILWKNSSGVEERIEINYSRHKIKYKLSPTTYCLKVKAAL 180
 DB 147 SPGTDSVMMALDGLSFTYSLILWKNSSGVEERIEINYSRHKIKYKLSPTTYCLKVKAAL 206
 OY 181 LTSMKIGVSPVHCITKTVENEL 203
 DB 207 LTSMKIGVSPVHCITKTVENEL 229

RESULT 4

ID R11958 standard; Protein: 557 AA.
 AC R11958;
 DT 18-JUL-1991 (first entry)
 DE Human alpha-interferon receptor protein.
 KM Human alpha IFN; IFN agonists; antiviral; anti tumour agent;
 KM drug targeting.
 OS Homo sapiens.
 FT Key Location/Qualifiers
 FT peptide 1..27 /label= signal peptide
 PN MO9105862-A.
 PD 02-MAY-1991.
 PF 19-OCT-1990; F00758.
 PF 20-OCT-1989; FR-013770.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PI Mogensen KE, Uze G, Lutfalla G, Gresser I;
 DR WPI: 91-148740/20.
 DR N-PSDB: Q11701.
 PT New human alpha-interferon receptor protein - useful for testing
 PT interferon agonists and in treatment or diagnosis
 PS Disclosure: fig 4; 30pp: French.
 CC This recombinant human alpha interferon (IFN) receptor protein is
 CC useful for the testing of IFN agonists and for treatment and diag-
 CC nosis of viral diseases and tumours. Antibodies raised against
 CC this protein can be used for blocking the receptor when required,
 CC eg where overexpression of alpha-IFN is harmful. The Abs are
 CC also useful for eg drug targeting. Variants of the protein,
 CC having residue 164 (Thr) replaced by Arg and an Asp inserted
 CC between residues 479 and 480, are also useful.
 SO Sequence 557 AA.

Query Match 100.0%; Score 1072; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 1.5e-101;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GKNLSPKQVEVDIIDDNFILRNRSDESGVNTFSFDYQKTMGMWIKLSGCCNITSTK 60
 DB 27 GKNLSPKQVEVDIIDDNFILRNRSDESGVNTFSFDYQKTMGMWIKLSGCCNITSTK 86
 OY 61 CNFSSLKLVYEEIKLRIRAKENTSSWYEDSFTPFRAKQIGPPEVHLEADKAIVYHI 120
 DB 87 CNFSSLKLVYEEIKLRIRAKENTSSWYEDSFTPFRAKQIGPPEVHLEADKAIVYHI 146
 OY 121 SPGTDSVMMALDGLSFTYSLILWKNSSGVEERIEINYSRHKIKYKLSPTTYCLKVKAAL 180

Db 147 SPGTRDSVMALDGLSFTSYSLIMKNSGVEERINISRHKIKLSPETTYCLAKVKAAL 206
 QY 181 LTRMKIGVSPVHCITKTVENEL 203
 Db 207 LTRMKIGVSPVHCITKTVENEL 229

RESULT 5
 R14488
 ID R14488 standard; Protein: 557 AA.
 AC R14488;
 DT 16-JAN-1992 (first entry)
 DE Complete interferon-alpha/beta receptor.
 KW IFN; autoimmune disease; graft rejection; histocompatibility.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 437..457
 FT /label= transmembrane
 FT 458..557
 FT /label= cytoplasmic
 PN FR2657881-A.
 PD 09-AUG-1991.
 PF 05-FEB-1990; 001298.
 PR 05-FEB-1990; FR-001298.
 PA (EUBI-) LAB EURO BIOTECHNO.
 PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
 PI Tovey MG, Uze G;
 PI WPI: 91-31978/44.
 DR N-PSDB: Q14240.
 PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
 PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
 PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
 PS Disclosure: Page 47: 52pp; French.
 CC The invention covers derivatives of the interferon-alpha and/or beta
 CC receptor obtained by deleting the transmembrane and cytoplasmic domains
 CC of the native receptor or by substitution. Potentially immunogenic
 CC epitopes are eliminated and the deriv. can be secreted from
 CC transformed cells. Soluble deriv.s block the activity of IFN alpha/beta
 CC and can be used to treat autoimmune diseases or to inhibit graft
 CC rejection. See also Q14239.
 SQ Sequence 557 AA;

Query Match 100.0%; Score 1072; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 1.5e-101;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNLKSPKVEVDIIDNFIILRNRSDESVGNTFSFDYOKTGMNWKILSGCQNTSTK 60
 Db 27 GNLKSPKVEVDIIDNFIILRNRSDESVGNTFSFDYOKTGMNWKILSGCQNTSTK 86
 QY 61 CNFSSKLNVYEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEAEKAIYIH 120
 Db 87 CNFSSKLNVYEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEAEKAIYIH 146
 QY 121 SPGTRDSVMALDGLSFTSYSLIMKNSGVEERINISRHKIKLSPETTYCLAKVKAAL 180
 Db 147 SPGTRDSVMALDGLSFTSYSLIMKNSGVEERINISRHKIKLSPETTYCLAKVKAAL 206
 QY 181 LTRMKIGVSPVHCITKTVENEL 203
 Db 207 LTRMKIGVSPVHCITKTVENEL 229

RESULT 6
 ID R28496
 AC R28496 standard; Protein: 557 AA.
 DT 31-MAR-1993 (first entry)
 DE Sequence of a soluble form of the interferon (IFN) receptor
 DE with a high affinity for IFN-alpha and -beta.
 KW Interferon receptor; alpha-interferon; beta-interferon.

OS Synthetic.
 PN WO9218626-A.
 PD 29-OCT-1992.
 PR 17-APR-1991; F00318.
 PR 17-APR-1991; WO-F00318.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
 PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
 PI Tovey M, Uze G;
 PI WPI: 92-382110/46.
 DR N-PSDB: Q30533.
 PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
 PT and beta - useful as immunosuppressants, for treating autoimmune
 PT diseases and transplant rejection
 PS Claim 3; Fig 2; 58pp; English.
 CC DNA encoding the water-soluble polypeptide with a high affinity for
 CC IFN-alpha and -beta is isolated by PCR, using appropriate
 CC oligonucleotides as primers and cloned cDNA as template. For example,
 CC bacteriophage lambda ZAP, containing the entire coding sequence of
 CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
 CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
 CC lacks the transmembrane and cytoplasmic domains. Both forms bind
 CC IFN in the same way as antibodies so are immunosuppressants e.g. for
 CC treating autoimmune diseases and graft rejection. They lack the
 CC toxic side-effects of known immunosuppressants such as steroids.
 SQ Sequence 557 AA;

Query Match 100.0%; Score 1072; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 1.5e-101;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNLKSPKVEVDIIDNFIILRNRSDESVGNTFSFDYOKTGMNWKILSGCQNTSTK 60
 Db 27 GNLKSPKVEVDIIDNFIILRNRSDESVGNTFSFDYOKTGMNWKILSGCQNTSTK 86
 QY 61 CNFSSKLNVYEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEAEKAIYIH 120
 Db 87 CNFSSKLNVYEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEAEKAIYIH 146
 QY 121 SPGTRDSVMALDGLSFTSYSLIMKNSGVEERINISRHKIKLSPETTYCLAKVKAAL 180
 Db 147 SPGTRDSVMALDGLSFTSYSLIMKNSGVEERINISRHKIKLSPETTYCLAKVKAAL 206
 QY 181 LTRMKIGVSPVHCITKTVENEL 203
 Db 207 LTRMKIGVSPVHCITKTVENEL 229

RESULT 7
 ID R42635
 AC R42635 standard; Protein: 557 AA.
 DT 20-APR-1994 (first entry)
 DE Human interferon receptor.
 KW IFN-R; extracellular domain; monoclonal antibody; viral infection;
 KW cell proliferation; allograft rejection; systemic lupus erythematosus;
 KW psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;
 KW immunodeficiency; measles virus; interferon-alpha-beta.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 1..436
 FT /label= extracellular_domain
 FT /note= "soluble, immunogenic form of IFN-R"
 PN EP-563487-A.
 PD 06-OCT-1993.
 PF 31-MAR-1992; 400902.
 PR 31-MAR-1992; EP-400902.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG;
 DR WPI: 93-312951/40.
 DR P-PSDB: R42635.
 PT Monoclonal antibody to human interferon type-I receptor - having
 PT neutralising activity against human type I interferon, used for

PT therapy and diagnosis
 PS Disclosure: Fig 3: 21pp: English.
 CC Monoclonal antibodies produced against soluble forms of the human
 CC interferon alpha-beta receptor based on the full-length human IFN-R
 CC sequence are claimed. The antibodies are useful for treatment and
 CC prophylaxis of disorders involving cell proliferation and/or viral
 CC infection.
 SO Sequence 557 AA:

Query Match 100.0%; Score 1072; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 1.5e-101;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GKNLSPQKVEVDIIDNFIILMNRSDSVGNVTFSPDYQKTGMNMWIKLSCGQNTSTK 60
 DB 27 GKNLSPQKVEVDIIDNFIILMNRSDSVGNVTFSPDYQKTGMNMWIKLSCGQNTSTK 86
 OY 61 CNFSSLKLVNVEEIKLRIRAEKENTSMWEVDSFTPRKAOIGPPEVHLEADKAIVIH 120
 DB 87 CNFSSLKLVNVEEIKLRIRAEKENTSMWEVDSFTPRKAOIGPPEVHLEADKAIVIH 146
 OY 121 SPGTRDSVMALDGLSTFTYSLIMKNSGVEERINISRHKIYKLSPEPTYCLKVAAL 180
 DB 147 SPGTRDSVMALDGLSTFTYSLIMKNSGVEERINISRHKIYKLSPEPTYCLKVAAL 206
 OY 181 LTSWKIGVSPVHCITTVENEL 203
 DB 207 LTSWKIGVSPVHCITTVENEL 229

RESULT 8

R75356
 ID R75356 standard; Protein: 557 AA.
 AC R75356;
 DT 16-OCT-1995 (first entry)
 DE Human IFN receptor.
 KW IFN receptor; interferon receptor; Interferon-alpha;
 KM Interferon-beta; monoclonal antibody; immunomodulator; AIDS.
 OS Homo sapiens.

FT Key Location/Qualifiers
 FT domain 1..436
 FT /label= Extracellular_domain
 FT W09507716-A.
 PD 23-MAR-1995.
 PR 16-SEP-1994; E03114.
 PR 17-SEP-1993; EP-402279.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benlzrl EJ, Tovey MG;
 DR N-PSDB; 086458.
 PT Compn. of monoclonal antibodies against interferon receptor -
 PT usetul as immuno/modulator, eg. for treating AIDS
 PS Disclosure: Fig. 3A-2B; 105pp; English.
 CC The amino acid sequence of human interferon class I receptor is
 CC given in R75356. A recombinant soluble form of the extracellular
 CC domain of this receptor (R71723) has been used to raise
 CC immunomodulatory monoclonal antibodies.
 SO Sequence 557 AA:

Query Match 100.0%; Score 1072; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 1.5e-101;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GKNLSPQKVEVDIIDNFIILMNRSDSVGNVTFSPDYQKTGMNMWIKLSCGQNTSTK 60
 DB 27 GKNLSPQKVEVDIIDNFIILMNRSDSVGNVTFSPDYQKTGMNMWIKLSCGQNTSTK 86
 OY 61 CNFSSLKLVNVEEIKLRIRAEKENTSMWEVDSFTPRKAOIGPPEVHLEADKAIVIH 120
 DB 87 CNFSSLKLVNVEEIKLRIRAEKENTSMWEVDSFTPRKAOIGPPEVHLEADKAIVIH 146

OY 121 SPGTRDSVMALDGLSTFTYSLIMKNSGVEERINISRHKIYKLSPEPTYCLKVAAL 180
 DB 147 SPGTRDSVMALDGLSTFTYSLIMKNSGVEERINISRHKIYKLSPEPTYCLKVAAL 206
 OY 181 LTSWKIGVSPVHCITTVENEL 203
 DB 207 LTSWKIGVSPVHCITTVENEL 229

RESULT 9

W21805
 ID W21805 standard; Protein: 434 AA.
 AC W21805;
 DT 23-SEP-1997 (first entry)
 DE Spliced-deleted interferon alpha-receptor form 1.
 KW Interferon alpha-receptor; IFNAR.
 OS Homo sapiens.

FT Key Location/Qualifiers
 FT domain 1..427
 FT /label= Extracellular_domain
 FT /note= "comprises amino acids 1-427 of the
 FT transmembrane IFNAR"
 FT 428..434
 FT /label= S-domain
 FT AU9475977-A.
 PN 11-MAY-1995.
 PD 20-OCT-1994; 075977.
 PR 24-OCT-1993; IL-107378.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (ABRA/) ABRAMOVICH C.
 PI Abramovich C, Ratovitski E, Revel M;
 DR WPI: 95-200634/27.
 PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Example 2; Fig 7; 46pp; English.
 CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 1
 CC (W21805) is characterised by a new domain (S) which follows an
 CC end-deleted extracellular domain when compared to transmembrane
 CC IFNAR (W21804). There is no transmembrane domain. The amino acid
 CC sequence is predicted from a cDNA clone (see also W73520) obtd.
 CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
 CC splice-deleted forms 1 and 2 (see also W21806) probably regulate
 CC the response of human cells to IFNs, either by acting as IFN
 CC antagonists or by regulating the activity of the multiple IFN
 CC subtypes. They can be expressed in host cells and used to inhibit,
 CC modulate or modify the activities of IFNs alpha and beta in cells,
 CC tissues and organisms, or for diagnostic purposes.
 SO Sequence 434 AA:

Query Match 99.5%; Score 1067; DB 1; Length 434;
 Best Local Similarity 99.5%; Pred. No. 3.5e-101;
 Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GKNLSPQKVEVDIIDNFIILMNRSDSVGNVTFSPDYQKTGMNMWIKLSCGQNTSTK 60
 DB 27 GKNLSPQKVEVDIIDNFIILMNRSDSVGNVTFSPDYQKTGMNMWIKLSCGQNTSTK 86
 OY 61 CNFSSLKLVNVEEIKLRIRAEKENTSMWEVDSFTPRKAOIGPPEVHLEADKAIVIH 120
 DB 87 CNFSSLKLVNVEEIKLRIRAEKENTSMWEVDSFTPRKAOIGPPEVHLEADKAIVIH 146
 OY 121 SPGTRDSVMALDGLSTFTYSLIMKNSGVEERINISRHKIYKLSPEPTYCLKVAAL 180
 DB 147 SPGTRDSVMALDGLSTFTYSLIMKNSGVEERINISRHKIYKLSPEPTYCLKVAAL 206
 OY 181 LTSWKIGVSPVHCITTVENEL 203
 DB 207 LTSWKIGVSPVHCITTVENEL 229

RESULT 10

W21806

ID W21806 standard; Protein: 496 AA.
 AC W21806;
 DT 23-SEP-1997 (first entry)
 DE Spliced-deleted interferon alpha-receptor form 2.
 KW Interferon alpha-receptor; IFNAR.
 OS Homo sapiens.
 FH Key
 FT domain
 FT 1.419
 FT /label= Extracellular_domain
 FT /note= "Comprises amino acid residues 1-413 and
 FT 422-427 of transmembrane IFNAR"
 FT 420..496
 FT domain
 FT /label= Intracellular_domain
 FT /note= "Comprises amino acids 481-557 of
 FT transmembrane IFNAR"
 PN AU9475977-A.
 PD 11-MAY-1995.
 PE 20-OCT-1994; 075977.
 PF 24-OCT-1993; IL-107378.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (ABRA/) ABRAMOVICH C.
 PI Abramovich C, Ratovitski E, Revel M;
 DR WPI: 95-200634/27.
 PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Example 3; Fig 7; 46pp; English.
 CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2
 CC (W21806) is characterised by a double deletion when compared to
 CC transmembrane IFNAR (W21804). The extracellular domain is
 CC shortened by 6 amino acid residues and is followed by a truncated
 CC intracellular domain. There is no transmembrane region. The amino
 CC acid sequence is predicted from a cDNA clone (see also T73521) obtd.
 CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
 CC splice-deleted forms 1 (see also W21805) and 2 may regulate the
 CC response of human cells to IFNs, either by acting as IFN
 CC antagonists or by regulating IFN activities. They can be expressed
 CC in host cells and used to inhibit, modulate or modify the
 CC activities of IFNs alpha and beta in cells, tissues and organisms,
 CC or for diagnostic purposes.
 SQ Sequence 496 AA;

Query Match 99.5%; Score 1067; DB 1; Length 496;
 Best Local Similarity 99.5%; Pred. No. 4.3e-101;
 Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GKNLKSPOKYEVDIIDNFI LRNNSDES VGNVTSFDYKGTGMWNKLSGCONITSTK 60
 DB 27 GKNLKSPOKYEVDIIDNFI LRNNSDES VGNVTSFDYKGTGMWNKLSGCONITSTK 86
 QY 61 CNFSSKLNVYEIEIKLRIRAEKENTSSWEVDSFTPRKAOIGPPEVHLEADKAIVIH 120
 DB 87 CNFSSKLNVYEIEIKLRIRAEKENTSSWEVDSFTPRKAOIGPPEVHLEADKAIVIH 146
 QY 121 SPOTKDSVMMALDGLSFTYSLIWKNSGVEERIENTYSRHKIYKLSPEPTYCLKVAAL 180
 DB 147 SPOTKDSVMMALDGLSFTYSLIWKNSGVEERIENTYSRHKIYKLSPEPTYCLKVAAL 206
 QY 181 LTSWKIGVSPVHCITKTVENEL 203
 DB 207 LTSWKIGVSPVHCITKTVENEL 229

RESULT 11
 ID W21804
 AC W21804 standard; Protein: 557 AA.
 DT 23-SEP-1997 (first entry)
 DE Transmembrane interferon alpha-receptor.
 KW Interferon alpha-receptor; IFNAR.
 OS Homo sapiens.
 FH Key
 FT domain
 FT 1.436

FT domain
 FT 437..457
 FT /label= Extracellular_domain
 FT domain
 FT 458..557
 FT /label= Transmembrane_domain
 FT /label= Intracellular_domain
 PN AU9475977-A.
 PD 11-MAY-1995.
 PE 20-OCT-1994; 075977.
 PF 24-OCT-1993; IL-107378.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (ABRA/) ABRAMOVICH C.
 PI Abramovich C, Ratovitski E, Revel M;
 DR WPI: 95-200634/27.
 PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Disclosure; Fig 7; 46pp; English.
 CC Human transmembrane interferon alpha receptor (IFNAR) (W21804)
 CC includes a 21-amino acid transmembrane region. Novel, splice-
 CC deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected
 CC that lack this transmembrane domain. These, soluble non-membrane
 CC bound polypeptides can be expressed in host cells and used to
 CC inhibit, modulate or modify the activities of interferons alpha
 CC and beta in cells, tissues and organisms, or for diagnostic
 CC purposes.
 SQ Sequence 557 AA;

Query Match 99.5%; Score 1067; DB 1; Length 557;
 Best Local Similarity 99.5%; Pred. No. 5e-101;
 Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GKNLKSPOKYEVDIIDNFI LRNNSDES VGNVTSFDYKGTGMWNKLSGCONITSTK 60
 DB 27 GKNLKSPOKYEVDIIDNFI LRNNSDES VGNVTSFDYKGTGMWNKLSGCONITSTK 86
 QY 61 CNFSSKLNVYEIEIKLRIRAEKENTSSWEVDSFTPRKAOIGPPEVHLEADKAIVIH 120
 DB 87 CNFSSKLNVYEIEIKLRIRAEKENTSSWEVDSFTPRKAOIGPPEVHLEADKAIVIH 146
 QY 121 SPOTKDSVMMALDGLSFTYSLIWKNSGVEERIENTYSRHKIYKLSPEPTYCLKVAAL 180
 DB 147 SPOTKDSVMMALDGLSFTYSLIWKNSGVEERIENTYSRHKIYKLSPEPTYCLKVAAL 206
 QY 181 LTSWKIGVSPVHCITKTVENEL 203
 DB 207 LTSWKIGVSPVHCITKTVENEL 229

RESULT 12
 ID W52296
 AC W52296 standard; Protein: 325 AA.
 DT 23-JUN-1998 (first entry)
 DE CRP4 protein.
 KW CRP4; Interleukin-10; IL-10; IL-10 receptor; allograft rejection;
 KW vaccine; photosensitivity; inflammation; autoimmune disease;
 KW septic shock; immune response; organ rejection; gene therapy.
 OS Homo sapiens.
 PN MO9802542-A1.
 PD 22-JAN-1998.
 PE 17-JUL-1997; U12455.
 PF 17-JUL-1996; US-683743.
 PA (UYNE-) UNIV NEW JERSEY.
 PI Kotenko SV, Pestka S;
 DR WPI: 98-110590/10.
 DR N-PSDB: V19874.
 PT New recombinant DNA - comprises sequences encoding interleukin-10
 PT and CRP4 linked to operator, useful, e.g. preventing allograft
 PT rejection
 PS Claim 2; Page -: 79pp; English.
 CC This sequence is the human CRP4 sequence, DNA encoding it is used in the
 CC recombinant DNA (1) of the invention. (1) comprises a sequence (S1)
 CC encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2)

CC encodinf CRFB4, both operably linked to expression control sequences.
CC Cells containing (1) may be used to identify agonists/antagonist of
CC IL-10. Agonists are potentially useful, e.g. for preventing allograft
CC rejection, as vaccine adjuvants, for treatment of photosensitivity,
CC inflammation, autoimmune disease and septic shock, while antagonists are
CC potentially useful for increasing immune responses against tumors,
CC viruses, bacteria and parasites (especially intracellular pathogens) and
CC for preventing organ rejection. A vector containing (1) is used to
CC restore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses
CC a dysfunctional IL10R and is able to bind IL-10 but not to transduce a
CC signal. Antisense CRFB4 sequences (especially ribozymes), can inhibit
CC IL-10 activity in cells. Antibodies specific for CRFB4 are used to
CC measure and localise CRFB4, for diagnosis of defective IL-10 activity.
CC Fragments of (1) are used as primers or probes to assay CRFB4-specific
CC RNA. Agonists/antagonists may be administered parenterally, orally or
CC rectally especially by intravenous injection or directly into a tumour or
CC allograft. 325 AA:
90 Sequence

Query Match	20.0%;	Score 214;	DB 1;	Length 325;
Best Local Similarity	30.5%;	Pred. No. 4.1e-14;		
Matches	60;	Conservative	39;	Mismatches 86;
			Indels	12;
			Gaps	7

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OY 7 POKVEVDIIDONFLIRMARSDSEGVNYTFSFDYOKTGDMNRIKLSGONITSRKCNSSL 66
Db 24 PENAMNSVNRKNTIOWSESPAFKGNLTFTAOY---LSYRIEODKCMNNTLTTECDSS- 79
OY 67 KLNYEEIKLRIRAE-KENTSSWEVDSTFPRKRAOIGPPEVHDEA-EDKAIVIHISPGT 124
Db 79 -LSKGDHTLIRVAFEDHSDWNI-TFCVYDOTTIICPMOVLEVADLSHMFLPKI 166
OY 125 KDSV-MMALDGL-SFTYSLIWMKNSGVEERIEINIRKAIYKLSPEYTCYKLVKALL 181
Db 137 ENEYETPMKKNVNSMTYNOGYMKNGFDEKFOIIPQYDFVLRLNLEPMYTCVQVGRFLP 196
OY 182 TSMKIGVYSPVHCITTT 198
Db 197 DRNKGEWSESPVCEQTT 213

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RESULT	13
ID	R75782
AC	R75782 standard; Protein; 332 AA.
DT	R75782;
DE	13-NOV-1995 (first entry)
DE	IFN-gamma receptor beta-subunit.
KM	Interferon-gamma receptor beta subunit; mIFN;
KM	Interferon-gamma-antagonist.
OS	Mus sp.
PM	Key
FT	peptide
FT	Location/Qualifiers
FT	1..18
FT	/label= Sig-peptide
FT	19..242
FT	/label= Extracellular_domain
FT	243..266
FT	/label= Transmembrane_anchoring_domain
FT	267..332
FT	/label= Cytoplasmic_domain
PN	W09516036-A.
PD	15-JUN-1985.
PF	07-DEC-1994; U14277.
PR	09-DEC-1993; US-164596.
PA	(AGUE//) AGUET M.
PA	(BOEH//) BOEHNI R.
PA	(HEMM//) HEMMI S.
PI	Aguet M, Boehni R, Hemmi S;
PI	WPI: 95-224321/29.
DR	N-RSD8: 090808.
DR	Novel Interferon gamma receptor beta chain polypeptide - for
PT	treatment of inflammatory bowel disease and liver damage
PT	Claim 3; Fig.2a; 86pp; English.
CC	The IFN-gamma receptor beta-subunit encoded by a cDNA clone derived

CC from mouse B-cells is given in R75782. Recombinant beta-subunit,
CC pref. with the transmembrane anchoring domain deleted or
CC inactivated and with the cytoplasmic domain deleted, may be
CC may be used to treat pathological conditions associated with endogenous
CC IFN-gamma production.
SQ Sequence 332 AA;

Query Match	18.6%;	Score 199;	DB 1;	Length 332;
Best Local Similarity	30.1%;	Pred. No. 1.4e-12;		
Matches	65;	Conservative	38;	Mismatches 81;
			Indels	32;
			Gaps	12

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0Y 4 LKSPQKVEVDIIDNFILRMNRDES-----VGNVTFSDYOKTGND-NWML--SGCQ 54
Db 29 LAAPLNPRLHLNYDEQILITWEPSPSSNDPRVYQVYVSF-----IDGSMHLNBNCT 82
0Y 55 NITSPCKNFS--LKLNVYE-EIKLIRAEKEN-TSSWYEVDSFPPRAQAGPPR-VH 108
Db 83 DITEKCOLTGGGRKLKLPHPFFYFLVYRAKRGYLTISKWYGLGFPOFYENWYGVPPKNIS 142
0Y 109 LEADKAVIHIISPQKDSVMALDGLSFYVSLIMKNSGVEERLNIYSRKKY--KL 166
Db 143 VTPGKSLVIEHSPED-----VEHGATFOYLVHYWMEKSEFQDQVYGGPFSKSIYGLN 197
0Y 167 SPETTYCLKVKAAL-LTSMKI---GVYSPHCITTT 198
Db 198 KPYRYVCLQTEAOILNNKRIKIPGILLSNVSCHETT 233

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RESULT	14
W79159	
ID	W79159 standard; Protein; 553 AA

DE 20-Nov-1998 (first entry)
 DE zcytor7 cytokine receptor polypeptide.
 KM zcytor7 cytokine receptor; ligand-binding polypeptide; kidney; pancreas
 KM type 2 cytokine receptor family; CBF2; prostate tissue; nervous tissue
 KM agonist; cell proliferation; cell differentiation; renal disease; human;
 KM neural disease; pancreatic disease.

Key	Location/Qualifiers
Domain	30..250
Domain	/note- "extracellular (ligand-binding) domain; sequence claimed in claim 1"
Domain	275..553
Domain	/note- "intracellular domain"
WO9837193-A1.	
PD	27-AUG-1998.
PF	18-FEB-1998; U03029.
PR	02-OCT-1997; US-945087.
PR	20-FEB-1997; US-803305.
PA	(ZYMO) ZYMOGENETICS INC.
PI	Adams RL, Farrah TM, Jelineberg AC, Kho CJ, Lok S, Whitmore TE;
DR	WPI: 98-480798/41.
DR	N-PSDB: V57515.
PT	Novel human Zcytor7 DNA encodes a type 2 cytokine receptor - useful for treating renal, neural, pancreatic and prostatic diseases
PS	Claim 1; Pages 55-59; 72pp; English.
CC	This represents the Zcytor7 cytokine receptor. Zcytor7 is a ligand-binding receptor polypeptide and is a novel member of the type 2 cytokine receptor family (CPRF2). An expression vector containing the Zcytor polynucleotide, operably linked to transcription promoter, a sequence encoding a transmembrane and intracellular domain, or both, and a transcriptional terminator can be used to transform host cells for the recombinant production of the polypeptide. The sequences can be used to study the Zcytor7 gene and to isolate ligands binding to it. Zcytor7 is preferentially expressed in the kidney, pancreas, prostate or nervous tissue. Antagonists of Zcytor7 can be used to stimulate proliferation and differentiation of cell in these organs. The antagonists and agonists can also be used in the treatment of renal, neural, pancreatic and prostate diseases.
Sequence	553 AA;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:17:53 ; Search time 23.82 Seconds

(without alignments)
123,039 Million cell updates/sec

Title: US-09-240-675-2_COPY_27_229

Perfect score: 1072

Sequence: 1 GRNLSPOKVEVDIIDDNFI.....WKIGYSPVCHIKTVEHEL 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 145308 seqs, 14437401 residues

Total number of hits satisfying chosen parameters: 145308

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents, AA:*
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4: /cgn2_6/ptodata/1/1aa/PCBUS.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1072	100.0	434	1 US-08-328-256-11	Sequence 11, Appl
2	1072	100.0	436	2 US-08-307-588-2	Sequence 2, Appl
3	1072	100.0	496	1 US-08-328-256-12	Sequence 12, Appl
4	1072	100.0	557	1 US-08-328-256-10	Sequence 10, Appl
5	1072	100.0	557	1 US-08-471-454-2	Sequence 2, Appl
6	1072	100.0	557	2 US-08-466-974-2	Sequence 2, Appl
7	1072	100.0	557	2 US-08-471-453-2	Sequence 2, Appl
8	1072	100.0	557	2 US-08-307-588-4	Sequence 3, Appl
9	490.5	45.8	202	4 PCT-US94-14277-3	Sequence 4, Appl
10	214	20.0	325	2 US-08-683-743-4	Sequence 4, Appl
11	199	18.6	332	4 PCT-US94-14277-2	Sequence 6, Appl
12	192	17.9	223	4 PCT-US94-14277-6	Sequence 6, Appl
13	172.5	16.1	221	2 US-08-943-087-56	Sequence 56, Appl
14	167.5	15.6	221	2 US-08-943-087-54	Sequence 54, Appl
15	166.5	15.5	221	2 US-08-943-087-50	Sequence 50, Appl
16	166.5	15.5	553	2 US-08-943-087-2	Sequence 2, Appl
17	166.5	15.5	553	2 US-08-943-087-14	Sequence 14, Appl
18	166.5	15.5	553	2 US-08-943-087-16	Sequence 16, Appl
19	166.5	15.5	553	2 US-08-943-087-18	Sequence 18, Appl
20	166.5	15.5	553	2 US-08-943-087-20	Sequence 20, Appl
21	166.5	15.5	553	2 US-08-943-087-22	Sequence 22, Appl
22	166.5	15.5	553	2 US-08-943-087-24	Sequence 24, Appl
23	166.5	15.5	553	2 US-08-943-087-26	Sequence 26, Appl
24	166.5	15.5	553	2 US-08-943-087-28	Sequence 28, Appl
25	166.5	15.5	553	2 US-08-943-087-30	Sequence 30, Appl
26	166.5	15.5	553	2 US-08-943-087-32	Sequence 32, Appl
27	166.5	15.5	553	2 US-08-943-087-34	Sequence 34, Appl
28	166.5	15.5	553	2 US-08-943-087-36	Sequence 36, Appl
29	166.5	15.5	553	2 US-08-943-087-38	Sequence 38, Appl

30	166.5	15.5	553	2 US-08-943-087-40	Sequence 40, Appl
31	166.5	15.5	553	2 US-08-943-087-42	Sequence 42, Appl
32	166.5	15.5	553	2 US-08-943-087-44	Sequence 44, Appl
33	166.5	15.5	553	2 US-08-943-087-46	Sequence 46, Appl
34	166.5	15.5	553	2 US-08-943-087-48	Sequence 48, Appl
35	165.5	15.4	221	2 US-08-943-087-52	Sequence 52, Appl
36	163.5	15.3	221	2 US-08-943-087-60	Sequence 60, Appl
37	160.5	15.0	221	2 US-08-943-087-68	Sequence 68, Appl
38	145	13.5	200	4 PCT-US94-14277-4	Sequence 4, Appl
39	142	13.2	337	2 US-08-906-713-2	Sequence 8, Appl
40	131.5	12.3	574	2 US-08-906-713-2	Sequence 2, Appl
41	111	10.4	489	4 PCT-US93-11110-1	Sequence 1, Appl
42	111	10.4	489	5 5221789-1	Patent No. 5221789
43	92	8.6	265	2 US-08-385-191A-14	Sequence 14, Appl
44	89.5	8.3	2213	1 US-08-727-034-3	Sequence 3, Appl
45	89	8.3	239	2 US-08-385-191A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-328-256-11
Sequence 11, Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: II 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ. ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-256-11

Query Match 100.0%; Score 1072; DB 1; Length 434;

Best Local Similarity 100.0%; Pred. No. 4.9e-112;

Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRNLSPOKVEVDIIDDNFIILRNRSDESYGNVTFSDYQKGMNWKSGCQNTSTK 60

Db 27 GNLSKSPKVEVDIIDNFIILRMNRSDSVGNVTFESFDYQKGMNWKILSGCONITSTK 86
QY 61 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIVIH 120
Db 87 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIVIH 146
QY 121 SPGRKDSVMALDGLSFTYSLILMKNSSGVEERENIYSRHKIKYKLSPEPTYCLKVAAL 180
Db 147 SPGRKDSVMALDGLSFTYSLILMKNSSGVEERENIYSRHKIKYKLSPEPTYCLKVAAL 206
QY 181 LTSKRIQVSPVHCIKITVENEL 203
Db 207 LTSKRIQVSPVHCIKITVENEL 229

RESULT 2
US-08-307-588-2
Sequence 2, Application US/08307588
Patent No. 5919453
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
NUMBER OF SEQUENCES: 4
TITLE OF INVENTION: INTERFERON
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/GUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-588-2

Query Match 100.0%; Score 1072; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 5e-112;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNLSKSPKVEVDIIDNFIILRMNRSDSVGNVTFESFDYQKGMNWKILSGCONITSTK 60
Db 27 GNLSKSPKVEVDIIDNFIILRMNRSDSVGNVTFESFDYQKGMNWKILSGCONITSTK 86

QY 61 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIVIH 120
Db 87 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIVIH 146
QY 121 SPGRKDSVMALDGLSFTYSLILMKNSSGVEERENIYSRHKIKYKLSPEPTYCLKVAAL 180
Db 147 SPGRKDSVMALDGLSFTYSLILMKNSSGVEERENIYSRHKIKYKLSPEPTYCLKVAAL 206
QY 181 LTSKRIQVSPVHCIKITVENEL 203
Db 207 LTSKRIQVSPVHCIKITVENEL 229

RESULT 3
US-08-328-256-12
Sequence 12, Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVTITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-256-12

Query Match 100.0%; Score 1072; DB 1; Length 496;
Best Local Similarity 100.0%; Pred. No. 6e-112;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNLSKSPKVEVDIIDNFIILRMNRSDSVGNVTFESFDYQKGMNWKILSGCONITSTK 60
Db 27 GNLSKSPKVEVDIIDNFIILRMNRSDSVGNVTFESFDYQKGMNWKILSGCONITSTK 86
QY 61 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIVIH 120
Db 87 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIVIH 146

OY 121 SPGTRDSVMMALDGLSTFYSLILMKNSGVEERIENTISRRKIYKLSPEYTYCLKVKAAAL 180
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DB 147 SPGTRDSVMMALDGLSTFYSLILMKNSGVEERIENTISRRKIYKLSPEYTYCLKVKAAAL 206
OY 181 LTSWKIGVSPVHCICKTTVENEL 203
|
DB 207 LTSWKIGVSPVHCICKTTVENEL 229

RESULT 4

US-08-328-256-10
; Sequence 10, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: ABRAMOVICH, Carolina
; APPLICANT: RAYOVITSKI, Edward
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,256
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107378
; FILING DATE: 24-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: REVEL-13
; REFERENCE/DOCKET NUMBER: 25,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-328-256-10

Query Match 100.0%; Score 1072; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 7.2e-112; Indels 0; Gaps 0;
Matches 203; Conservative 0; Mismatches 0;

OY 1 GKNLSPQKVEVDIIDNFIILMNRSDSVGNVTFSPDYOKTGMDNMWIKLSGCONITSTK 60
|
DB 27 GKNLSPQKVEVDIIDNFIILMNRSDSVGNVTFSPDYOKTGMDNMWIKLSGCONITSTK 86
OY 61 CNFSSLKLVYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPEVHLAEADKAIYIHI 120
|
DB 87 CNFSSLKLVYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPEVHLAEADKAIYIHI 146
OY 121 SPGTRDSVMMALDGLSTFYSLILMKNSGVEERIENTISRRKIYKLSPEYTYCLKVKAAAL 180
|
DB 147 SPGTRDSVMMALDGLSTFYSLILMKNSGVEERIENTISRRKIYKLSPEYTYCLKVKAAAL 206
OY 181 LTSWKIGVSPVHCICKTTVENEL 203

DB 207 LTSWKIGVSPVHCICKTTVENEL 229
|

RESULT 5

US-08-471-454-2
; Sequence 2, Application US/08471454
; Patent No. 5731169
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LUTFALLA, Georges
; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,454
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 13-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-471-454-2

Query Match 100.0%; Score 1072; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 7.2e-112; Indels 0; Gaps 0;
Matches 203; Conservative 0; Mismatches 0;

OY 1 GKNLSPQKVEVDIIDNFIILMNRSDSVGNVTFSPDYOKTGMDNMWIKLSGCONITSTK 60
|
DB 27 GKNLSPQKVEVDIIDNFIILMNRSDSVGNVTFSPDYOKTGMDNMWIKLSGCONITSTK 86
OY 61 CNFSSLKLVYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPEVHLAEADKAIYIHI 120
|
DB 87 CNFSSLKLVYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPEVHLAEADKAIYIHI 146
OY 121 SPGTRDSVMMALDGLSTFYSLILMKNSGVEERIENTISRRKIYKLSPEYTYCLKVKAAAL 180
|
DB 147 SPGTRDSVMMALDGLSTFYSLILMKNSGVEERIENTISRRKIYKLSPEYTYCLKVKAAAL 206
OY 181 LTSWKIGVSPVHCICKTTVENEL 203

Db 207 LTRKIGVSPVHCITVENEL 229

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|||||
RESULT 6
US-08-466-974-2
; Sequence 2, Application US/08466974
; Patent No. 5861258
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LUTFALLA, Georges
; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,974
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-466-974-2
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Query Match 100.0%; Score 1072; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 7.2e-112;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GKNLSPQKVEVDIIDNFIILRNRSDESVGNVTFSDYQKGTGMNWKILSGCONITSTK 60
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Db 27 GKNLSPQKVEVDIIDNFIILRNRSDESVGNVTFSDYQKGTGMNWKILSGCONITSTK 86
|||||
Db 61 CNFSSKLNVVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIVYIH 120
|||||
Db 87 CNFSSKLNVVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIVYIH 146
|||||
Db 121 SPGRKDSVMAALDGLSFTSYSLILKKNSSGVEERIENTISYRHKIKLSPETTYCLKVAAL 180
|||||
Db 147 SPGRKDSVMAALDGLSFTSYSLILKKNSSGVEERIENTISYRHKIKLSPETTYCLKVAAL 206
|||||
Db 181 LTRKIGVSPVHCITVENEL 203

Db 207 LTRKIGVSPVHCITVENEL 229

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RESULT 7
US-08-471-453-2
; Sequence 2, Application US/08471453
; Patent No. 586153
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LUTFALLA, Georges
; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,453
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-471-453-2
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Query Match 100.0%; Score 1072; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 7.2e-112;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GKNLSPQKVEVDIIDNFIILRNRSDESVGNVTFSDYQKGTGMNWKILSGCONITSTK 60
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Db 27 GKNLSPQKVEVDIIDNFIILRNRSDESVGNVTFSDYQKGTGMNWKILSGCONITSTK 86
|||||
Db 61 CNFSSKLNVVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIVYIH 120
|||||
Db 87 CNFSSKLNVVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIVYIH 146
|||||
Db 121 SPGRKDSVMAALDGLSFTSYSLILKKNSSGVEERIENTISYRHKIKLSPETTYCLKVAAL 180
|||||
Db 147 SPGRKDSVMAALDGLSFTSYSLILKKNSSGVEERIENTISYRHKIKLSPETTYCLKVAAL 206
|||||
Db 181 LTRKIGVSPVHCITVENEL 203

Db 207 LTSMKIGVSPVHCITKTVEENL 229

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RESULT 8
US-08-307-588-4
; Sequence 4, Application US/08307588
; Patent No. 5919453
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MAGUIRE, Deborah
; APPLICANT: PLAYEC, Ivan
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; TITLE OF INVENTION: INTERFERON
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,588
; FILING DATE: 05-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00770
; FILING DATE: 30-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92400902.0
; FILING DATE: 31-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard P.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5390
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-307-588-4

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Query Match 100.0%; Score 1072; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 7.2e-112;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GKNLSPKQVEVDIIDDFILRMNRSDESGVGNVTFESFYOKTGMDNMWIKLSGCONITSTK 60
Db 27 GKNLSPKQVEVDIIDDFILRMNRSDESGVGNVTFESFYOKTGMDNMWIKLSGCONITSTK 86
QY 61 CNFSSLKLVYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPEVHLEAEDKAIYIHI 120
Db 87 CNFSSLKLVYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPEVHLEAEDKAIYIHI 146
QY 121 SPGRKDSYMAALDGLSTFTYSLIMKNSSGVEERIEINYSRHKIKYKLSPEYTYCKVKAAAL 180
Db 147 SPGRKDSYMAALDGLSTFTYSLIMKNSSGVEERIEINYSRHKIKYKLSPEYTYCKVKAAAL 206
QY 181 LTSMKIGVSPVHCITKTVEENL 203
Db 207 LTSMKIGVSPVHCITKTVEENL 229

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RESULT 9
PCT-US94-14277-3
; Sequence 3, Application PC/TUS9414277
; GENERAL INFORMATION:
; APPLICANT: Aguet, Michel
; APPLICANT: Bohml, Ruth
; APPLICANT: Hemmi, Silvio
; TITLE OF INVENTION: Receptor subunit Polypeptides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14277
; FILING DATE: 07-DEC-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/164596
; FILING DATE: 09-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 866PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 202 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US94-14277-3

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Query Match 45.8%; Score 490.5; DB 4; Length 202;
Best Local Similarity 48.3%; Pred. No. 2.4e-47;
Matches 98; Conservative 34; Mismatches 69; Indels 1; Gaps 1;

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QY 2 KNLSPKQVEVDIIDDFILRMNRSDESGVGNVTFESFYOKTGMDNMWIKLSGCONITSTK 61
Db 1 ENLKPENIDXYIIDDFILRMNRSDESGVGNVTFESFYOKTGMDNMWIKLSGCONITSTK 60
QY 62 NFSSLKLVYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPEVHLEAEDKAIYIHI 120
Db 61 EFSILDINXYIKQFVRRAEGNSTSSWNEVDPIPTAHMSPVEVLEAEDKAIYIHI 120
QY 121 SPGRKDSYMAALDGLSTFTYSLIMKNSSGVEERIEINYSRHKIKYKLSPEYTYCKVKAAAL 180
Db 121 SPGRKDSYMAALDGLSTFTYSLIMKNSSGVEERIEINYSRHKIKYKLSPEYTYCKVKAAAL 202
QY 181 LTSMKIGVSPVHCITKTVEENL 202
Db 181 PSLLKHSNYSSTXOCISTTVANK 202

```

RESULT 10
US-08-683-743-4
; Sequence 4, Application US/08683743
; Patent No. 5843697
; GENERAL INFORMATION:
; APPLICANT: Pestka, Sidney

APPLICANT: Kotenko, Serguei
TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
TITLE OF INVENTION: CHAIN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,743
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FRAGMENT TYPE:
US-08-683-743-4

Query Match 20.0%; Score 214; DB 2; Length 325;
Best Local Similarity 30.5%; Pred. No. 4.9e-16;
Matches 60; Conservative 39; Mismatches 86; Indels 12; Gaps 7;
OY 7 POKVEVDIIDNFIILNRMSDESVCNVTFSFYQKTGMDNMTKLSGCONITSTKCNFSSL 66
DB 24 PENVMNSVNFENKNILOMESPAFAKGNLTFTAGY---LSYRLFQDKCMNTLTTECDSS- 79
OY 67 KLVNVEEIKLRIRAE-KENTSSWYEVDSFTPPRKAQIGPPEVHLBA-EDKAIIVHISPGT 124
DB 79 -LSKRGDHLIRAFRAFEHSDWNI-FTCPYVDOTIIGPCKQVEVLADSLHMRFLAPKI 136
OY 125 KDSV-MMALDGL--SFTYSLIWNKSSGVEERIEINISRHKIYKLSPEPTYCLKYKALL 181
DB 137 ENEYETMTMKKNVNSMTYVNWQKNGTDEKFOITPOYDFEVLRLNEPWTTCVQVGRCLP 196
OY 182 TSMKIGVSPVHCITKT 198
DB 197 DRNKGWSEPVCEQTT 213

RESULT 11
PCT-US94-14277-2
Sequence 2, Application PC/TUS9414277
GENERAL INFORMATION:
APPLICANT: Aguet, Michel
APPLICANT: Bohml, Ruth
APPLICANT: Hemmi, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patln (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/223-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-2

Query Match 18.6%; Score 199; DB 4; Length 332;
Best Local Similarity 30.1%; Pred. No. 2.4e-14;
Matches 65; Conservative 38; Mismatches 81; Indels 32; Gaps 12;
OY 4 LKSPQVEVDIIDNFIILNRMSDES-----VGNVTFSPDYQKTGMD-NWIKL--SGCQ 54
DB 29 LAELNPRHLHXNDQILTWEPSSNDPRVYQVEXSF-----IDGSMHRLLEENCT 82
OY 55 NITSTKCNFSS--LKINYE-EIKLRIRAEKEN-TSSWYEVDSFTPPRKAQIGPPE-VH 108
DB 83 DITETKCDLNGGGRKLFPHPTFVFLVRARAGNLTSKWGLLEPFQYEWNTVGPKNIS 142
OY 109 LEADKAIIVHISGCTDSVMALDGLSFTYSLIWNKSSGVEERIEINISRHKIY--KL 166
DB 143 VTPKGSILVHFSPFD---VFHGATFOYLVAHYWEKSETQOQVEGPKNSNIVLGNL 197
OY 167 SPETTYCLKYKAAAL-LTSMKI---GVYSPVHCITKT 198
DB 198 KPYRVYCLQTEPAQLLNKKIRPAGLLSNVSCHETT 233

RESULT 12
PCT-US94-14277-6
Sequence 6, Application PC/TUS9414277
GENERAL INFORMATION:
APPLICANT: Aguet, Michel
APPLICANT: Bohml, Ruth
APPLICANT: Hemmi, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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1      SOFTWARE:      patin (Genentech)
2      CURRENT APPLICATION DATA:
3      APPLICATION NUMBER:      PCT/US94/142777-6
4      FILING DATE:      07-DEC-1994
5      CLASSIFICATION:
6      PRIOR APPLICATION DATA:
7      APPLICATION NUMBER:      08/164596
8      FILING DATE:      09-DEC-1993
9      ATTORNEY/AGENT INFORMATION:
10     NAME:      Love, Richard B.
11     REGISTRATION NUMBER:      34,659
12     REFERENCE/DOCKET NUMBER:      866PCT
13     TELECOMMUNICATION INFORMATION:
14     TELEPHONE:      415/225-5530
15     TELEFAX:      415/952-9881
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Query Match	17.9%	Score 192;	DB 4;	Length 223;
Best Local Similarity	29.6%	Pred. No. 8.1e-14;		
Matches 64; Conservative	37;	Mismatches 83;	Indels 32;	Gaps 12

QY 4 LKSPQKVEVDIIDDNFLLRNRSDES-----VQNTFFSFQYQTGMD-WMIK!-SGCQ 54
Db 10 LARLNPRLHLTYNDQIITWEPSPSSNDPRVYQVEXSF-----IDGSHRLLEPNC 63
QY 55 NITSTCKNFSS--LKLNYVE-EIKLRIRAKEN-TSSWYEVDSFTFPFRAQIOPPE-VH 108
Db 64 DITFKCDLTGGRKULKEPHFPFYELRLRAKRGULTSMWGLEPFQYEHYNTVQPPKNIS 123
QY 109 LEADKALVHISQGTQDSVMAALDGLSFYSLIIMKSSGVERIENTISRKRIY-KL 166
Db 124 VTPKGSGLVHFSPFD-----VFHGATFQTLVHYWEKSEFQOGEVGPFSKNSIYVGNL 178
QY 167 SPETTYCLKVAAL-LTSMKI---GVSPVHCITTT 198
Db 179 KPRVYICQIOTEROLILKKKKTIRPGLGLSNVSCHETT 214

RESULT 13
US-08-943-087-56

1
2 PATENT NO.: 5945511
3
4 GENERAL INFORMATION:
5
6 APPLICANT: Lok, Si
7
8 APPLICANT: Kho, Choon J.
9
10 APPLICANT: Jelmberg, Anna C.
11
12 APPLICANT: Adams, Robyn L.
13
14 APPLICANT: Whitmore, Theodore E.
15
16 TITLE OF INVENTION: CYTOKINE RECEPTOR
17
18 NUMBER OF SEQUENCES: 60
19
20 CORRESPONDENCE ADDRESS:
21
22 ADDRESSEE: Zymogenetics, Inc.
23
24 STREET: 1201 Eastlake Avenue East
25
26 CITY: Seattle
27
28 STATE: WA
29
30 COUNTRY: USA
31
32 ZIP: 98102
33
34 COMPUTER READABLE FORM:
35
36 MEDIUM TYPE: Diskette
37
38 COMPUTER: IBM Compatible
39
40 OPERATING SYSTEM: DOS
41
42 SOFTWARE: FASTEO for Windows Version 2.0
43
44 CURRENT APPLICATION DATA:
45
46 APPLICATION NUMBER: US/08/943,087
47
48 FILING DATE:
49
50

CLASSIFICATION: 536
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-56

Query Match	16.18;	Score 172.5;	DB 2;	Length 221;
Best Local Similarity	26.68;	Pred. No. 1.2e-11;		
Matches 50; Conservative	35;	Mismatches 86;	Indels 17;	Gaps 5;

QY	4	LKSQKVEVDIIDDNFILNRNSRSEVYG--NTEFEFDYQXGMDWIKLSCQNTSPKCN	62
		: :	
Db	8	LPRKANTTFELSIINKNVLOMTPEBGLOGVATTYVOYFIYGQKKWLNKSECRNINRTYCD	67
		: :	
QY	63	FSSLNLNVEEBIKLIRA-EKENTSSWYEVDSFPTPEKKAQIGPPEVHLAEADKAIVHIS	120
		: :	
Db	68	LSAETSDYEHQYAKVAIKNSCKSKMAEGRFYPLESDQIGPPEVALTJDEKSIIVLVS	127
		: :	
QY	122	PGTR-----DSYKALDGLSFTYSLILMKNSSGVEERIENTIYSRHKIYK--LSPET	170
		: :	
Db	128	APKFKKNRPEDLLPYVSMOOIYSNLKYNSVLNTKSNRTMSOCVTV---HFLVLTWLEPNT	183
		: :	
QY	171	TYCELVKKA	178
		: : : : :	
Db	184	LYCVHVES	191
		: : : : :	

RESULT 14

Sequence 54, Application US/08943087
 Patent No. 5945511
 GENERAL INFORMATION:
 APPLICANT: Lok, SI
 APPLICANT: Kuo, Choon J.
 APPLICANT: Jelmberg, Anna C.
 APPLICANT: Adams, Robyn L.
 APPLICANT: Whitmore, Theodore E.
 APPLICANT: Farrah, Theresa M.
 TITLE OF INVENTION: CYTOKINE RECEPTOR
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Zymogenetics, Inc.
 STREET: 1201 Eastlake Avenue East
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTEO for Windows Version 2.0.
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/943,087
 FILING DATE:
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/803,305
 FILING DATE: 20-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Lunn, Paul G
 REGISTRATION NUMBER: 32,743
 REFERENCE/DOCKET NUMBER: 96-24C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678
 TELEX:
 INFORMATION FOR SEQ ID NO: 54:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 221 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-943-087-54

Query Match	15.6%	Score 167.5	DB 2	Length 221
Best Local Similarity	26.1%	Pred No. 4.5e-11		
Matches 49	Conservative 34	Mismatches 88	Indels 17	Gaps 5

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QY      4 LKSPQKVEVDIIDNFIILKMRNRSQSVG-NYTFEFDYQKMDWIKLISGCONITSRKN 62
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      8 LPRANITFELSMKNVLOMTPEPGLOGVKTYYIVQYFLIGQKKWMLKSECRNINFTYCD 67
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      63 FSSKLNVYEEIKLIRI-EKENTSSWYENDSFPPRKAQIGPBEVHLEADKAIYHIS 121
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      68 LSAERSDYEHQYAKKAIWGTCKSKMAESGRFPFLIETQIGPREVALTLTDEKSIYVL 127
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      122 PGR-----DSVMALDGLSFTYSLIKWKSQGYEERIEIYTSRHAIYK--LSPET 170
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      128 APEKMRNPEDLPVYSMOOLYSLNKLYNSVLTKSKNRMWSOCVTR---HTLVLTWLEPNT 183
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QY      171 TYCLKVKA 178
      1 : : : :
Db      184 LYCVAVES 191

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```

1  APPLICATION NUMBER: 08/803,305
2  FILING DATE: 20-FEB-1997
3  ATTORNEY/AGENT INFORMATION:
4  NAME: Lunn, Paul G
5  REGISTRATION NUMBER: 32,743
6  REFERENCE/DOCKET NUMBER: 96-24C11
7  TELECOMMUNICATION INFORMATION:
8  TELEPHONE: 206-442-6627
9  TELEFAX: 206-442-6678
10 TELE:
11
12 INFORMATION FOR SEQ. ID NO: 50:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 221 amino acids
15 type: amino acid
16 STRANDEDNESS: single
17 TOPOLOGY: linear
18 MOLECULE TYPE: protein
19 FRAGMENT TYPE: internal
20
21 US-08-943-087-50

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Query Match	15.5%	Score 166.5	DB 2	Length 221
Best Local Similarity	26.1%	Pred. No. 5.8e-11		
Matches 49	Conservative 34	Mismatches 88	Indels 17	Gaps 5

QY	4	LKSOKEVLDIIDDNFILNMRSDSEVG-NYTFEFEDYOKTMDWIKLISCONTPSRKN	62
		: : : : : : : : : : : : : : : : : : : :	
Db	8	LPRANNTIFLSTINKNVLOMTPEBGLOGVATYTVQVFTTGGOKWMLKSECRNINRTYCD	67
QY	63	FSSKLNLNTEBEIKLIRIA-EKENTSSWEYDSEFTPFERKAOIGPPEVHLLEADKAIVHIS	121
		: : : : : : : : : : : : : : : : : : : :	
Db	68	LSAETSDVEHQYAKVAINMOTKRSKMAESGRFYPLETQIGPPEVALTTDEKSI SVLT	127
QY	122	PGTR-----DSVMALDGLSFTYSLILMKKSSGVEERIENTYSRKHIIYK--LSPET	170
		: : : : : : : : : : : : : : : : : : : :	
Db	128	APETKRRNPEDLPVSMOOIYSNLKYNSVLTNKSIRMSOCVTN---HTLVLTWLEPNT	183
QY	171	TYGLKVKKA	178
Db	184	LYCVHVES	191

Search completed: June 1, 2000, 04:17:54
Job time: 15448 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2000, 04:35:09 ; Search time 64.83 seconds
(without alignments)
183.585 Million cell updates/sec

Title: US-09-240-675-2_COPY_27_229

Perfect score: 1072
Sequence: 1 GKNLSPKQVEVDIIDDFILRMNRSDESVCNVTFSPYQGTGMDNWKLSGCCNITSTK 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

PIR_63: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1072	100.0	557	2 A32694	interferon alpha/b
2	708	66.0	560	2 S27387	interferon alpha r
3	525.5	49.0	590	2 A45283	interferon alpha/b
4	219	20.4	273	2 G04418	cytokine receptor
5	216	20.1	349	2 JC6311	interferon receptor
6	214	20.0	325	2 A47003	cytokine receptor
7	199	18.6	332	2 A49947	interferon gamma r
8	144	13.4	337	2 I38500	interferon gamma r
9	111	10.4	489	2 A31555	interferon gamma r
10	97.5	9.1	6831	2 T27934	hypothetical prote
11	97.5	9.1	6839	2 S57242	twitcln - Caenorh
12	97.5	9.1	7160	2 T27935	hypothetical prote
13	95.5	8.9	925	2 T29585	hypothetical prote
14	92.5	8.6	292	1 KFE03	tissue factor prec
15	92	8.6	477	2 A34368	interferon gamma r
16	90.5	8.4	1304	1 A46546	leukocyte common a
17	90	8.4	315	1 S14222	chalcone reductase
18	89.5	8.3	2033	2 T09123	hybrid receptor So
19	89.5	8.3	2215	2 T00348	Lr11 protein - mou
20	89	8.3	331	2 A54295	interferon alpha/b
21	89	8.3	331	2 S59501	interferon recepto
22	89	8.3	515	2 S59502	interferon recepto
23	89	8.3	1152	2 S20106	hypothetical prote
24	88	8.2	515	2 I39073	interferon alpha-b
25	87.5	8.2	575	2 A49667	interleukin-10 rec
26	87.5	8.2	6805	2 S20901	tlfln - rabbit (fr
27	87	8.1	639	2 JC1391	tlfln - type molecula
28	87	8.1	26926	1 I38344	tlfln, cardiac mus
29	86.5	8.1	429	2 S57773	26S proteasome reg
30	85.5	8.0	295	1 KFH03	tissue factor prec

31	85.5	8.0	578	2 I56215	interleukin-10 rec
32	84.5	7.9	623	1 VGBE68	glycoprotein E - h
33	84.5	7.9	1220	2 S64916	probable membrane
34	83.5	7.8	306	2 A25698	probable protein x
35	82.5	7.7	406	2 B64432	capsular polysacch
36	82.5	7.7	1068	2 S01519	hypothetical prote
37	82	7.6	415	2 S12357	hypothetical prote
38	82	7.6	817	2 A48721	interleukin-5 rece
39	81.5	7.6	1009	2 I KFR83	tissue factor prec
40	81	7.6	292	2 C64483	hypothetical prote
41	81	7.6	1120	2 S67208	hypothetical prote
42	81	7.6	1375	2 T13822	frizzled gene prot
43	81	7.6	1526	2 T13823	frizzled gene prot
44	80	7.5	780	1 S39110	valosin-containing
45	80	7.5	878	1 A40091	interleukin-3 rece

ALIGNMENTS

RESULT 1

A32694 Interferon alpha/beta receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 22-Jun-1990 #sequence, revision 22-Jun-1990 #text, change 22-Oct-1999

C:Accession: A32694; S17112

R:Uze, G.; Luftalla, G.; Gresser, I.

Cell 60, 225-234, 1990

A:Title: Genetic transfer of a functional human interferon alpha receptor into mos

A:Reference number: A32694; MUID:90124632

A:Accession: A32694

A:Molecule type: mRNA

A:Residues: 1-557 <UZE>

A:Cross-references: GB:003171; NID:g184645; PIDN:AAA52730.1; PID:g306914

R:Luftalla, G.

submitted to the EMBL Data Library, July 1991

A:Description: The structure of the human interferon alpha/beta receptor gene.

A:Reference number: S17112

A:Accession: S17112

A:Molecule type: DNA

A:Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUM>

A:Cross-references: EMBL:X00459; NID:932671

C:Genetics:

A:Gene: GDB:IFNAR1; IFNAR; IFRC

A:Cross-references: GDB:120078; OMIM:107450

A:Map position: 21q22.1-21q22.1

A:Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3

C:Keywords: cytokine receptor; glycoprotein; transmembrane protein

F:1-21/Domain: transmembrane #status predicted <TRN1>

F:437-455/Domain: transmembrane #status predicted <TRN2>

F:50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydrate

Query Match 100.0%; Score 1072; DB 2; Length 557;

Best Local Similarity 100.0%; Pred. No. 3e-87;

Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GKNLSPKQVEVDIIDDFILRMNRSDESVCNVTFSPYQGTGMDNWKLSGCCNITSTK	60
DB	27	GKNLSPKQVEVDIIDDFILRMNRSDESVCNVTFSPYQGTGMDNWKLSGCCNITSTK	86
QY	61	CNFSLLKNVYEIKLRIRAEKENTSSVEYDSFPPKKAQIGPPEVHLEADKAIVIH	120
DB	87	CNFSLLKNVYEIKLRIRAEKENTSSVEYDSFPPKKAQIGPPEVHLEADKAIVIH	146
QY	121	SPGTDSTWMAALDGLSFTYSLIKNSSGVEERINITSRRKIYKLSPEYTYCKLVKAA	180
DB	147	SPGTDSTWMAALDGLSFTYSLIKNSSGVEERINITSRRKIYKLSPEYTYCKLVKAA	206
QY	181	LTSWKIGVSPVHCIKITVENEL 203	
DB	207	LTSWKIGVSPVHCIKITVENEL 229	

RESULT 2
 S27387
 Interferon alpha receptor type 1 precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S27387; S33770
 R:Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
 FEBS Lett. 313, 255-259, 1992
 A:Title: Specific antiviral activities of the human alpha interferons are determined at
 A:Reference number: S27387; MUID:93076908
 A:Accession: S27387
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-560 <MOU>
 A:Cross-references: EMBL:X68443; NID:q431; PIDN:CAA48484.1; PID:q432
 A:Experimental source: MDBK cells
 R:Lim, J.K.; Langer, J.A.
 Biochim. Biophys. Acta 1173, 314-319, 1993
 A:Title: Cloning and characterization of a bovine alpha interferon receptor.
 A:Reference number: S33770; MUID:93305725
 A:Accession: S33770
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-421, 'V', 423-560 <LIM>
 A:Cross-references: EMBL:L06320; NID:q163187; PIDN:AAA02571.1; PID:q163188
 A:Experimental source: lung
 C:Keywords: antiviral; cytokine receptor; transmembrane protein
 F:1-24/domain: signal sequence #status predicted <Stic>
 F:25-560/Product: interferon alpha receptor type 1 #status predicted <Mat>

Query Match	66.0%;	Score 708;	DB 2;	Length 560;
Best Local Similarity	67.2%;	Pred. No. 5.1e-55;		
Matches 137; Conservative	28;	Mismatches 35;	Indels 4;	Gaps 4;

Qy	3	NLKSPQKAEVJIIIDNDFLLRNRRSDSEVGANTFSDYDQKTMDMWIKRISGCGONTSTFCN	62
Db	27	NLK - PENVEIHIIIDNFLLKNSSSESKANTFSDADYIIGTDMMKKLSGCCHITSTKCN	85
Qy	63	FSSLKL-NVYEIEIKLRIPAER-ENTSSWYEVDSFTPFPKAAIGPPEVHLEAEDKAIVHI	120
Db	86	FSSVELNVFEKIELRIAREGNMNTSWYEPFPFLLEAQIGPPDVHLEAKDAKAILLTI	148
Qy	121	S-PGTGRDSVMALDGLSTTYTSLILTKNSSGVGEERIENTYSHHKIKYKLSPTETLYCKYKAA	175
Db	146	SPPGTKDISIMAMPRSSFRYSVVIWKNSSSLEERTETVPEDKIKYLKSPIETCYCLKYAE	205
Qy	180	LITSWKIGVSPVHCIKTTVENEL	203
Db	206	LRLQSRVGCYSPVYCINTTERHKV	229

RESULT 3
A:Accession: A45283
Interferon alpha/beta receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1998
C:Accession: A45283; #148423; 148424; 148425; 148426; 148427; 148428; 148429
R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogenssen, K.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
A:Title: Behavior of a cloned mouse interferon alpha/beta receptor expressed in homospice
A:Reference number: A45283; MUID:92262522
A:Accession: A45283
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-590 <GB>
A:Cross-references: CB:MB96641; NID:g194111; PIDN:AAA37890.1; PID:g194112
A:Note: sequence extracted from NCBI backbone (NCBIN:102354, NCBIIP:102357)
R:Lutfalla, G.; Uze, G.
Gene 148, 343-346, 1994
A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-freq
A:Reference number: 148423; MUID:95047447

A:Accession:148423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 116-125 <RES>
A:Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1; PID:g755810
A:Accession: 148424
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 127-224 <RE2>
A:Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1; PID:g755811
A:Accession: 148425
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 243-264 <RE3>
A:Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1; PID:g510261
A:Accession: 148426
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 265-375 <RE4>
A:Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1; PID:g510262
A:Accession: 148427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 397-424 <RE5>
A:Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.1; PID:g755812
A:Accession: 148428
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 426-445 <RE6>
A:Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1; PID:g755813
A:Accession: 148429
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 473-590 <RE7>
A:Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA65008.1; PID:g510265
C:Genetics:
A:Gene: IFNAR
A:Introns: 177/3; 331/1
C:Keywords: cytokine receptor; transmembrane protein

[illegible]

A:Molecule type: DNA
A:Residues: 1-273 <LUT>
A:Cross-references: EMBL:U08988; NID:g571255; PID:g571256
C:Genetics:
A:Gene: GDB:CRFB4; CRF2-4
A:Cross-references: GDB:138168; OMIM:123889
A:Map position: 21922.1-21922.2
A:Introns: 17/1, 58/2, 111/1, 166/3, 216/1

Query Match	20.48;	Score 219;	DB 2;	Length 273;	.
Best Local Similarity	30.58;	Pred. NO. 3.9e-12;			
Matches 60;	Conservative 41;	Mismatches 84;	Indels 12;	Gaps 7;	

QY 7 POKVEEIIIDNFIILNNRSDSESGVNTFSPDYXOTGMWMIKLSGCONITTSRKCNSSL 66
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 124 PENRBMSVNRKNLQWESSPAFGNLFTTQY----LSYRIPODKCMNLTLEDCPSS- 79

QY 67 KLANYEIEIKLRAE-KENTSSWEVDSTFPFRKAQIGPEPVHLEADKAVIH-ISPGT 124
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 79 -LSKYGDHTLTRAAFEADEHSDMVNI--TFCPVDDTIIGPPMGQEVLDDSLHRFLAPKI 136

QY 125 KDVS-MALDGL--SFYSLLIMKNSSSVERIERINISRKIKYLSPETTYCLKVRAALL 181
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 137 ENERYETMMKNVVSNMYSMTYNVOVMKNGDEKFOIPPOYDFEVLBNLEPMITYCVQVRGLP 196

QY 182 TSMKIGVYSPVHCJTKT 198
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 197 DRNKAGEWSEPYCEOTT 213

```

RESULT      5
JC6311
Interferon receptor-class II cytokine receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999
C:Accession: JC6311
R:Gibbs, V.C.: Pennica, D.
Gene 186, 97-101, 1997
A:Title: CRF2-1: Isolation of cDNA clones encoding the human and mouse proteins
A:Reference number: JC6311
A:Accession: JC6311
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-349 <GIB>
A:Cross-references: GB:U53696

```

Query Match	20.1%	Score 216;	DB 2;	Length 349;
Best Local Similarity	28.6%	Pred. No. 1e-11;		
Matches	58;	Conservative 43;	Mismatches 76;	Indels 26;
			Gaps	8

[illegible]

RESULT 6
AA7003
cytokine receptor family class II protein CRF2-4 precursor - human
C:Species: Homo sapiens (mn)

C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1997
C:Accession: A47003
R:Lutfulalla, G.; Gardner, K.; Uze, G.
Genomics 16, 366-373, 1993
A:Title: A new member of the cytokine receptor gene family maps on chromosome 21 at
A:Reference number: A47003; PMID:93300510
S:Accession: A47003

[illegible]

RESULT 7
A49947
Interferon gamma receptor beta subunit - mouse
N.Altenerate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor; t
C.Species: Mus musculus (house mouse)
C.Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C.Accession: A49947
R.Hemmi, S.; Bohnl, R.; Stark, G.; Di Marco, F.; Aguet, M.
Cell 76, 803-810, 1994
A>Title: A novel member of the interferon receptor family complements functionality
A.Reference number: A49947; MUID:9410381

A:Cross-references: GB:569336; NID:954584; PIDN:AAB30165.1; PID:9545842
A:Experimental source: early B-cell line y16
A:Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIPI:145656)
C:Keywords: cytokine receptor

	Query Match	18.6%	Score 199:	DB 2:	Length 332:
	Best Local Similarity	30.1%	Pred. No. 3e-10:		
	Matches 65:	Conservative 38:	Mismatches 81:	Indels 32:	Gaps
Qy	4	LKSPQKVEVDIIDDNFLRMNRDES-----VGNVFESFDYKGTGMD-IMIKL--SGCQ	54		
Db	29	LAAPNLPRLHLNYDQILITWPPSSSDPRAVYQVYSF-----IDGSMHRLLEPNC	82		
Qy	55	NITSTKCNFSS--LKLNVYE-EIKLRIRAEKN-TSSWYEVDSFTFPFRAQIGPPE-VH	108		
Db	83	DITETKCOLTGCGRLKLPNPFYFLVLRARAGULSKWGLEPFOYIENVTYVGPNNIS	142		
Qy	109	LEADKAIIVIHISPGTKDSVMALADGLSFTYSLIMNNSGVEERLENIYSRHKIY--KL	166		
Db	143	VTPGKGLVITHFSPFD-----YHGKNTFOVLIVHWKESLSEIQDQVCGPFRKNSIVLGNL	197		


```

RESULT 11
S57242
twlitchin - Caenorhabditis elegans
N:Alternate names: myosin-regulating protein
N:Contains: protein kinase (EC 2.7.1.1)
C:Species: Caenorhabditis elegans
C:Date: 28-Oct-1995 #sequence_revision 24-Oct-1997 #text_change 18-Jun-1999
C:Accession: S57242; S07571; S06797; S57218
R:Benian, G.M.; L'Hernault, S.W.; Morris, M.E.
Submitted to the EMBL Data Library, February 1993
A:Description: Additional sequence complexity within twitching of Caenorhabditis elegans
A:Reference number: S57242
A:Accession: S57242
A:Molecule type: DNA
A:Residues: 1-6839 <BEN1>
A:Cross-references: EMBL:LI0351
R:Benian, G.
Submitted to the EMBL Data Library, November 1989
A:Reference number: S07571
A:Accession: S07571
A:Molecule type: DNA
A:Residues: 792-6839 <BEN2>
A:Cross-references: EMBL:X15423; NID:66897; PIDN:CAA33463.1; PID:66898
R:Benian, G.M.; Kiff, J.E.; Neckelmann, N.; Moerman, D.G.; Waterston, R.H.
Nature 342, 45-50, 1989
A:Title: Sequence of an unusually large protein implicated in regulation of myosin activity
A:Reference number: S06797; MUID:90044042
A:Accession: S06797
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 806-1175; 1178-1998, 'Y', 2000-3040, 'I', 3042-3335, 'I', 3337-5693; 5696-6359, 'I', 6
A:Cross-references: EMBL:X15423
R:Benian, G.M.; L'Hernault, S.W.; Morris, M.E.
Genetics 134, 1097-1104, 1993
A:Title: Additional sequence complexity in the muscle gene, unc-22, and its encoded protein
A:Reference number: S57218; MUID:93387664
A:Accession: S57218
A:Molecule type: DNA
A:Residues: 2-99; 108-194, 'Q', 196-206; 374-468; 658-753 <BEN4>
A:Experimental source: var. Bristol
C:Comment: Lack of unc-22 leads to a constant twitching of the body muscles.
C:Genetics:
A:Gene: unc-22
A:Map position: IV
A:Introns: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/3; 60
132/3; 6691/3; 6776/1; 6808/3
C:Superfamily: twlitchin; fibronectin type III repeat homology; immunoglobulin homology;
C:Keywords: ATP; autophosphorylation; duplication; muscle; phosphotransferase; serine/th
R:806-899, 899-990, 991-1083, 1084-1175, 1178-1273, 1474-1567, 1770-1864, 2066-2158, 2358-2450, 2
96-5790, 6263-6356, 6386-6478, 6541-6635, 6649-6742, 6745-6838/Region: motif 2
F:1274-1372, 1373-1473, 1568-1670, 1671-1769, 1865-1964, 1965-2065, 2159-2258, 2259-2357, 2451-2
29, 4215-4313, 4314-4415, 4416-4516, 4612-4710, 4711-4811, 4908-5009, 5010-5109, 5110-5210, 5399-
F:5940-6197/Domain: protein kinase homology <kin>
F:5948-5956/Region: protein kinase ATP-binding motif
F:5971/Active site: lys #status predicted

```

```

Query Match 9.1%; Score 97.5; DB 2: Length 6839;
Best Local Similarity 22.8%; Pred. No. 15;
Matches 44: Conservative 22; Mismatches 74; Indels 53; Gaps 10;

```

```

OY 4 LKSPK---VEV-DIIDNFILRMNRSESVGNVTFSDYOK--TGMDNMIKLSGCONI 56
DB 1864 LDRPSPNCPLEVSDFEDFNLSMKPPDDGGEPIEYVEKLDATGRWVP---CAKV 1920
OY 57 TSTKCNFSSKLNVYEIKLRIRA-EKENTSSWYEVDSFTPRKAQIGPEVHLEADKA 115
DB 1921 KOTKAHIDLKKG--QTYQFRKAVNKEGASDALSTDKTKAKNPIDEGCKT----- 1971

```

```

OY 116 IVIHISPEKDSVMALDGLSFTYSLIIV---KNSGVEERIENTYSHKIKYKSPETTY 172
DB 1971 -----GTPDYVMDADRVS-----LEMEPPKSDG-----APITQY 2001
OY 173 CLKVKAALLTSMK 185
DB 2002 VIEKKGKGRDMQ 2014

```

RESULT 12

hypothetical protein ZK617.1b - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C:Accession: T27935; T28031

R:White, S.

Submitted to the EMBL Data Library, May 1996

A:Reference number: Z20442

A:Accession: T27935

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-7160 <WIL>

A:Cross-references: EMBL:Z73897; PIDN:CAA98065.1; GSPDB:GN00022; CESP:ZK617.1b

R:Harris, B.

Submitted to the EMBL Data Library, May 1996

A:Reference number: Z20458

A:Accession: T28031

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-7160 <WIL2>

A:Cross-references: EMBL:Z73899; PIDN:CAA98082.1; GSPDB:GN00022; CESP:ZK617.1b

A:Experimental source: clone ZK829

C:Genetics:

A:Gene: CESP:ZK617.1b

A:Map position: 4

A:Introns: 10/3; 61/3; 135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 542/3; 574, 3067/1; 3141/3; 3269/1; 6473/3; 7012/3; 7097/1; 7129/3

```

Query Match 9.1%; Score 97.5; DB 2: Length 7160;
Best Local Similarity 22.8%; Pred. No. 15;
Matches 44: Conservative 22; Mismatches 74; Indels 53; Gaps 10;

```

```

OY 4 LKSPK---VEV-DIIDNFILRMNRSESVGNVTFSDYOK--TGMDNMIKLSGCONI 56
DB 2185 LDRPSPNCPLEVSDFEDFNLSMKPPDDGGEPIEYVEKLDATGRWVP---CAKV 2241
OY 57 TSTKCNFSSKLNVYEIKLRIRA-EKENTSSWYEVDSFTPRKAQIGPEVHLEADKA 115
DB 2242 KDTKAHIDLKKG--QTYQFRKAVNKEGASDALSTDKTKAKNPIDEGCKT----- 2292
OY 116 IVIHISPEKDSVMALDGLSFTYSLIIV---KNSGVEERIENTYSHKIKYKSPETTY 172
DB 2292 -----GTPDYVMDADRVS-----LEMEPPKSDG-----APITQY 2322
OY 173 CLKVKAALLTSMK 185
DB 2323 VIEKKGKGRDMQ 2335

```

RESULT 13

hypothetical protein F55F8.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T29585

R:Gallung, S.; Scheet, P.; Kemp, K.

Submitted to the EMBL Data Library, November 1996

A:Description: The sequence of C. elegans cosmid F55F8.

A:Reference number: Z20647

A:Accession: T29585

A:Status: preliminary; translated from GB/EMBL/DBJ


```

Db 41 PTNVLKSYNLPVYCWETQNM---QTPIFTQVKYISGSW---TDSCNISDHCC---- 92
QY 66 LKLNVEEIK-----LRIRAE-KENTSSWYEVDSFTPFRAQIGPP--EVHLEAEDKA 115
Db 92 ---NIGQIMYPDVSAARVAKYAGKESDYARSKFELMCKGKVGPPGLEIRRKKEQL 148
QY 116 IVIHISP-----GTRDSVMAALDG---LSFTYSLIMKNSSGVEERIENTISRHKIKYLS 167
Db 149 SYLVFHPPEVVVNGESOGIMEG-DGSTCYTFDYTYVEHNRSG-----EILHTKHVKEKE 202
QY 168 PETTYC-LKVKALITS 183
Db 203 CNETLCELNISVSTLDS 219

```

Search completed: June 1, 2000, 04:35:14
 Job time: 14294 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:38:50 ; Search time 34.71 Seconds

(without alignments)
178.115 Million cell updates/sec

Title: US-09-240-675-2_COPY_27_229

Perfect score: 1072

Sequence: 1 GKNLSPQKVEVDIIDNFI.....WKIGYSPVHCITVENEL 203

ALIGNMENTS

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 83857 seqs, 30454973 residues

83857

Total number of hits satisfying chosen parameters:

83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1072	100.0	557	1	INR1_HUMAN
2	708	66.0	560	1	INR1_BOVIN
3	693	64.6	560	1	INR1_SHEEP
4	525.5	49.0	590	1	INR1_MOUSE
5	214	20.0	325	1	INR1_MOUSE
6	144	13.4	337	1	INR1_MOUSE
7	111	10.4	489	1	INR1_MOUSE
8	95.5	8.9	925	1	INR1_MOUSE
9	92.5	8.6	292	1	INR1_MOUSE
10	92	8.6	477	1	INR1_MOUSE
11	90.5	8.4	1304	1	INR1_MOUSE
12	90	8.4	315	1	INR1_MOUSE
13	89.5	8.3	530	1	INR1_MOUSE
14	89	8.3	515	1	INR1_MOUSE
15	87.5	8.2	575	1	INR1_MOUSE
16	87	8.1	639	1	INR1_MOUSE
17	85.5	8.0	295	1	INR1_MOUSE
18	85.5	8.0	578	1	INR1_MOUSE
19	84.5	7.9	623	1	INR1_MOUSE
20	83.5	7.8	306	1	INR1_MOUSE
21	83.5	7.8	536	1	INR1_MOUSE
22	82.5	7.7	1068	1	INR1_MOUSE
23	82	7.6	415	1	INR1_MOUSE
24	81.5	7.6	292	1	INR1_MOUSE
25	80	7.5	486	1	INR1_MOUSE
26	80	7.5	780	1	INR1_MOUSE
27	80	7.5	878	1	INR1_MOUSE
28	80	7.5	993	1	INR1_MOUSE
29	78.5	7.3	896	1	INR1_MOUSE
30	78	7.3	1124	1	INR1_MOUSE
31	77.5	7.2	274	1	INR1_MOUSE
32	77.5	7.2	2131	1	INR1_MOUSE
33	77	7.2	377	1	INR1_MOUSE
34	77	7.2	460	1	INR1_MOUSE

35	77	7.2	620	1	Y241_MYCGE
36	76	7.1	504	1	MYCGE_HUMAN
37	76	7.1	3898	1	MYCGE_HUMAN
38	75.5	7.0	695	1	MYCGE_HUMAN
39	75.5	7.0	1447	1	MYCGE_HUMAN
40	75	7.0	254	1	MYCGE_HUMAN
41	75	7.0	376	1	MYCGE_HUMAN
42	75	7.0	998	1	MYCGE_HUMAN
43	75	7.0	1450	1	MYCGE_HUMAN
44	75	7.0	1997	1	MYCGE_HUMAN
45	74.5	6.9	262	1	MYCGE_HUMAN

RESULT 1
INR1_HUMAN
ID INR1_HUMAN STANDARD: PRT; 557 AA.
AC P17181;
DT 01-AUG-1990 (Rel. 15, Created)
DR 01-AUG-1990 (Rel. 15, Last sequence update)
DE 15-FEB-2000 (Rel. 39, Last annotation update)
GN INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Euthera; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90124632.
RA Uze G., Lutfalla G., Gresser I.;
RT "Genetic transfer of a functional human interferon alpha receptor
into mouse cells: cloning and expression of its cDNA."
RL Cell 60:225-234(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92129376.
RA Lutfalla G., Gardiner K., Proudhon D., Viehl E., Uze G.;
RT "The structure of the human interferon alpha/beta receptor gene."
RL J. Biol. Chem. 267:2802-2809(1992).
RN [3]
RP PHOSPHORYLATION BY TYR2.
RX MEDLINE: 95059042.
RA Collierman J., Witte M., Krishnan K., Krolewski J.;
RT "Direct binding to and tyrosine phosphorylation of the alpha subunit
of the type I interferon receptor by p135tyr2 tyrosine kinase."
RL Mol. Cell. Biol. 14:8133-8142(1994).
CC - FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
SUBUNITS THEMSELVES.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC - TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND
EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.
CC - PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYR2 TYROSINE KINASE.
CC - SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC - SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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or send an email to license@isb-sib.ch).
CC - EMBL: J03171; AAA52730.1; -
CC - EMBL: X60459; CAA42992.1; -
CC - PIR: A32694; A32694.
CC - PIR: S17112; S17112.
CC - MIM: 107450; -

KM Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;
 RX Phosphorylation.
 FT SIGNL 1 27 POTENTIAL.
 FT CHAIN 28 557 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 FT DOMAIN 28 436 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 437 457 POTENTIAL.
 FT DOMAIN 458 557 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 199 220 BY SIMILARITY.
 FT MOD.RES 466 466 PHOSPHORYLATION (BY TYR2) (PROBABLE).
 FT MOD.RES 481 481 PHOSPHORYLATION (BY TYR2) (PROBABLE).
 FT MOD.RES 50 50 POTENTIAL.
 FT CARBOHYD 58 58 POTENTIAL.
 FT CARBOHYD 81 81 POTENTIAL.
 FT CARBOHYD 86 88 POTENTIAL.
 FT CARBOHYD 110 110 POTENTIAL.
 FT CARBOHYD 172 172 POTENTIAL.
 FT CARBOHYD 254 254 POTENTIAL.
 FT CARBOHYD 313 313 POTENTIAL.
 FT CARBOHYD 314 314 POTENTIAL.
 FT CARBOHYD 376 376 POTENTIAL.
 FT CARBOHYD 416 416 POTENTIAL.
 FT CARBOHYD 433 433 POTENTIAL.
 FT VARIANT 168 168 L -> V.
 FT CONFLICT 17 17 /Frid-VAR.002717.
 FT SEQUENCE 557 AA: 63525 MW: 0F6744C8A1ADB673 CRC64;

Query Match 100.0%; Score 1072; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 1,1e-88;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKNIKSPQKVEVDIIDDNFILRNRSDESGVNTFSFDYKGTGDMNRIKSGCONITSTK 60
 DB 27 GKNIKSPQKVEVDIIDDNFILRNRSDESGVNTFSFDYKGTGDMNRIKSGCONITSTK 86
 QY 61 CNFSSLNLYVEEIKLRRAKENTSSWYEDSFTPRKAOIGPEVHLEAEDKAIYIH 120
 DB 87 CNFSSLNLYVEEIKLRRAKENTSSWYEDSFTPRKAOIGPEVHLEAEDKAIYIH 146
 QY 121 SPGRKDSVMAALDGLSFTYSLIMKNSGVEERINISRKIKYLSPEPTYCLVKYAA 180
 DB 147 SPGRKDSVMAALDGLSFTYSLIMKNSGVEERINISRKIKYLSPEPTYCLVKYAA 206
 QY 181 LTSWKIGVSPVHCITKTVENEL 203
 DB 207 LTSWKIGVSPVHCITKTVENEL 229

RESULT 2
 INRL_BOVIN STANDARD; PRT; 560 AA.
 AC 004790;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
 GN IFNARI OR IFNAR.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Bovine; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LONG;
 RX MEDLINE; 93076908.
 RA Mouchel-Viehl E., Lutfalla G., Mogensen K.E., Uze G.;
 RT "Specific antiviral activities of the human alpha interferons are
 determined at the level of receptor (IFNAR) structure.";
 RL FEBS Lett. 313:255-259(1992).
 RN [12]

RP SEQUENCE FROM N.A.
 RA MEDLINE; 93305725.
 RA Lim J.-K., Langer J.A.;
 RT "Cloning and characterization of a bovine alpha interferon receptor.";
 RL Blochim. Biophys. Acta 1173:314-319(1993).
 CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA- AND BETA-
 CC SUBUNITS THEMSELVES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTRAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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DR EMBL; X68443; CAA48484.1; -
 DR EMBL; L06320; AAA02571.1; -
 DR PIR; S33770; S33770.
 DR PIR; S27387; S27387.
 DR PFAM; PF00041; fn3; 1.
 KM Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNL 1 24 BY SIMILARITY.
 FT CHAIN 25 560 INTERFERON-ALPHA/BETA RECEPTOR ALPHA

FT DOMAIN 25 437 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 438 458 POTENTIAL.
 FT DOMAIN 459 560 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 199 220 BY SIMILARITY.
 FT DISULFID 47 47 BY SIMILARITY.
 FT CARBOHYD 47 47 POTENTIAL.
 FT CARBOHYD 55 55 POTENTIAL.
 FT CARBOHYD 85 85 POTENTIAL.
 FT CARBOHYD 109 109 POTENTIAL.
 FT CARBOHYD 172 172 POTENTIAL.
 FT CARBOHYD 254 254 POTENTIAL.
 FT CARBOHYD 313 313 POTENTIAL.
 FT CARBOHYD 377 377 POTENTIAL.
 FT CARBOHYD 434 434 POTENTIAL.
 FT CONFLICT 422 422 F -> V (IN REF. 2).
 FT SEQUENCE 560 AA: 63818 MW: 66D76B72861ED11 CRC64;

Query Match 66.0%; Score 708; DB 1; Length 560;
 Best Local Similarity 67.2%; Pred. No. 4,6e-56;
 Matches 137; Conservative 28; Mismatches 35; Indels 4; Gaps 4;

QY 3 NIKSPQKVEVDIIDDNFILRNRSDESGVNTFSFDYKGTGDMNRIKSGCONITSTKCN 62
 DB 27 NIK-PEVVEIHIIDNFFLKNSSSVKNVTSADYQILGIDNMKLSGCCQITSTKCN 85
 QY 63 FSSSLK-LNVEEIKLRRAK-ENTSSWYEDSFTPRKAOIGPEVHLEAEDKAIYIH 120
 DB 86 FSSVELENVEEIKLRRAK-ENTSSWYEDSFTPRKAOIGPEVHLEAEDKAIYIH 145
 QY 121 S-PTGRKDSVMAALDGLSFTYSLIMKNSGVEERINISRKIKYLSPEPTYCLVKYAA 179
 DB 146 SPGRKDSVMAALDGLSFTYSLIMKNSGVEERINISRKIKYLSPEPTYCLVKYAA 205
 QY 180 LTSWKIGVSPVHCITKTVENEL 203
 DB 206 LTSWKIGVSPVHCITKTVENEL 229

RESULT 3
 INRL_SHEEP STANDARD; PRT; 560 AA.
 ID INRL_SHEEP
 AC Q28389; Q95206;

DT	01-NOV-1997	(Rel. 35, Created)	
DT	01-NOV-1997	(Rel. 35, Last sequence update)	
DT	15-FEB-2000	(Rel. 39, Last annotation update)	
DE	INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)		
DE	(INTERFERON ALPHA/BETA RECEPTOR-1).		
GN	IFNARI OR IFNAR.		
OS	Ovis aries (Sheep).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
OC	Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;		
OC	Cephalinae; Ovis.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-ENDOMETRIUM:		
RX	MEDLINE; 97135690.		
RA	Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;		
RT	"Structure of an ovine interferon receptor and its expression in		
RT	endometrium";		
RL	J. Mol. Endocrinol. 17:207-215(1996).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-ENDOMETRIUM:		
RX	MEDLINE; 98006426.		
RA	Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;		
RT	"Molecular cloning of ovine and bovine type I interferon receptor		
RT	subunits from uterl. and endometrial expression of messenger		
RT	ribonucleic acid for ovine receptors during the estrous cycle and		
RT	pregnancy";		
RL	Endocrinology 138:4757-4767(1997).		
CC	-1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE		
CC	I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS		
CC	INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-		
CC	SUBUNITS THEMSELVES.		
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT		
CC	CONCEPTUS AT DAY 15 OF PREGNANCY.		
CC	-1- SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.		
CC	-1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.		
CC	-----		
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CC	-----		
DR	EMBL; X95939; CAA65183.1; -.		
DR	EMBL; U65978; AAB84231.1; -.		
DR	PFAM; PF00041; fn3.1.		
KW	Receptor; Transmembrane; Glycoprotein; Signal.		
FT	SIGNAL	1	24
FT	CHAIN	25	560
FT	-----		
FT	DOMAIN	25	437
FT	TRANSMEM	438	458
FT	DOMAIN	459	560
FT	DISULFID	76	84
FT	DISULFID	199	220
FT	CARBOHYD	47	47
FT	CARBOHYD	55	55
FT	CARBOHYD	85	85
FT	CARBOHYD	108	108
FT	CARBOHYD	109	109
FT	CARBOHYD	172	172
FT	CARBOHYD	222	222
FT	CARBOHYD	285	285
FT	CARBOHYD	313	313
FT	CARBOHYD	359	359
FT	CARBOHYD	377	377
FT	CARBOHYD	434	434
FT	CONFLICT	352	352
FT	CONFLICT	522	522
SO	SEQUENCE	560 AA;	63918 MW;
			E7198A1905D4805C CRC64;

[illegible]

FT CARBOHYD 214 214 POTENTIAL.
 FT CARBOHYD 314 314 POTENTIAL.
 FT CARBOHYD 370 370 POTENTIAL.
 FT CARBOHYD 409 409 POTENTIAL.
 FT CARBOHYD 413 413 POTENTIAL.
 SQ SEQUENCE 590 AA; 65776 MW; 7EC6DF370185D3A CRC64;

Query Match 49.0%; Score 525.5; DB 1; Length 590;
 Best Local Similarity 51.0%; Pred. No. 1, le-39;
 Matches 104; Conservative 36; Mismatches 63; Indels 1; Gaps 1;

QY 1 GKNLSPQKVEVDIIDNFILRNKSDSEVGNVTFSDYQKTDGMDNMIKSGCONITSTK 60
 DB 86 CEFSLDTNVIYIKTORVRAEGNSTSWNEVDFIPEYTAHMSPEVRLAEDKALVH 145
 QY 120 ISPGTDSVMALDGLSFTSYSLIMKNSGVEERIEIYSRHKIYKLSPTTYCLVKAA 179
 DB 146 ISPPGDGNMALEKSPSTTIRIMOKSSSDKTIINSTIYVEKIPPELTTCLEVKAI 205
 QY 180 LLSMKIGVSPVHCIRKTYENEL 203
 DB 206 HPLKKHSNYSYVOICISTYVANKM 229

RESULT 5

CRF4_HUMAN STANDARD; PRT; 325 AA.

AC 008334;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.
 GN CRF4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-FETAL BRAIN;
 RA Lutfalla G., Gardiner K., Uze G.;
 RT "A new member of the cytokine receptor gene family maps on chromosome 21 at less than 35 kb from IFNAR."
 RL Genomics 16:366-373(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96054036.
 RA Lutfalla G., McInnis M.G., Antonarakis S.E., Uze G.;
 RT "Structure of the human CRF4 gene: comparison with its IFNAR neighbor."
 RL J. Mol. Evol. 41:338-344(1995).

CC - FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC - SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC - SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC EMBL: Z17227; CAA78933.1;
 CC EMBL: U08988; AAA86872.1;
 CC PIR: A47003; A47003.
 CC HSP: P13726; IDAN.

DR MM: 123889; -
 KM Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 325
 FT DOMAIN 20 220
 FT TRANSFM 221 249
 FT DOMAIN 250 325
 FT DISULFID 66 74
 FT CARBOHYD 188 209
 FT CARBOHYD 49 49
 FT CARBOHYD 102 102
 FT CARBOHYD 161 161
 FT CARBOHYD 124 123
 FT CONFLICT 269 273
 FT CONFLICT 274 325
 SQ SEQUENCE 325 AA; 37011 MW; 66706C79F8514B23 CRC64;

Query Match 20.0%; Score 214; DB 1; Length 325;
 Best Local Similarity 30.5%; Pred. No. 4, 2e-12;
 Matches 60; Conservative 39; Mismatches 86; Indels 12; Gaps 7;

QY 7 POKVEVDIIDNFILRNKSDSEVGNVTFSDYQKTDGMDNMIKSGCONITSTKNESSL 66
 DB 24 PENVRNNSVNFKNILQWESPFAKGNLTFTAOY---LSYRFODKCMNTLTEDCFSS- 79
 QY 67 KLVYEEIKLRIRAE-KENTSSWYEVDSFTPRKAQIGPPEVHLBA-EDKAVIHISPT 124
 DB 79 -LSKYGDTLRRAFADEHSDVNI-TPCPYDDITIGPPKQGVAVLDSLHMRLLAKI 136
 QY 125 KDSV-MMALDGL-SFTSYSLIMKNSGVEERIEIYSRHKIYKLSPTTYCLVKAAAL 181
 DB 137 ENEYETWTKKNYNSMTYVQYWKNGTDEKQITPQYDFEVLRLNEPWTYCVQVRCGLP 196
 QY 182 TSMKIGVSPVHCIRKTYENEL 198
 DB 197 DRNKGWSEPVCEQT 213

RESULT 6

INGS_HUMAN STANDARD; PRT; 337 AA.

AC P38484;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSUCER-1).
 GN IFNGR2 OR IFNGT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LUNG FIBROBLAST;
 RX MEDLINE: 94170380.
 RA Soh J., Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R., Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.;
 RT "Identification and sequence of an accessory factor required for activation of the human interferon gamma receptor."

CC - FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO INTERACT WITH GAF, JAK1, AND/OR JAK2.
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC - SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC - SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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DR EMBL: 005875; AAA16955.1; -
DR EMBL: 005877; AAA16956.1; -
DR MIM: 147569; -
DR PFM: PF00041; fn3; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 337 INTERFERON-GAMMA RECEPTOR BETA CHAIN.
FT DOMAIN 28 247 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 248 268 POTENTIAL.
FT DOMAIN 269 337 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 56 85 POTENTIAL.
FT CARBOHYD 85 85 POTENTIAL.
FT CARBOHYD 110 110 POTENTIAL.
FT CARBOHYD 137 137 POTENTIAL.
FT CARBOHYD 219 219 POTENTIAL.
FT CARBOHYD 231 231 POTENTIAL.
FT VARIANT 64 64 R -> Q.
FT SEQUENCE 337 AA; 37834 MW; 18C61B10AD90E509 CRC64; /FTID-VAR.002718.

Query Match 13.4%; Score 144; DB 1; Length 337;
Best Local Similarity 24.7%; Pred. No. 8; 1e-06;
Matches 56; Conservative 39; Mismatches 86; Indels 46; Gaps 12;

OY 4 LKSPQKVEVDIIDDNFILRM-----NRSDSEGVNTSFYQKGMWIKLS----- 52
DB 30 LPAPHKPKRLNAGVLSMEVALNSRPPVYRQVRYTQSK-----WFTADIMSTGV 84
OY 52 GQONTSTKCNSS-----LKLNVYEIKLRIRAKENT-SSMYEVDSTPRKAOI 102
DB 85 NCTQITAECDFTASPSKGFPPDENV-----TLRLRAELGALHSAAWVTPFOHINNTV 140
OY 103 GPPEVHLE---AEKRAIVIHISPGTKDSYVMAALDGLSFTYSLIMKNSGVEERENIYS 159
DB 141 GPPE-NIEVTPGEGSLINFSSPFIDISTAF-----FCYVYHYME--KGIGQVYGPR 193
OY 160 RKRIV--KLSPETTYCLAKYKALLTS---WKIGVSPHCKITVE 200
DB 194 SSSISLDNLKPSRYVCLQVADQLWKNKSNIFRVGHLSNISCYETMAD 240

RESULT 7
INGR_HUMAN STANDARD: PRT; 489 AA.
AC P15260;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDM119).
GN IFNGR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89003065.
RA Aguet M., Dembic Z., Merlin G.;
RT "Molecular cloning and expression of the human interferon-gamma
RT receptor";
RL Cell 55:273-280(1988).
RN [2]
RP DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.
RX MEDLINE: 93183911.
RA Stuber D., Friedlein A., Fountoulakis M., Lahm H.-W., Garotta G.;
RT "Alignment of disulfide bonds of the extracellular domain of the
RT interferon gamma receptor and investigation of their role in
RT biological activity";

RL Biochemistry 32:2423-2430(1993).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.
RX MEDLINE: 95342235.
RA Walter M.R., Windsor W.T., Nagabhushan T.L., Lundell D.J., Lunn C.A.,
RA Zaudowy P.J., Narula S.K.;
RT "Crystal structure of a complex between interferon-gamma and its
RT soluble high-affinity receptor";
RL Nature 376:230-235(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 COMPLEX WITH ANTIBODY.
RX MEDLINE: 98035727.
RA Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A.,
RA Winkler F.K., Robinson J.A.;
RT "Neutralizing epitopes on the extracellular interferon gamma receptor
RT (IFNGAMR), alpha-chain characterized by homology scanning mutagenesis
RT and X-ray crystal structure of the A6 fab-IFNGAMR1-108 complex";
RL J. Mol. Biol. 273:882-897(1997).
CC - FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
CC INTERFERON-GAMMA DIMER.
CC - SUBUNIT: MONOMER.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC - PM: PHOSPHORYLATED AT SER/THR RESIDUES.
CC - SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC - SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC - SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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DR EMBL: J03143; AAA52731.1; -
DR PIR: A31555; A31555.
DR PDB: 1JRH; 25-MAR-98.
DR MIM: 107470; -
DR MIM: 209950; -
KW Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;
KW Immunoglobulin domain; 3D-structure.
FT SIGNAL 1 17
FT CHAIN 18 489 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
FT DOMAIN 18 245 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 246 266 POTENTIAL.
FT DOMAIN 267 489 CYTOPLASMIC (POTENTIAL).
FT DISULFID 77 85
FT DISULFID 122 167
FT DISULFID 195 200
FT DISULFID 214 235
FT CARBOHYD 34 34 POTENTIAL.
FT CARBOHYD 79 79 POTENTIAL.
FT CARBOHYD 86 86 POTENTIAL.
FT CARBOHYD 179 179 POTENTIAL.
FT CARBOHYD 240 240 POTENTIAL.
FT SEQUENCE 489 AA; 54404 MW; DCF95374D8F47400 CRC64;

Query Match 10.4%; Score 111; DB 1; Length 489;
Best Local Similarity 22.2%; Pred. No. 0.012;
Matches 45; Conservative 41; Mismatches 83; Indels 34; Gaps 7;

OY 3 LKSPQKVEVDIIDDNFILRMNRSDSEGVNT-TEFSDYQKGMWIKLSGQNTITSTKC 61
DB 28 SVPTPTNTVITISYNNNPVYWEY--QINPQVDFVEYKNGVKNSWIDACINISHHYC 85
OY 62 NFSSKLNVYEIKRITA---EKENTSSKVEVDSFTPRKAOIGPPEVHLEAEKAVI 118
DB 86 NISDHWGPPNSLWVRAVAGQKE--SAVAKSEFAVCRGKGIGPPPLDIRKEKQMTI 143
OY 119 HI-----SPGTX-----DSYVMALDGLSFTYSLIMKNSGVEERINNI 157

Db 144 DIFHPVANGDEQVEDDYDETCYIRVNYVYVAMNGSEIOYKILTKR-----EDDCDEI 198
 OY 158 YSRHKYKLSPEPTYCKVKAAL 180
 Db 199 QCOLAIPVSSLNSQYCVSAGCVL 221

RESULT 8
 PMP2_CAEEL STANDARD: PRT: 925 AA.

AC P01341; 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG.
 GN F55F8.3
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 OC Rhabditina; Rhabditioidea; Rhabditidae; Pelodierinae; Caenorhabditis.
 RN [1]

RP SEQUENCE FROM N.A.
 RC SRRAIN-BRISTOL N2:
 RA Gattung S., Scheet P., Kemp K.:
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: BELONGS TO THE PMP2 FAMILY OF WD-REPEAT PROTEINS.
 CC -----
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CC
 DR EMBL: U00447; AAB37807.1; -
 DR WORMPEP; F55F8.3; CE11192.
 DR PRINTS: PR00320; GPROTEINBRP.
 DR PROSITE: PS00678; WD_REPEATS; 1.
 DR PPM: PFO0400; WD40; 4.
 KW Hypothetical protein; Repeat; WD repeat.
 FT REPEAT 188 218 WD1.
 FT REPEAT 358 388 WD2.
 FT REPEAT 400 430 WD3.
 FT REPEAT 486 514 WD4.
 FT REPEAT 524 554 WD5.
 FT REPEAT 599 627 WD6.
 SQ SEQUENCE 925 AA; 103899 MW; 439F35881B398CD1 CRC64;

Query Match 8.9%; Score 95.5; DB 1; Length 925;
 Best Local Similarity 25.7%; Pred. No. 0.64;
 Matches 38; Conservative 19; Mismatches 70; Indels 21; Gaps 4;

OY 44 MDNWKISGCONIT--STKCNFSSLKLNVEET--KLRIRAKENTSSWYVDSFTPRK 99
 Db 1 MDNFKLSNCGIYVYRDGQVAFSKDQSVISPIGNKLSIFDLRNNTSKTLDIDCNVNIKR 60
 OY 100 AQIGPPEVHLEADKAIYIH-----SPGTKSVYMAALDGLSFTY---SL 142
 Db 61 LSTISPGSYHLLASDERGVHVFHLLSEFKITTFRSNKRPIGSLWSPATRAVAICRENDIQ 120
 OY 143 IMKNSGVEERIENTISRKIKYKLSPEP 170
 Db 121 IHFGKSIENKYNVNFSLSRKIKLSDDS 148

RESULT 9
 TF_BOVIN STANDARD: PRT: 292 AA.
 ID TF_BOVIN
 AC P30931;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).
 GN F3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Bovinae; Bos.
 RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE-ADRENAL GLAND;
 RX MEDLINE: 92109720.
 RA Takeyenko Y., Muta T., Miyata T., Iwanaga S.;
 RT "CDNA and amino acid sequences of bovine tissue factor."
 RL Biochem. Biophys. Res. Commun. 181:1145-1150(1991).
 CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
 CC CIRCULATING FACTOR VII OR VIIA. THE [TF-VIIA] COMPLEX ACTIVATES
 CC FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
 CC PROPAGATION OF THE COAGULATION PROTEINASE CASCADE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

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CC
 DR EMBL: S74147; AAB20755.1; -
 DR PIR: JQ1319; KFB03.
 DR HSSP: P24055; 1A21.
 DR PRINTS: PR00346; TISSUEFACTOR.
 DR PROSITE: PS00621; TISSUE_FACTOR; 1.
 DR PPM: PFO1108; Tissue_fac; 1.
 KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
 KW Palmitate.
 FT SIGNAL 1 35
 FT CHAIN 36 292
 FT DOMAIN 36 248
 FT TRANSMEM 249 271
 FT DOMAIN 272 292
 FT SITE 46 48
 FT CARBOHYD 43 43
 FT CARBOHYD 153 153
 FT CARBOHYD 181 181
 FT DISULFID 81 89
 FT DISULFID 215 238
 FT LIPID 274 274
 SQ SEQUENCE 292 AA; 32475 MW; 5E471D92BFBCE163 CRC64;

Query Match 8.6%; Score 92.5; DB 1; Length 292;
 Best Local Similarity 22.7%; Pred. No. 0.28;
 Matches 40; Conservative 35; Mismatches 70; Indels 31; Gaps 9;

OY 44 MDNWKISGCONITSKCNFS--SLKLNVEEIKLRIRAKENTSS-----WYVDSFTP 96
 Db 74 LGNW--KNCFTYTNTECVTDEIYKNNVRETYLARIASLPATSSSTVPPPTNSPEFTP 131
 OY 97 FRRAGQGP-----EVHLEADKAIYIHISPGTDSYMAALD---GLSFTYSLII 143
 Db 132 YLENTNGOPTIOSFEQGVGKLVNTYQDARTLV-----ANS AFLSLRDVFGKDLNVTLY 186
 OY 144 WK NSGVEERIENTISRKIKYKLSPEPTYCKVKAALTSKIKIGYSPVHDKT 198
 Db 187 WKASSTGKKRATN--TNGFLIDVDXGNYCFHQAIVL--SRVVKQSPSPICKT 239

RESULT 10
 INGR_MOUSE STANDARD: PRT: 477 AA.
 ID INGR_MOUSE
 AC P15261;

DT 01-APR-1990 (Rel. 14, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR.
 GN IFNGR1 OR IFNGR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eukaryota; Rodentia; Sciurognathi; Muridae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90083245.
 RT "Expression cloning of the murine interferon gamma receptor cDNA."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:9248-9252(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90046824.
 RA Gray P.W., Leong S., Fennie E.H., Farrar M.A., Pingel J.T.,
 RA Fernandez-Luna J., Schneider R.D.;
 RT "Cloning and expression of the cDNA for the murine interferon gamma
 RT receptor."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8497-8501(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90093370.
 RA Hemmi S., Peghini P., Metzler M., Merlin G., Dembic Z., Aguet M.;
 RT "Cloning of murine interferon gamma receptor cDNA: expression in
 RT human cells mediates high-affinity binding but is not sufficient to
 RT confer sensitivity to murine interferon gamma."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:9901-9905(1989).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90036866.
 RA Kumar C.S., Muthukumaran G., Frost L.J., Noe M., Ahn Y.H.,
 RA Mariano T.M., Pestka S.;
 RT "Molecular characterization of the murine interferon gamma receptor
 RT cDNA."
 RL J. Biol. Chem. 264:17939-17946(1989).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90154099.
 RA Cofano F., Moore S.K., Tanaka S., Yuhki N., Landolfo S.,
 RA Appella E.;
 RT "Affinity purification, peptide analysis, and cDNA sequence of the
 RT mouse interferon gamma receptor."
 RL J. Biol. Chem. 265:4064-4071(1990).
 RN [6]
 RP SEQUENCE OF 1-28 FROM N.A.
 RX MEDLINE: 95197006.
 RA Raval P., Obici S., Russell S.W., Murphy W.J.;
 RT "Characterization of the 5' flanking region and gene encoding the
 RT mouse interferon-gamma receptor."
 RL Gene 154:219-223(1995).
 CC -1- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
 CC INTERFERON-GAMMA DIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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 CC -----
 DR EMBL: M28995; AAA37895.1; ALT_INIT.
 DR EMBL: M26713; AAA37896.1; -
 DR EMBL: M28333; AAA37898.1; -
 DR EMBL: M25764; AAA39177.1; -

DR EMBL: J05265; AAA39178.1; -
 DR EMBL: U05960; AAA80980.1; -
 DR PIR: A34368; A34368.
 DR PIR: A34423; A34423.
 DR PIR: A34508; A34508.
 DR PIR: A35468; A35468.
 DR PIR: A36224; A36224.
 DR HSSP: P15260; 10RN.
 DR MCD: MGI:107655; IFNGR.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;
 FT CHAIN 1 22
 FT SIGNAL 1 22
 FT CHAIN 23 477
 FT DOMAIN 23 253
 FT TRANSMEM 254 277
 FT DOMAIN 278 477
 FT DISULFID 83 91
 FT DISULFID 128 174
 FT DISULFID 203 208
 FT DISULFID 222 243
 FT CARBOHYD 61 61
 FT CARBOHYD 85 85
 FT CARBOHYD 186 186
 FT CARBOHYD 204 204
 FT CARBOHYD 211 211
 FT CONFLICT 95 95
 SQ SEQUENCE 477 AA; 52271 MW; A1FC6E9BA0B20A CRC64;
 Query Match 8.68; Score 92; DB 1; Length 477;
 Best Local Similarity 23.48; Pred. No. 0.57;
 Matches 46; Conservative 33; Mismatches 80; Indels 38; Gaps 12;
 Oy 7 POKVEVDIDNFIILRNRSDESVGNVTFSPDYQ-KTGMQWIKLSGQONTSTKCNSS 65
 Db 41 PTNVLKYNINLPVYCYMEYQNS--OTPIYVQKYYSGW--TDSCINISDHC----- 92
 Oy 66 LKLVYERIK-----LRRAE-KENTSSVYEVDSFTPFKQAIGPP-EVHLBADKA 115
 Db 92 ---NYGGIMYPDVSAARVAKVKGKESDVARSKFELMCLKGVGPGLEIRKKEEQL 148
 Oy 116 IVYHISP-----GTRDSYMAALDG---LSFTYSLILINKSSGVREIRNITSRKIKYKLS 167
 Db 149 SVLVFHPVYVNVGSGQTFMG-DGSTCYTFDYTVYVEHNRSQ-----ELHTKHTVEKEE 202
 Oy 168 PETTYC-LKVKALITS 183
 Db 203 CNETLCELINISVSTLDS 219
 RESULT 11
 CD45_HUMAN STANDARD; PRT; 1304 AA.
 ID CD45_HUMAN
 AC P08575; 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE LEUKOCYTE COMMON ANTIGEN PRECURSOR (EC 3.1.3.48) (L-CA) (CD45 ANTIGEN)
 DE (T200).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eukaryota; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-LYMPHOCTES;
 RX MEDLINE: 88061067.
 RA Streuli M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;
 RT "Differential usage of three exons generates at least five different
 RT mRNAs encoding human leukocyte common antigens."
 RL J. Exp. Med. 166:1548-1566(1987).
 RN [2]
 RP FUNCTION.

CC	DISCUSSION OF VARIOUS FORMS, AND PARTIAL SEQUENCE.
RX	MEDLINE: 95279874.
RA	*Novick D., Cohen B., Tal N., Rubinstein M.: RT Soluble and membrane-anchored forms of the human IFN-alpha/beta receptor.";
RL	J. Leukoc. Biol. 57:712-718(1995).
CC	- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. THE LONG AND CC SOLUBLE FORMS ARE DIRECTLY INVOLVED IN SIGNAL TRANSDUCTION DUE TO CC THEIR INTERACTION WITH THE TYR KINASE, JAK1. THE LONG FORM ALSO CC INTERACTS WITH THE TRANSCRIPTIONAL FACTORS, STAT1 AND STAT2. BOTH CC FORMS ARE POTENT INHIBITORS OF TYPE I IFN ACTIVITY.
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	- ALTERNATIVE PRODUCTS: THREE ISOFORMS; A LONG FORM/IFNAR2-2 (SHOWN CC HERE), A SHORT FORM/IFNAR2-1 AND A SOLUBLE FORM/IFNAR2-3/P40; ARE CC PRODUCED BY ALTERNATIVE SPLICING.
CC	- PPM: UPON BINDING, IFNAR2 IS PHOSPHORYLATED ON TYROSINE RESIDUES. CC - SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC	-----
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DR	EMBL: L42243; AAB46417.1; JOINED.
DR	EMBL: L42238; AAB46417.1; JOINED.
DR	EMBL: L42233; AAB46417.1; JOINED.
DR	EMBL: L42340; AAB46417.1; JOINED.
DR	EMBL: L42323; AAB46417.1; JOINED.
DR	EMBL: L42241; AAB46417.1; JOINED.
DR	EMBL: L42242; AAB46417.1; JOINED.
DR	EMBL: L42243; AAB46418.1; JOINED.
DR	EMBL: L42339; AAB46418.1; JOINED.
DR	EMBL: L42340; AAB46418.1; JOINED.
DR	EMBL: L42323; AAB46418.1; JOINED.
DR	EMBL: L42241; AAB46419.1; JOINED.
DR	EMBL: L42243; AAB46419.1; JOINED.
DR	EMBL: L42338; AAB46419.1; JOINED.
DR	EMBL: L42239; AAB46419.1; JOINED.
DR	EMBL: L42340; AAB46419.1; JOINED.
DR	EMBL: L42241; AAB46419.1; JOINED.
DR	EMBL: L42242; AAB46419.1; JOINED.
DR	EMBL: L41944; AAB46415.1; JOINED.
DR	EMBL: L41943; AAB46414.1; JOINED.
DR	EMBL: L41942; AAB46413.1; JOINED.
DR	EMBL: L41941; AAB46412.1; JOINED.
DR	EMBL: L41940; AAB46411.1; JOINED.
DR	EMBL: L41939; AAB46410.1; JOINED.
DR	EMBL: L41938; AAB46409.1; JOINED.
DR	EMBL: L41937; AAB46408.1; JOINED.
DR	EMBL: L41936; AAB46407.1; JOINED.
DR	EMBL: L41935; AAB46406.1; JOINED.
DR	EMBL: L41934; AAB46405.1; JOINED.
DR	EMBL: L41933; AAB46404.1; JOINED.
DR	EMBL: L41932; AAB46403.1; JOINED.
DR	EMBL: L41931; AAB46402.1; JOINED.
DR	EMBL: L41930; AAB46401.1; JOINED.
DR	EMBL: L41929; AAB46400.1; JOINED.
DR	EMBL: L41928; AAB46399.1; JOINED.
DR	EMBL: L41927; AAB46398.1; JOINED.
DR	EMBL: L41926; AAB46397.1; JOINED.
DR	EMBL: L41925; AAB46396.1; JOINED.
DR	EMBL: L41924; AAB46395.1; JOINED.
DR	EMBL: L41923; AAB46394.1; JOINED.
DR	EMBL: L41922; AAB46393.1; JOINED.
DR	EMBL: L41921; AAB46392.1; JOINED.
DR	EMBL: L41920; AAB46391.1; JOINED.
DR	EMBL: L41919; AAB46390.1; JOINED.
DR	EMBL: L41918; AAB46389.1; JOINED.
DR	EMBL: L41917; AAB46388.1; JOINED.
DR	EMBL: L41916; AAB46387.1; JOINED.
DR	EMBL: L41915; AAB46386.1; JOINED.
DR	EMBL: L41914; AAB46385.1; JOINED.
DR	EMBL: L41913; AAB46384.1; JOINED.
DR	EMBL: L41912; AAB46383.1; JOINED.
DR	EMBL: L41911; AAB46382.1; JOINED.
DR	EMBL: L41910; AAB46381.1; JOINED.
DR	EMBL: L41909; AAB46380.1; JOINED.
DR	EMBL: L41908; AAB46379.1; JOINED.
DR	EMBL: L41907; AAB46378.1; JOINED.
DR	EMBL: L41906; AAB46377.1; JOINED.
DR	EMBL: L41905; AAB46376.1; JOINED.
DR	EMBL: L41904; AAB46375.1; JOINED.
DR	EMBL: L41903; AAB46374.1; JOINED.
DR	EMBL: L41902; AAB46373.1; JOINED.
DR	EMBL: L41901; AAB46372.1; JOINED.
DR	EMBL: L41900; AAB46371.1; JOINED.
DR	EMBL: L41899; AAB46370.1; JOINED.
DR	EMBL: L41898; AAB46369.1; JOINED.
DR	EMBL: L41897; AAB46368.1; JOINED.
DR	EMBL: L41896; AAB46367.1; JOINED.
DR	EMBL: L41895; AAB46366.1; JOINED.
DR	EMBL: L41894; AAB46365.1; JOINED.
DR	EMBL: L41893; AAB46364.1; JOINED.
DR	EMBL: L41892; AAB46363.1; JOINED.
DR	EMBL: L41891; AAB46362.1; JOINED.
DR	EMBL: L41890; AAB46361.1; JOINED.
DR	EMBL: L41889; AAB46360.1; JOINED.
DR	EMBL: L41888; AAB46359.1; JOINED.
DR	EMBL: L41887; AAB46358.1; JOINED.
DR	EMBL: L41886; AAB46357.1; JOINED.
DR	EMBL: L41885; AAB46356.1; JOINED.
DR	EMBL: L41884; AAB46355.1; JOINED.
DR	EMBL: L41883; AAB46354.1; JOINED.
DR	EMBL: L41882; AAB46353.1; JOINED.
DR	EMBL: L41881; AAB46352.1; JOINED.
DR	EMBL: L41880; AAB46351.1; JOINED.
DR	EMBL: L41879; AAB46350.1; JOINED.
DR	EMBL: L41878; AAB46349.1; JOINED.
DR	EMBL: L41877; AAB46348.1; JOINED.
DR	EMBL: L41876; AAB46347.1; JOINED.
DR	EMBL: L41875; AAB46346.1; JOINED.
DR	EMBL: L41874; AAB46345.1; JOINED.
DR	EMBL: L41873; AAB46344.1; JOINED.
DR	EMBL: L41872; AAB46343.1; JOINED.
DR	EMBL: L41871; AAB463

FT	VARSPIC	332	515	MISSING (IN ISOFORM 2-1).
FT	CONFLICT	10	10	F -> V (IN REF. 2 AND 4).
FT	CONFLICT	151	151	M -> V (IN REF. 3).
SO	SEQUENCE	515 AA:	57758 MM:	4D7730D93AA739F4 CRC64:
Query Match	Best Local Similarity	8.3%;	Score 89;	DB 1;
Matches	46;	Conservative	26;	Mismatches
			83;	Indels
			48;	Gaps
			10;	
OY	18	NF--ILKRNBSDESGVNTSFQYQKGMNWR-LSGCONITSTKCNFSLKINYEEI	74	
Db	47	NFRSLSLKELKNHISVPTHYLLTYLTKSPEDLLVVKNCATFTSSFCDDLDEMRSYHEAY	106	
OY	75	KLIRAEKENT-----SSWYEVD-SFTPRKKAQIGPEVHLEAEADKAIVHIS-PGTR	125	
Db	107	VTVLEGFGKNTLTPLSCSNFWLAIDMSE-----PPEEYIGFTNHIVNWKFPSTV	158	
OY	126	DSVMALDGLSFTYSLSLTKMNSGVEERIEVYISRRK-----IKLSPTTT	171	
Db	159	E-----EELQFDLSLVY-----EEQSEGIYVKKHKEPKINGMNSGNTFYIIDKLIPNTN	205	
OY	172	YCLKVKALLTSWKIGVSPVHC	194	
Db	206	YCVSYLEHSDQAV-IKSPKLC	227	
RESULT	15			
ID	IL10R_MOUSE	STANDARD;	PRT;	575 AA.
AC	061727;			
DT	15-JUL-1998	(Rel. 36, Created)		
DT	15-JUL-1998	(Rel. 36, Last sequence update)		
DT	15-DEC-1998	(Rel. 37, Last annotation update)		
DE	INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).			
GN	IL10RA OR IL10R.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-C57BL/6 X AJ F1; TISSUE-HEMATOPOIETIC;			
RX	MEDLINE: 94068585.			
RA	HO A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;			
RI	"A receptor for interleukin 10 is related to interferon receptors."			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).			
CC	-1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation			
CC	at the European Bioinformatics Institute. There are no restrictions on			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/).			
CC	or send an email to license@isb-sib.ch .			
CC				
DR	EMBL: L12120; AAA16156.1; -			
DR	MGI: 96538; IL10RA.			
KW	Receptor; Transmembrane; Glycoprotein; Signal.			
FT	SIGNAL	1	16	POTENTIAL.
FT	CHAIN	17	575	INTERLEUKIN-10 RECEPTOR.
FT	DOMAIN	17	241	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	242	262	POTENTIAL.
FT	DOMAIN	263	375	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	204	225	POTENTIAL.
FT	CARBOHYD	50	50	POTENTIAL.
FT	CARBOHYD	66	66	POTENTIAL.
FT	CARBOHYD	113	113	POTENTIAL.
FT	CARBOHYD	182	182	POTENTIAL.
FT	CARBOHYD	238	238	POTENTIAL.

SO SEQUENCE 575 AA; 64248 MM; 820B9CD576F686B7 CRC64;

Query Match 8.2%; Score 87.5; DB 1; Length 575;
Best Local Similarity 20.0%; Pred. No. 1.8;
Matches 47; Conservative 38; Mismatches 89; Indels 61; Gaps 10;

```
QY 1 GKNLKSPOKEVDIIDDNFILRW---NRSDSVGNVTFSPDYOKTGMDNNIKLSGCONT 56
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 23 GTELPSPSPYVWFENAFQOHLHWKPIPNQSESTYEVAL---KQYGNSTWMDIHCRKA 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 57 TSTKCNFSSKLNYEE---IKLRIRA-EKENTSSWEVDS-FPFKRAQIGPEVHLEA 111
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 79 QALSCDLTFTLIDLHRSYGRARAVDNSOYSNWTTEFT----- 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 112 EDKAIYIHISPTKDSV-MMALDGLSEFYSLIMKNSGVEERIEIYSRHKIYKLS--- 168
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 123 VDEVIL-----TVDSVTLKAMDGIYGTIHPRPRTIIPAGDEYEQVFKDLRVYKISIRK 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 168 -----PET-----TYCLKYKALLTSMKIGVYSPVHCITVE 200
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 177 FSELKNATKRYKOEFTLTPVIGVRKFCVKVLPRLSRINKAEWSEEQCLLITTE 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: June 1, 2000, 04:38:52
Job time: 14315 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:38:06 ; Search time 69.16 Seconds

(Without alignments)
203.511 Million cell updates/sec

Title: us-09-240-675-2_COPY_27_229

Perfect score: 1072

Sequence: 1 GKNLKSPOKVEVDIIDNFI.....WKIGVSPVHCITVTENEL 203

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SPREMBL.12.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plant:*
10: sp_prokaryote:*
11: sp_rickettsia:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	415.5	38.8	569	13	O9YHWO gallus gall
2	215	20.1	349	11	Q61180 mus musculu
3	199	18.6	332	11	Q63953 mus musculu
4	179	16.7	341	13	O9YHWO gallus gall
5	107	10.0	484	4	O14936 homo sapien
6	97.5	9.1	6048	5	O23020 caenorhabd
7	97.5	9.1	6831	5	O23550 caenorhabd
8	97.5	9.1	7160	5	O23551 caenorhabd
9	90.5	8.4	1143	4	O16614 homo sapien
10	89.5	8.3	2033	11	O54711 mus musculu
11	89.5	8.3	2213	6	O95209 oryctolagu
12	89.5	8.3	2215	11	O88307 mus musculu
13	89	8.3	239	4	O15467 homo sapien
14	87.5	8.2	504	4	O93624 homo sapien
15	87.5	8.2	6875	6	O28733 oryctolagu
16	87	8.1	26926	4	O10466 homo sapien
17	86.5	8.1	429	3	O06103 saccharomyc
18	86	8.0	508	13	O9YHWO gallus gall
19	84.5	7.9	1220	3	O12465 saccharomyc
20	84.5	7.9	2214	4	O92673 homo sapien

21	82.5	7.7	406	1	O58459	O58459 methanococ
22	82	7.6	817	13	O07784	O07784 gallus gall
23	82	7.6	1093	11	O70535	O70535 rattus norv
24	81	7.6	1009	1	O58863	O58863 methanococ
25	81	7.6	1120	3	O08773	O08773 saccharomyc
26	81	7.6	1375	5	O94537	O94537 dirosophila
27	81	7.6	1526	5	O94538	O94538 dirosophila
28	81	7.6	2340	11	O60705	O60705 mus musculu
29	80.5	7.5	513	4	O94977	O94977 homo sapien
30	80	7.5	513	11	O35664	O35664 mus musculu
31	79.5	7.4	431	10	O23861	O23861 brassica ca
32	79.5	7.4	1074	2	O9X257	O9X257 thermotoga
33	79	7.4	247	11	O35663	O35663 mus musculu
34	79	7.4	248	11	O35983	O35983 mus musculu
35	79	7.4	430	10	O23854	O23854 brassica ca
36	79	7.4	513	11	O35238	O35238 mus musculu
37	79	7.4	531	11	O62319	O62319 mus musculu
38	79	7.4	828	5	O9X439	O9X439 caenorhabd
39	78.5	7.3	395	5	O01531	O01531 caenorhabd
40	78.5	7.3	497	12	P89031	P89031 ovine papil
41	78.5	7.3	1825	5	O61210	O61210 caenorhabd
42	78	7.3	331	11	O55205	O55205 mus musculu
43	78	7.3	373	11	O55203	O55203 mus musculu
44	78	7.3	746	12	O90754	O90754 foot-and-mo
45	77.5	7.2	342	5	P91305	P91305 caenorhabd

ALIGNMENTS

RESULT	1	PREDIMINARY	PRT	569 AA.
O9YHWO	O9YHWO			
AC	O9YHWO			
DT	01-MAY-1999 (TREMBL)	10, Created		
DT	01-MAY-1999 (TREMBL)	10, Last sequence update		
DT	01-MAY-1999 (TREMBL)	10, Last annotation update		
DE	INTERFERON ALPHA/BETA RECEPTOR 1.			
GN	IFNAR1.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;			
CC	Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-LAYER.			
RA	REBOU J., GARDINER K., MONNERON D., UZE G., LUTPALLA G.;			
RT	"Comparative genomic analysis of the Interferon/Interleukin-10			
RT	receptor gene cluster."			
RL	Genome Res. 0:0-0(1999).			
DR	EMBL; AF082664; AAD13669.1; -.			
KW	Receptor.			
SO	SEQUENCE	569 AA;	64055 MW;	F99BC099 CRC32;

Query Match	38.8%;	Score 415.5;	DB 13;	Length 569;
Best Local Similarity	45.1%;	Pred. No. 1e-29;		
Matches	92;	Conservative	36;	Mismatches 65;
				Indels 11;
				Gaps 6;
OY	3	NLKSPOKVEVDIIDNFIILRNRSDESGVTFFSPDQ-----KTGMDNWKLSGCONIT	57	
DB	31	NLKSPODQYAVAVNTFLMNTYGDGT-NYTFSAQYOCFDDLTSEPEMELSGCONVS	89	
OY	58	STKNFSLKLVVEEIKLRIRAE-KENTSSWYEDSFTPEPKAQIGPPEVHLEADKAI	116	
DB	90	HTEDFSALIRAYVTDHTRIRARREKSPWSSIFEMIPYEINQIGPELALDSINGAI	149	
OY	117	VIHSFGKSDV--MMALDGLSFTYSLIKNNSGVEERINYSRKIKYLSPEYTYCL	174	
DB	150	KINISPEANQVRKM--LISVFYKYNVIMNNSNV-EKVASLIPDIVINDLAPEYTYCL	207	
OY	175	KVKAAALLSWKIGVSPVHCITKT	198	
DB	208	KVQATVPLEDKGGLFSPHCITKT	231	


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QY 122 -PCTKDSVMMALDGL--STFYSLIMKNSGVEERINISRKH---ITYKLSPEITYCK 175
DB 137 PAADREHDKWSLKQYGVSWYIRILYK--RGSNKKVIHIDTKHNSSELLSQLPWTIYCIO 194
QY 176 VKAALLTSW-KIGVSPVHCIRKT 198
DB 195 VQ-CVTPENKKTGERSELCQRT 217

RESULT 5
ID Q14936 PRELIMINARY: PRT: 484 AA.
AC Q14936:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89003065.
RA AGUET M., DEMBIC Z., MERLIN G.;
RT "Molecular cloning and expression of the human interferon-gamma
RT receptor."
RL Cell 55:273-280(1988).
RN [2]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE: 97246734.
RA MERLIN G., VAN DER LEDE B.-J.M., MCKUNE K., KNEZEVIC N.,
RA BANNARATH W., KOMOUIN N., VIEGAS-PROUIGNOT E., KIEFER H., AGUET M.,
RA DEMBIC Z.;
RT "The gene for the ligand binding chain of the human interferon gamma
RT receptor."
RL Immunogenetics 45:413-421(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX DEMBIC Z.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U19247; AAC52064.1; -.
DR EMBL: U19241; AAC52064.1; JOINED.
DR EMBL: U19242; AAC52064.1; JOINED.
DR EMBL: U19243; AAC52064.1; JOINED.
DR EMBL: U19244; AAC52064.1; JOINED.
DR EMBL: U19245; AAC52064.1; JOINED.
DR EMBL: U19246; AAC52064.1; JOINED.
SQ SEQUENCE 484 AA; 53818 MW; EBC99D1F CRC32;

Query Match 10.0%; Score 107; DB 4; Length 484;
Best Local Similarity 22.5%; Pred. No. 0.066;
Matches 40; Conservative 39; Mismatches 61; Indels 38; Gaps 7;

QY 3 NLSPQVEVDIIDDNFIILMNRSDSEVGNV-TFSPDYQTKGMDNWKLSGCCONITSTKC 61
DB 28 SVPTPTVVTIESYNNMNIYVMEY--QIMPOVPFTVEVKYGVKNSEMIACINISHNYC 85
QY 62 NFSLSKLNYEEIKLRIR--EKENTSSWYEVDSFTPPRKAQIGPEVHLAEDKAIYI 118
DB 86 NISDHVGDPSNSLWRYKAKAYGQK--SAVAKSEEFVAVCGDKIGPKLDIRKEEKQIM 143
QY 119 HISPGTKDSVMMALDGLSFTYSLIMKNSGVEERINISRKHIYKLSPEITYCKLV 176
DB 144 DI-----FHPVSFV-----NGDEGEVD-----YDEFTTCYIRV 171

RESULT 6
ID Q23020 PRELIMINARY: PRT: 6048 AA.
AC Q23020: 027232;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
```

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DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE TWITCHIN.
GN UNC-22 OR ZK617.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RX MEDLINE: 90044042.
RA BENJAN G.M., KIEF J.E., NECKELMANN N., MOERMAN D.G., WATERSON R.H.;
RT "Sequence of an unusually large protein implicated in regulation of
RT myosin activity in C. elegans."
RL Nature 342:45-50(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RX MEDLINE: 93387664.
RA BENJAN G.M., L'HERNAULT S.N., MORRIS M.E.;
RT "Additional sequence complexity in the muscle gene, unc-22, and its
RT encoded protein, twitchin, of Caenorhabditis elegans."
RL Genetics 134:1097-1104(1993).
RN [3]
RP SEQUENCE FROM N.A.
RA HARRIS B.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: X15423; CAA33463.1; -.
DR EMBL: 273899; CAA98081.1; ALT. INIT.
DR EMBL: 273897; CAA98081.1; JOINED.
DR HSP: 063450; IAO6.
DR PFAM: PF00041; I03; 31.
DR PFAM: PF00047; I9; 13.
DR PFAM: PF00069; PKinase; 1.
DR PRINTS: PR00014; FNTYPEITI.
KW Myosin; Kinase.
SQ SEQUENCE 6048 AA; 668449 MW; 1977C602 CRC32;

Query Match 9.1%; Score 97.5; DB 5; Length 6048;
Best Local Similarity 22.8%; Pred. No. 12;
Matches 44; Conservative 22; Mismatches 74; Indels 53; Gaps 10;

QY 4 LNSPQK---VEV-DIIDDNFIILMNRSDSEVGNVTFSPDYQK--TGMDNWKLSGCCONI 56
DB 1073 LRPSPKPNGLPSVDFEDNLMKPPDDGGEPELEYEVEKLTATGRWVP---CAKV 1129
QY 57 TETKCFSSSLKINYEIEIKLRIR--EKENTSSWYEVDSFTPPRKAQIGPEVHLAEDKA 115
DB 1130 KOTKAHIDGLKKG--QTYOFKVAVKNKESASDALSTDKTKAKNPYDEPKT----- 1180
QY 116 IYHISPGTKDSVMMALDGLSFTYSLIW---KNSGVEERINISRKHIYKLSPEITY 172
DB 1180 -----GTPDVYDDHADAVS-----LEWEPPKSDG-----APIQY 1210

QY 173 CLKVKAALLTSWK 185
DB 1211 VIEKKGKGRDQW 1223

RESULT 7
ID Q23550 PRELIMINARY: PRT: 6831 AA.
AC Q23550:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE UNC-22 PROTEIN.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
```

RA WHITE S.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: 273897; CAA98064.1; -
 DR EMBL: 273899; CAA98064.1; JOINED.
 DR HSSP: P02751; 1FNA.
 DR PFAM: PF00041; fn3; 31.
 DR PFAM: PF00047; 19; 17.
 DR PFAM: PF00069; PKinase; 1.
 DR PRINTS: PRO0014; FNTYPEIII.
 DR PRINTS: PRO0014; FNTYPEIII.
 SO SEQUENCE 6831 AA; 752579 MW; 0A66C38 CRC32;

Query Match 9.1%; Score 97.5; DB 5; Length 6831;
 Best Local Similarity 22.8%; Pred. No. 14;
 Matches 44; Conservative 22; Mismatches 74; Indels 53; Gaps 10;

QY 4 LKSPQK---VEV-DIIDNFIILRNNSDESIGNVTFSDYOK--TGMDNWKISGCONI 56
 DB 1856 LDRPSKNGPLEVSDVEEDNLNLSKRPDDGGEPIEYEVKLDITAGRWVP---CAKV 1912
 QY 57 TSTKCNFSSLLKLVYEIKLRIR- EKENTSSWYEVDSFTPRKAQIGPEVHLEADKA 115
 DB 1913 KDTKAHIDGLKKG--QTYQFVKAVKKEGASDALSTDKTKAKNPYDEPKT----- 1963
 QY 116 IVIHISPGTKDSYMAALDGLSTFTSLTIW---KNSGVEERIENTYSRHKIYKLSPEPTY 172
 DB 1963 -----GTPDYVDMADRVIS-----LEWEPKSDG-----APITQY 1993
 QY 173 CLKVKAALLTSWK 185
 DB 1994 VIEKKGKRGDMQ 2006

RESULT 8
 ID Q23551 PRELIMINARY; PRT; 7160 AA.
 AC Q23551;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE ZK617.1B PROTEIN.
 GN ZK617.1B.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
 OC Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HARRIS B.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BEKKS M.,
 RA BONFIELD J., BORTON J., CONNELL M., COPESEY T., COOPER J., COULSON A.,
 RA CAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIKEN L., ROOPRA A., SAUNDERS D., SHOMKKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOULDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans";
 RT Nature 368:32-38(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA WHITE S.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: 273899; CAA98082.1; -
 DR EMBL: 273897; CAA98082.1; JOINED.
 DR EMBL: 273897; CAA98082.1; JOINED.
 DR EMBL: 273899; CAA98082.1; JOINED.

DR HSSP: P02751; 1FNA.
 DR PFAM: PF00041; fn3; 31.
 DR PFAM: PF00047; 19; 17.
 DR PFAM: PF00069; PKinase; 1.
 DR PRINTS: PRO0014; FNTYPEIII.
 DR PRINTS: PRO0014; FNTYPEIII.
 SO SEQUENCE 7160 AA; 789211 MW; EDD567FE CRC32;

Query Match 9.1%; Score 97.5; DB 5; Length 7160;
 Best Local Similarity 22.8%; Pred. No. 15;
 Matches 44; Conservative 22; Mismatches 74; Indels 53; Gaps 10;

QY 4 LKSPQK---VEV-DIIDNFIILRNNSDESIGNVTFSDYOK--TGMDNWKISGCONI 56
 DB 2185 LDRPSKNGPLEVSDVEEDNLNLSKRPDDGGEPIEYEVKLDITAGRWVP---CAKV 2241
 QY 57 TSTKCNFSSLLKLVYEIKLRIR- EKENTSSWYEVDSFTPRKAQIGPEVHLEADKA 115
 DB 2242 KDTKAHIDGLKKG--QTYQFVKAVKKEGASDALSTDKTKAKNPYDEPKT----- 2292
 QY 116 IVIHISPGTKDSYMAALDGLSTFTSLTIW---KNSGVEERIENTYSRHKIYKLSPEPTY 172
 DB 2292 -----GTPDYVDMADRVIS-----LEWEPKSDG-----APITQY 2322
 QY 173 CLKVKAALLTSWK 185
 DB 2323 VIEKKGKRGDMQ 2335

RESULT 9
 ID Q16614 PRELIMINARY; PRT; 1143 AA.
 AC Q16614;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE T200 LEUKOCYTE COMMON ANTIGEN (CD45, LC-A) PRECURSOR (EC 3.1.3.48)
 DE (CD45, LC-A).
 GN PTPRC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87275816.
 RA RALPH S.J., THOMAS M.L., MORTON C.C., TROMBRIDGE I.S.;
 RT "Structural variants of human T200 glycoprotein (Leukocyte-common
 antigen).";
 RT EMBO J. 6:1251-1257(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE: 89009812.
 RA HALL L.R., STREUBI M., SCHLOSSMAN S.F., SAITO H.;
 RT "Complete exon-intron organization of the human leukocyte common
 antigen (CD45) gene";
 RT J. Immunol. 141:2781-2787(1988).
 RL EMBL: M23462; AAD15273.1; JOINED.
 DR EMBL: M23461; AAD15273.1; JOINED.
 DR EMBL: M23462; AAD15273.1; JOINED.
 DR EMBL: M23463; AAD15273.1; JOINED.
 DR EMBL: M23464; AAD15273.1; JOINED.
 DR EMBL: M23465; AAD15273.1; JOINED.
 DR EMBL: M23466; AAD15273.1; JOINED.
 DR EMBL: M23467; AAD15273.1; JOINED.
 DR EMBL: M23468; AAD15273.1; JOINED.
 DR EMBL: M23469; AAD15273.1; JOINED.
 DR EMBL: M23470; AAD15273.1; JOINED.
 DR EMBL: M23471; AAD15273.1; JOINED.
 DR EMBL: M23472; AAD15273.1; JOINED.
 DR EMBL: M23473; AAD15273.1; JOINED.
 DR EMBL: M23474; AAD15273.1; JOINED.
 DR EMBL: M23475; AAD15273.1; JOINED.
 DR EMBL: M23476; AAD15273.1; JOINED.
 DR EMBL: M23477; AAD15273.1; JOINED.
 DR EMBL: M23478; AAD15273.1; JOINED.

DR EMBL: M23479; AAD15273.1; JOINED.
DR EMBL: M23480; AAD15273.1; JOINED.
DR EMBL: M23481; AAD15273.1; JOINED.
DR EMBL: M23482; AAD15273.1; JOINED.
DR EMBL: M23483; AAD15273.1; JOINED.
DR EMBL: M23484; AAD15273.1; JOINED.
DR EMBL: M23485; AAD15273.1; JOINED.
DR EMBL: M23486; AAD15273.1; JOINED.
DR EMBL: M23487; AAD15273.1; JOINED.
DR EMBL: M23488; AAD15273.1; JOINED.
DR EMBL: M23489; AAD15273.1; JOINED.
DR EMBL: M23490; AAD15273.1; JOINED.
DR EMBL: M23491; AAD15273.1; JOINED.
DR EMBL: Y00062; CAA68269.1; .
DR HSSP: P18052; 1YFO.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00102; Y_PHOSPHATASE.
DR PRINTS: PR00700; PRTPHPTASE.
DR SIGNAL: Alternative splicing; Hydrolase.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 1143
SQ SEQUENCE 1143 AA; 130897 MW; 97A3A561 CRC32;

Query Match 8.4%; Score 90.5; DB 4; Length 1143;
Best Local Similarity 20.9%; Pred. No. 6.1;
Matches 36; Conservative 23; Mismatches 60; Indels 53; Gaps 6;

QY 27 DESVGVNTPSFYQKGMNMIKSCGONITKCNFSSLKLVNVEIKLRPAEENIS 86
DB 66 DEKVAITVDYLYNK-----ETKLFYAKLVNENVEC-----GNNTC 102
QY 87 SWYEDSFTPFRAQIGPEVHLEADKAIVIHISPT----- 125
DB 103 TNEVHNMLECKNNAVSISHNSTADKLLIDVPGVEKFKQLHDTQVEKADTICLKW 162
QY 125 KQSVWALDGLSFTYSL---LIWKNSSGVEERIEIENYSRHKIKYLSPEPTY 172
DB 163 KNIETFTCDQNTITRYFGQGNMIFDK---EIKLENLEPEHE-YKCDSEILY 210

RESULT 10
OS4711 PRELIMINARY; PRT; 2033 AA.
AC OS4711;
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE SORILIN-RELATED RECEPTOR, LDLR CLASS A REPEATS-CONTAINING PRECURSOR (GP250) (FRAGMENT).
GN SORL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA HERANUS-BONGMEYER I., HAMPE W., SCHINKE B., METHNER A., NYKJAER A.,
MECH. Dev. 0:0-0(1997).
RL EMBL: AF01816; AAC16739.1; .
DR HSSP: P01130; 1AJV.
DR MGD: MGI:1202296; Sorl1.
DR PROSITE: PS01209; LDLRA_1; 10.
DR PFAM: PF00041; fn3; 4.
DR PFAM: PF00057; ldl_recept_a; 11.
DR PFAM: PF00058; ldl_recept_b; 5.
KW Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 2033 AA; 227305 MW; DC8108CD CRC32;

Query Match 8.3%; Score 89.5; DB 11; Length 2033;
Best Local Similarity 19.2%; Pred. No. 16;
Matches 33; Conservative 33; Mismatches 77; Indels 29; Gaps 7;
QY 18 NFILMNRSDSEV-----GNV-TFSFDYQKGMNMIKSCGONITSTKCNFS 64
DB 1474 NQQLNREDEGVILGHAPPVHTGLIREYIVESRSGSKMAQRAASNTEK----- 1530
QY 65 SKLVNVEEIKLRPAEENISSWYEDSFTPFRAQIGPEVHLEADKAIV----- 118
DB 1530 NLLNALVTVRY-AAVTSRGIGNMDSKSIITIKGVIAQAPNIIHSDYDENSLSFTLMD 1588
QY 118 --THSPGKDSVWALDGLSFTYSLLIWKNSGVEERIEIENYSRHKIKYLS 167
DB 1589 GDIKVY-GYVNLFWSPFAHQKQKTLSPFRGSAISHKVSNL-TAHTSYEIS 1638

RESULT 11
Q95209 PRELIMINARY; PRT; 2213 AA.
AC Q95209;
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE LR11.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RX MEDLINE: 96394640.
RA YAMAZAKI H., BUDO H., KUSUNOKI J., SEIMIYA K., KANAKI T., MORISAKI N.,
SCHNEIDER W.J., SAITO Y.;
RT "Elements of neural adhesion molecules and a yeast vacuolar protein
RT sorting receptor are present in a novel mammalian low density
RT lipoprotein receptor family member";
RL J. Biol. Chem. 271:24761-24768(1996).
DR EMBL: D86350; BAA13075.1; .
DR HSSP: P01130; 1AJV.
DR PROSITE: PS01209; LDLRA_1; 10.
DR PFAM: PF00057; ldl_recept_a; 11.
DR PFAM: PF00058; ldl_recept_b; 4.
DR PFAM: PF00041; fn3; 5.
DR PRINTS: PR00261; LDLRECEPTOR.
DR PRINTS: PR00014; FNTYPEIII.
KW Glycoprotein.
SQ SEQUENCE 2213 AA; 247764 MW; B35F3995 CRC32;

Query Match 8.3%; Score 89.5; DB 6; Length 2213;
Best Local Similarity 17.1%; Pred. No. 17;
Matches 32; Conservative 36; Mismatches 76; Indels 43; Gaps 7;

QY 6 SFQKVEVDIIDN---FILMNRSDSEVGNV-TFSFDYQKGMNMIKSCGONITSTK 61
DB 1652 APQNLQLSLHGEDEVIGHWSPPTHGLIREYIVESRSGSKVWTERAASNTEK- 1711
QY 62 NFSSKLNVYEIKLRPAEENISSWYEDSFTPFRAQIGPEVHLEADKAIVIHIS 121
DB 1711 ---NLVNTLYTVRY-AAVTSRGIGNMDSKSIITIKGVIAQAPNIIHSDYDENS 1760
QY 122 PGTKDSVWALDGLSFTYSL-----LIWKNSSGVEER-----IENYSRHKIKY 165
DB 1760 -----NSLSFTLVDCNIKIVGVVNLFWAFDTHKQEKTKMNFQSGSVSHKYN 1808
QY 166 LSPETTY 172
DB 1809 LTAQTAY 1815

RESULT 12
088307

ID 088307 PRELIMINARY; PRT; 2215 AA.
AC 088307;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE LK11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA KANAI T., BUJO H., HIRAYAMA S., TANAKA K., YAMAZAKI H., SEIMIYA K.,
RA MORISAKI N., SCHNEIDER W.J., SAITO Y.;
RT "Developmental regulation of Iril expression in murine brain.";
RL DNA Cell Biol. 0:0-0(1998);
DR EMBL: AB015790; BAA31219.1; -;
DR HSSP: P01130; IAUJ.
DR PROSITE: P501209; LDURA_1; 10.
DR PFAM: PF00057; Idl_recept_a; 11.
DR PFAM: PF00058; Idl_recept_b; 5.
DR PFAM: PF00041; fn3; 4.
DR PRINTS: PR00261; LDLRECEPTOR.
DR PRINTS: PR00014; FNTPEPIT.
KW Glycoprotein.
SQ SEQUENCE 2215 AA; 247021 MW; DFEBCF8 CRC32;

Query Match 8.3%; Score 89.5; DB 11; Length 2215;
Best Local Similarity 19.2%; Pred. No. 17;
Matches 33; Conservative 33; Mismatches 77; Indels 29; Gaps 7;

OY 18 NFIIRNRSDSEV-----GNV--TFSPDYOKTGMNNTKLSGCONITSTKCNFS 64
DB 1656 NQLSLNREEGVILGMARPVHTGILREYIEYISGSKMNASQPAASNSTEIK----- 1712
OY 65 SLALNVEEIKLRIRAKENTSSWEYDSTPFRKAQIGPPEVLEADKAIV----- 118
DB 1712 NLNLALYTRV-AAVTSRGIKMSDSTTKIGKVIAQPNHIDYDENSLSFTLTM 1770
OY 118 --IHISGTDSVMALDGLSTYSLIKMNSGVEERENIYSRKIYLS 167
DB 1771 GDIKVN-GYVYNLFMSFDAKOEKTLFRGSGALSHKVSNT-TAHTSYEIS 1820

RESULT 13
ID 015467 PRELIMINARY; PRT; 239 AA.
AC 015467;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE SOLUBLE IFN ALPHA/BETA RECEPTOR PRECURSOR.
GN IFNABR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE: 95279874.
RA NOVICK D., COHEN B., TAL N., RUBINSTEIN M.;
RT "Soluble and membrane-anchored forms of the human IFN-alpha/Beta
receptor.";
RL J. Leukoc. Biol. 57:712-718(1995).
CC -1- SIMILARITY BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
KW EMBL: X89814; CAA61940.1; -;
KW Receptor; Signal.
FT SIGNAL 1 26 SOLUBLE IFN ALPHA/BETA RECEPTOR BETA
FT CHAIN 27 239 CHAIN
SQ SEQUENCE 239 AA; 27336 MW; 9DA1F03E CRC32;

Query Match 8.3%; Score 89; DB 4; Length 239;
Best Local Similarity 22.7%; Pred. No. 1.1;
Matches 46; Conservative 26; Mismatches 83; Indels 48; Gaps 10;

OY 18 NF--ILNRNRSDSEVGNVTFSPDYOKTGMNNTK-LSCONTSTKCNFSIKLVYEIR 74
DB 47 NRSILSWLKNHSHVPTTYITLITIMSKPEDLKVKKNCANTRFCDLTDMSRSTHEAY 106
OY 75 KLIRAKENT-----SSWEVD-STPFRKAQIGPPEVLEADKAIVIHIS-PGTR 125
DB 107 VYVLEEGSCNTLIFSCSHNFMLAIDMSEF-----PPEFIVFTNINMVAFFPSIV 158
OY 126 DSVMALDGLSTYSLIKMNSGVEERENIYSRK-----IYKISPEPT 171
DB 159 E-----EELQDLSIV-----EEOSEGIVKAKHPKMGSGNFTIYIDKLIPNTN 205
OY 172 YCLKVKAAALLTSWKIGVSPVHC 194
DB 206 YCVSVYLEHSDQAV-IKSPKLC 227

RESULT 14
ID 099624 PRELIMINARY; PRT; 504 AA.
AC 099624;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE TRANSPORTER PROTEIN.
GN G17.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA LATIF F., LERMAN M., MINNA J., DUH F.M., KOONIN E., BADER S.;
RT Submitted (FEB-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL: U49082; AAB47236.1; -;
DR PFAM: PF01490; Ab_trans; 1.
SQ SEQUENCE 504 AA; 55772 MW; C41A273E CRC32;

Query Match 8.2%; Score 87.5; DB 4; Length 504;
Best Local Similarity 25.5%; Pred. No. 4;
Matches 41; Conservative 35; Mismatches 64; Indels 21; Gaps 7;

OY 55 NITSTKCNFSIKLVYEIRAKEN--TSSWEYDSTP-----RKAQIGPPEV 107
DB 245 NFNNTGNSSHVEI-VKEVQLQVEPEASAFCTPSYFTLNSOTAVTIPIMAFVCHPEV 303
OY 108 -----HLEMDKAIVIHISPGTKDSVMALDGLSTYSLIKMNSGVEERENIYSRK 162
DB 304 LPITYELKDPSSKKWQHIS-NLSIAVMYIMFLALFYGLFTFN--GVESELHLYTS--- 358
OY 163 IYKLSPEPTCYCKVKAALLTSWKIGVSPVHCIKTVENEL 203
DB 358 --KVDPFDVILCVRAVAVTAVTLVPIVPRRAIQML 396

RESULT 15
ID 028733 PRELIMINARY; PRT; 6875 AA.
AC 028733;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE TITIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-CE12;
 RA LABEIT S.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-6805 FROM N.A.
 RC STRAIN-CE12;
 RX MEDLINE: 92258380.
 RA LABEIT S., GAUTEL M., LAKEY A., TRINICK J.;
 RT "Towards a molecular understanding of titin."
 RL EMBO J. 11:1711-1716(1992).
 RN [3]
 RP SEQUENCE OF 4305-5320 FROM N.A.
 RC TISSUE-PSOAS MUSCLE;
 RX MEDLINE: 90238553.
 RA LABEIT S., BARLOW D.P., GAUTEL M., GIBSON T., HOLT J., HSIEH C.L.,
 RA FRANCKE U., LEONARD K., WARDALE J., WHITING A., TRINICK J.;
 RT "A regular pattern of two types of 100-residue motif in the sequence
 of titin."
 RL Nature 345:273-276(1990).
 DR EMBL: X64696; CAA45937.1; -;
 DR EMBL: X17329; CAA35207.1; -;
 DR HSSP: P56276; 1TLK.
 DR PRAM: PF00041; fn3: 50.
 DR PRAM: PF00047; 19: 3.
 KW Myosin; Muscle protein.
 FT NON_TER 1
 FT NON_TER 6875
 SO SEQUENCE 6875 AA; 759127 MW; ESD3B61F CRC32;

Query Match 8.2%; Score 87.5; DB 6; Length 6875;
 Best Local Similarity 21.0%; Pred. No. 1.1e+02;
 Matches 48; Conservative 24; Mismatches 70; Indels 87; Gaps 9;

OY 2 KNLKSPQKVEVDITDDNFILMNRSDSVGNVTFSDYQKTMQDNWIKLSC--QNTIST 59
 DB 233 RNLKIP-----DVSSDRCITRMDDPEDD-----GGCEIQNYILE 266
 OY 60 KCNFSSLKLVY-----EIKLRIRAEKE-----NTSSWEVDSFTPF 97
 DB 267 KCEKRWVMSYTSATVLTPTGTVRLIEGNEYIRVRRAENKIGTGPTESKPIAKTKYD 326
 OY 98 RKAQIGPPEVHLEADRAIVT-----HISPGTKDSVMWALDGLSFTYSL 142
 DB 327 RPRGRPDPEVTYKVSKEETVWVSPREYDGKRSITGYLEKKEKHSVRN----- 375
 OY 143 IWKSSGVEERIEINISYKRIYKLSPEPTYCLAKYKALLTSMKIGYVSP 191
 DB 375 VPVNRKSAIPER-----RLKYQNLIPGHEYQFRVKA---ENEIGVGE 413

Search completed: June 1, 2000, 04:38:14
 Job time: 14306 sec

OM of: US-09-240-675-1_COPY_27_229 to: A_Geneseq_36:*

Date: May 31, 2000 7:05 PM

About: Results were produced by the Gencore software, version 4.5,
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Command line parameters:

-MODEL=frame+np.model -DEV=xlp
-O/cg2_1/USPTO.spool/US09240675/runat.30052000.164311.24603/app_query.fasta.1
-DB=A_Geneseq_36 -QMT=fastan -SUFFIX=modif.rag -GAP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPT=0.000 -LOOPTXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAP=10.000 -XGAPEXT=0.500
-FCAP=6.000 -FCAPEXT=7.000 -YCAP=10.000 -YCAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -STAR=1 -MATRIX=blomsun62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pcr
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfes -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US09240675 -NCP=6 -ICPV=3 -NO_XLPHY -WAIT
-THREADS=1

Search information block:

Query: US-09-240-675-1_COPY_27_229
Query length: 203
Database: A_Geneseq_36:*Database sequences: 188963
Database length: 23686106
Search time (sec): 60.370000

score_list:

Sequence	Strd Orig	ZScore	Escore	Len	Documentation
A_Geneseq_36:W21805	340.00	795.63	1.8e-37	434	Spliced-deleted interferon alpha
A_Geneseq_36:R14487	340.00	795.58	1.8e-37	436	Soluble interferon-alpha/beta
A_Geneseq_36:R28495	340.00	795.58	1.8e-37	436	Sequence of a soluble form of
A_Geneseq_36:R21723	340.00	795.58	1.8e-37	436	IFN receptor extracellular doma
A_Geneseq_36:R21806	340.00	794.38	1.8e-37	496	Spliced-deleted interferon alpha
A_Geneseq_36:R11958	340.00	793.29	1.9e-37	557	Human alpha-interferon receptor
A_Geneseq_36:R14488	340.00	793.29	1.9e-37	557	Complete interferon-alpha/beta
A_Geneseq_36:R28495	340.00	793.29	1.9e-37	557	Sequence of a soluble form of
A_Geneseq_36:R42635	340.00	793.29	1.9e-37	557	Human interferon receptor. Mond
A_Geneseq_36:R75356	340.00	793.29	1.9e-37	557	Human IFN receptor. Compn. of
A_Geneseq_36:R21804	340.00	793.29	1.9e-37	557	Transmembrane interferon alpha
A_Geneseq_36:W93941	75.00	146.53	0.0771	1429	Human bix protein. Breast cand
A_Geneseq_36:W93962	62.00	151.40	1.97	30	Human bix immunogenic peptide 1.
A_Geneseq_36:W52296	61.50	127.90	3.70	325	CRP4 protein. New recombinant
A_Geneseq_36:W07702	61.00	121.89	4.79	543	Mouse ETS2 repressor factor (ER
A_Geneseq_36:R82404	61.00	121.58	4.82	561	Human SRE-2BP analogue GEN 506G
A_Geneseq_36:R96994	59.00	113.57	5.72	1321	Mouse IRS-2. New insulin rece
A_Geneseq_36:W59912	59.00	108.97	10.56	1291	Amino acid sequence of the mut
A_Geneseq_36:R57474	59.00	100.66	12.61	3135	P. falciparum transmission bid
A_Geneseq_36:R87511	58.00	108.96	13.66	999	Human c-met protooncogene recep
A_Geneseq_36:R61117	57.50	117.98	12.80	335	Yeast presequence COX IV-wheat
A_Geneseq_36:R41227	56.50	113.71	18.14	409	910 SLG protein. Isolated cDNA
A_Geneseq_36:R76075	56.50	111.90	18.86	496	Cardamylphosphate-synthase hom
A_Geneseq_36:R82399	56.00	121.06	17.63	164	Human G3BP protein. New ubiquit
A_Geneseq_36:R92593	56.00	114.77	20.17	321	Rice cultivar IR58024A atp6b
A_Geneseq_36:R66850	56.00	114.32	20.37	337	Rice mitochondrial protein (337
A_Geneseq_36:R74752	56.00	111.86	20.37	337	Rice mitochondrial protein (337
A_Geneseq_36:R59856	55.00	119.09	21.47	438	Maize id protein. Id gene contr
A_Geneseq_36:R20231	55.50	119.09	20.91	178	Human endothelin-2 vasoconstr
A_Geneseq_36:R23784	55.50	109.09	25.96	523	Precursor ET-2 sequence. Human
A_Geneseq_36:W22776	55.00	114.19	26.41	264	Toway p30 elicitor. DNA constr
A_Geneseq_36:R60610	55.00	114.19	26.41	264	Toway p30 elicitor. DNA constr
A_Geneseq_36:R02084	55.00	113.03	27.08	299	Camphor Class II acyl-ACP thioe
A_Geneseq_36:W09297	55.00	113.03	27.08	299	Camphor Class II acyl-ACP thioe
A_Geneseq_36:R87468	55.00	113.03	27.08	299	Camphor Class II acyl-ACP thioe
A_Geneseq_36:R29171	55.00	110.74	28.44	382	Camphor thioesterase. New plant
A_Geneseq_36:R74148	55.00	110.74	28.44	382	Camphor thioesterase. DNA const
A_Geneseq_36:W44336	55.00	110.74	28.44	382	Camphor PCR-generated thioest
A_Geneseq_36:R87463	55.00	110.74	28.44	382	Camphor C14 acyl ACP thioest
A_Geneseq_36:Y04998	55.00	110.59	28.53	388	Mycobacterium species protein s

A_Geneseq_36:Y04994 + 55.00 105.95 31.51 637 | Mycobacterium species prot.
A_Geneseq_36:W56309 + 55.00 103.21 33.42 854 | Class II S-receptor kinase
A_Geneseq_36:W22602 - 55.00 95.90 39.08 1864 | Tylosin synthase ORF2 p.
A_Geneseq_36:R47812 + 54.50 107.30 34.81 485 | Sequence of amino acid tra

seq_name: A_Geneseq_36:W21805

seq_documentation_block:

ID W21805 standard; Protein: 434 AA.
AC W21805:
DT 23-SEP-1997 (first entry)
DE Spliced-deleted interferon alpha-receptor form 1.
KW Interferon alpha-receptor; IFNAR.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..427
FT /label= Extracellular domain
FT /note= "comprises amino acids 1-427 of the
FT transmembrane IFNAR"
FT 428..434
FT /label= S_domain
PN A09475977-A.
PD 11-MAY-1995.
PE 20-OCT-1994; 075977.
PR 24-OCT-1993; IL-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PI (ABRA/) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M:
DR WPI; 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Example 2; Fig 7; 46pp; English.
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 1
CC (W21805) is characterised by a new domain (S) which follows an
CC end-deleted extracellular domain when compared to transmembrane
CC IFNAR (W21804). There is no transmembrane domain. The amino acid
CC sequence is predicted from a cDNA clone (see also T73520) obtd.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 and 2 (see also W21806) probably regulate
CC the response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating the activity of the multiple IFN
CC subtypes. They can be expressed in host cells and used to inhibit,
CC modulate or modify the activities of IFNs alpha and beta in cells,
CC tissues and organisms, or for diagnostic purposes.
SQ Sequence 434 AA:

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_27_229 x W21805 ..

Align seg 1/1 to: W21805 from: 1 to: 434

1 ATGATGCGTCGTCGCGGCGGACGACCTATGTCGCGCGGCGG 50
|||||
1 MethevalValLeuLeuGlyAlaThrThrLeuValLeuAlaValGI 17
17 yProTirpValLeuSerAlaAlaAlaGlyGlyAsnLeuLysSerProG 34
101 AAAAAGTAGAGCTGCATCATGATGACCACTTATCTGAGGTGAAC 150
|||||
34 IntyValGluValAspIleIleAspAspAsnPhelIleLeuArgTyrAsn 50
151 AGAGCCATGATGCTGCGGGAATGATGACTTTTCATTCATTCATAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67

201 A 201
|
67 s 67

seq_name: A_Geneseq_36:R14487

seq_documentation_block:

ID R14487 standard; Protein: 436 AA.
AC R14487; 16-JAN-1992 (first entry)
DE Soluble Interferon-alpha/Beta receptor.
KW IFN; autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
PN FR2657881-A.
PD 09-AUG-1991.
PF 05-FEB-1990; 001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Tovey MG, Uze G;
DR WPI: 91-319778/44.
DR N-PSDB; Q14239.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Claim 2: Page 45; 53pp; French.
CC The transmembrane and cytoplasmic domains of the native IFN receptor have been deleted to obtain a soluble, circulating form of the receptor. Potentially immunogenic epitopes have thus been eliminated.
CC Derivatives obtained by substitution or deletion of this sequence are also claimed as are hybrid molecules comprising the soluble receptor (or deriv.) and an immunoglobulin such as IgG1.
CC See also Q14240.
SQ Sequence 436 AA;

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_27_229 x R14487 ..

Align seg 1/1 to: R14487 from: 1 to: 436

1 ATGATGCTGCTCTCTGGCGGCGAGACCTAGTCTGTCGCCGCTGG 50
|
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGCTGTGTCGCCGAGCGAGTGAATAAATCTAAATCTCCTC 100
|
17 yProTrrPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTAGAGGTCGACATCATGATGACAACTTATCTGAGGTGGAAC 150
|
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
151 AGGAGCATGATGCTGTCGGGAATGATGATCTTTTCATTCATATCAAAA 200
|
51 ArgSerAspGluSerValGlyAsnValThrPheserPhesAspTryGlnLy 67
201 A 201
|
67 s 67

seq_name: A_Geneseq_36:R28495

seq_documentation_block:

ID R28495 standard; Protein: 436 AA.
AC R28495;
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the Interferon (IFN) receptor

DE with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-Interferon; beta-Interferon.
OS Synthetic.

PN WO9218626-A.
PD 29-OCT-1992.
PF 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PI Tovey M, Uze G;
DR WPI: 92-382110/46.
DR N-PSDB; Q30532.
PT Water soluble polypeptide(s) strongly bind Interferon(s) alpha and beta - useful as immunosuppressants, for treating auto-immune diseases and transplant rejection
PS Claim 2: Fig 1: 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, CC bacteriophage lambda ZAP, containing the entire coding sequence of CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos CC Q30534 and Q30535. R28496 represents the complete receptor. R28495 CC lacks the transmembrane and cytoplasmic domains. Both forms bind CC IFN in the same way as antibodies so are immunosuppressants e.g. for CC treating autoimmune diseases and graft rejection. They lack the CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 436 AA;

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_27_229 x R28495 ..

Align seg 1/1 to: R28495 from: 1 to: 436

1 ATGATGCTGCTCTCTGGCGGCGAGACCTAGTCTGTCGCCGCTGG 50
|
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGCTGTGTCGCCGAGCGAGTGAATAAATCTAAATCTCCTC 100
|
17 yProTrrPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTAGAGGTCGACATCATGATGACAACTTATCTGAGGTGGAAC 150
|
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
151 AGGAGCATGATGCTGTCGGGAATGATGATCTTTTCATTCATATCAAAA 200
|
51 ArgSerAspGluSerValGlyAsnValThrPheserPhesAspTryGlnLy 67
201 A 201
|
67 s 67

seq_name: A_Geneseq_36:R17123

seq_documentation_block:

ID R17123 standard; Protein: 436 AA.
AC R17123;
DT 16-OCT-1995 (first entry)
DE IFN receptor extracellular domain.
KW IFN receptor; Interferon receptor; Interferon-alpha; Interferon-beta; monoclonal antibody; Immunomodulator; AIDS.
OS Homo sapiens.
PN WO9507716-A.
PD 23-MAR-1995.
PF 16-SEP-1994; E03114.
PR 17-SEP-1993; EP-402279.

PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benizri EJ, Tovey MG:
DR WPL: 95-131187/17.
DR N-PSDB: 086457.
PT Compr. of monoclonal antibodies against interferon receptor -
PT useful as immuno:modulator, eg. for treating AIDS
PS Disclosure: F19.2A-2B; 105p; English.
CC A recombinant soluble form of the human interferon class I receptor
CC protein extracellular domain, given in R11723, was expressed in
CC either E. coli or COS cell hosts. The protein was used to raise
CC immunomodulatory monoclonal antibodies.
SQ Sequence 436 AA;

```
alignment_scores: ?
    Quality: 340.00      Length: 67
    Ratio: 5.075         Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.00000
```

alignment_block:
US-09-240-675-1_COPY_27_229 x R71723

Align seg 1/1 to: R71723 from: 1 to: 436

1 ATATGATGTCGTCCTCCTGGGGCGGAGAACCCATGAGTCGTCGCGCGTGG 50
1 MetMetValValLeuLeuLysValAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTGTCTCCGACGCCGCGAGGTGGAAAAATCTAAATCTCTCTC 1000
17 yProTPValLeuSerAlaAlaAlaG1yG1yysAsnLeuLysSerProG 34
101 AAAAAGTAGGTCGACATCATAGATGACAACTTATCTCAGGTGGAAAC 1500
34 LmYsValGluValAspL1e1LeuAspAsnPhelLeuAlaTrpAsn 50
151 AGGAGCGATGAGTCTCTCGGAGATGTGACTTTTCATTCGATTATCAAAA 2000
51 ArgSerAspGluSerValG1yAsnValTrpPheSerPheAspTyrGlnLy 67
201 A 201
67 s 67

seq_name: A_Geneseq_36:W21806

```
seq_documentation_block:
```

ID	W21806	standard; protein; 496 AA.
AC	W21806;	
DT	23-SEP-1997	(first entry)
DE	Spliced-deleted interferon	alpha-receptor form 2
KW	interferon alpha-receptor; IFNAR.	

Key	Location/Qualifiers
domain	1. .419

FT	/label-Extracellular_domain
FT	/note-"comprises amino acid residues 1-413 and
FT	422-427 of transmembrane IFNAR"
FT	420..496
FT	domain

FT	/label= intracellular_domain	481-557 of
FT	/note= "comprises amino acids	
FT	transmembranal IFNAR"	

PN	AU9475977-A.
PD	11-MAY-1995.

PF 20-OCT-1994; 075977.
PR 24-OCT-1993; IL-107378.

PA (YEDA) YEDA RES & DEV CO LTD.
PA (ABRA/) ABRAMOVICH C.

PI Abramovich C, Ratovitski E, Revel M,
DR WPI; 95-200634/27.

PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s),
PS Example 3; Fig 7; 46pp; English.

CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2
CC (w21806) is characterised by a double deletion when compared to
CC transmembranal IFNAR (w21804). The extracellular domain is
CC shortened by 6 amino acid residues and is followed by a truncated
CC intracellular domain. There is no transmembrane region. The amino
CC acid sequence is predicted from a cDNA clone (see also.T73521) obtcd
CC from human myeloma U265 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 (see also W21805) and 2 may regulate the
CC response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating IFN activities. They can be expressed
CC in host cells and used to inhibit, modulate or modify the
CC activities of IFNs alpha and beta in cells, tissues and organisms,
CC or for diagnostic purposes.

SO Sequence 496 AA.

```
alignment_scores:
  quality: 340.00
  ratio: 5.075
  gaps: 0
  percent similarity: 100.000
  percent identity: 100.000
```

alignment_block:
US-09-240-675-1_COPY_27_229 x W21806

Align seg 1/1 to: W21806 from: 1 to: 496

1 ATATGGTGTCTCTCTCTGGCGCGCGACGACCTTAGTCGTCGCGCGGG 50
1 MethevalValLeuLeuLysValArthrThrLeuValLeuValAlaValG1 17
51 CCGATGGGTGTTCGCCGACGCCGAGGTGGAATAATCAATCTCTC 100
17 yProTIPValLeuSerAlaAlaIGLYG1LYlsAsnLeuLysSerProG 34
101 AAAAAAGTAGAGTGGCAGACATCAAGATGACAACTTATCTCGAGTGGAC 150
34 InLysValG1LysValAspIleIleAspAspAsnPheIleLeuATyrAsn 50
151 AGGAGCGATGAGTCTGTCTCGGAAATGTGACTTTTCATCTCGATTCAAAA 200
51 ArgSerAspLysSerValG1LysValLThrPheSerPheAspTyrG1nLys 67
201 A 201
67 s 67

seq_name: A_Geneseq_36:R11958

```
seq_documentation_block:
ID   R1958 standard; protein; 557 AA

```

DT 18-JUL-1991 (first entry)
DE Human alpha-interferon receptor protein.
KW Human alpha IFN; IFN agonists; antiviral; anti tumour agent; drug targetting.

OS	Homo sapiens.	Location/Qualifiers
FH	Key	1..27
FT	peptide	/label= signal peptide
FT		

PN	WO9105862-A.
PD	02-MAY-1991.
PF	19-OCT-1990.

PR 20-OCT-1989; FR-013770
PA (CNRS) CNRS CENT NAT I

PI Mogensen KE, Uze G, Lutfalla G, Gresser I,
WPI; 91-148740/20.
DR

DR N-PSDB, Q11701.
PT New human alpha-interferon receptor protein - useful for testing

PT Interferon agonists and in treatment or diagnosis
PS Disclosure; fig 4; 30pp; French.

CC This recombinant human alpha interferon (IFN) receptor protein is
CC useful for the testing of IFN agonists and for treatment and diag
CC nosis of viral diseases and tumours. Antibodies raised against

CC this protein can be used for blocking the receptor when required,
CC eg where overexpression of alpha-IFN is harmful. The Abs are
CC also useful for eg drug targeting. Variants of the protein,
CC having residue 164 (Thr) replaced by Arg and an Asp inserted
CC between residues 479 and 480, are also useful.
SQ Sequence 557 AA;

alignment_scores: Length: 67
Quality: 340.00 Gaps: 0
Ratio: 5.075
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R11958 ..

Align seg 1/1 to: R11958 from: 1 to: 557

```
1 ATGATGTCGTCCTCCTGCGCGACGACCTAGTCGTCGCGCGG 50
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
|||||
51 CCCATGGGTGTGTCGCCGACGCCAGTGGAAAAATCTAAATCTCTC 100
|||||
17 yProtrpValLeuSerAlaAlaAlaGlyLysAsnLeuLysSerProG 34
|||||
101 AAAAGTACAGTGCACATCATAGACAACTTCTCTGAGGTGGAC 150
|||||
34 InLysValGluValAspIleIleAspAspAsnPhelLeuArgTrpAsn 50
|||||
151 AGGACGATGAGTCTGCGGAGTGTGACTTTTCATTCGATTATCAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
```

201 A 201
67 s 67

seq_name: A_Geneseq_36:R14488

seq_documentation_block:

ID R14488 standard; Protein: 557 AA.

AC R14488;

DT 16-JAN-1992 (first entry)

DE Complete interferon-alpha/beta receptor.

KW IFN; autoimmune disease; graft rejection; histocompatibility.

OS Homo sapiens.

FT Key Location/Qualifiers

FT domain 437..457

FT /label= transmembrane

FT domain 458..557

FT /label= cytoplasmic

FN FR2657881-A.

PD 09-AUG-1991.

PE 05-FEB-1990: 001298.

PR 05-FEB-1990: FR-001298.

PA (EUBI-) LAB EURO BIOTECHNO.

PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;

P1 Tovey M, Uze G;

DR N-PSDB: Q14240.

PT New water-soluble polypeptide(s) with affinity for IFN-alpha and

PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,

PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.

PS Disclosure: Page 47: 52pp; French.

CC The invention covers derivatives of the interferon-alpha and/or beta

CC receptor obtained by deleting the transmembrane and cytoplasmic domains

CC of the native receptor or by substitution. Potentially immunogenic

CC epitopes are eliminated and the deriv. can be secreted from

CC transformed cells. Soluble deriv's block the activity of IFN alpha/beta

CC and can be used to treat autoimmune diseases or to inhibit graft

CC rejection. See also Q14239.

SQ Sequence 557 AA;

alignment_scores: Length: 67
Quality: 340.00 Gaps: 0
Ratio: 5.075
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R14488 ..

Align seg 1/1 to: R14488 from: 1 to: 557

```
1 ATGATGTCGTCCTCCTGCGCGACGACCTAGTCGTCGCGCGG 50
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
|||||
51 CCCATGGGTGTGTCGCCGACGCCAGTGGAAAAATCTAAATCTCTC 100
|||||
17 yProtrpValLeuSerAlaAlaAlaGlyLysAsnLeuLysSerProG 34
|||||
101 AAAAGTACAGTGCACATCATAGACAACTTTCATTCGATTATCAAA 150
|||||
34 InLysValGluValAspIleIleAspAspAsnPhelLeuArgTrpAsn 50
|||||
151 AGGACGATGAGTCTGCGGAGTGTGACTTTTCATTCGATTATCAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
```

201 A 201
67 s 67

seq_name: A_Geneseq_36:R28496

seq_documentation_block:

ID R28496 standard; Protein: 557 AA.

AC R28496;

DT 31-MAR-1993 (first entry)

DE Sequence of a soluble form of the interferon (IFN) receptor

DE with a high affinity for IFN-alpha and -beta.

KW Interferon receptor; alpha-interferon; beta-interferon.

OS Synthetic.

PN MO9218626-A.

PD 29-OCT-1992.

PF 17-APR-1991: F00318.

PR 17-APR-1991: WO-F00318.

PA (EUBI-) LAB EURO BIOTECHNOLOGIE.

PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,

P1 Tovey M, Uze G;

DR N-PSDB: Q30533.

PT Water soluble polypeptide(s) strongly bind interferon(s) alpha

PT and beta - useful as immunosuppressants, for treating autoimmune

PT diseases and transplant rejection

PS Claim 3: Fig 2; 58pp; English.

CC DNA encoding the water-soluble polypeptide with a high affinity for

CC IFN-alpha and -beta is isolated by PCR, using appropriate

CC oligonucleotides as primers and cloned cDNA as template. For example,

CC bacteriophage lambda ZAP, containing the entire coding sequence of

CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos

CC Q30534 and Q30535. R28496 represents the complete receptor. R28495

CC lacks the transmembrane and cytoplasmic domains. Both forms bind

CC IFN in the same way as antibodies so are immunosuppressants e.g. for

CC treating autoimmune diseases and graft rejection. They lack the

CC toxic side-effects of known immunosuppressants such as steroids.

SQ Sequence 557 AA;

alignment_scores: Length: 67
Quality: 340.00 Gaps: 0
Ratio: 5.075
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R28496 ..

Align seg 1/1 to: R28496 from: 1 to: 557

```

1 ATGATGCTGCTCTCTGGGCGCGAGCACTAGTGTCTGCTGCGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValAlaValAlG1 17
51 CCCATGGGTGTTCGCCGAGCCGAGTGAATAATCTAAATCTCC 100
17 yProTriPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAAGTAGAGGTGACATCATAGATGACACTTATCTGAGTGAAC 150
34 InLysValGluValAspIleIleAspAspAsnPhelIleuArgTriPasn 50
151 AGGACCGATGACTGTCTGGGAAATGTACTTTTCATTGATTACAAA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLys 67
201 A 201
1
67 s 67

```

seq_name: A_Geneseq_36:R42635

seq_documentation_block:

ID R42635 standard: Protein: 557 AA.

```

AC R42635;
DT 20-APR-1994 (first entry)
DE Human interferon receptor.
KW IFN-R; extracellular domain; monoclonal antibody; viral infection;
KW cell proliferation; allograft rejection; systemic lupus erythematosus;
KW psoriasis; multiple sclerosis; Behcet's disease; aplastic anaemia;
KW immunodeficiency; measles virus; interferon-alpha-beta.
OS Homo sapiens.
FH key Location/Qualifiers
FT domain 1..436
FT /label= extracellular domain
FT /note= "soluble, immunogenic form of IFN-R"
PD 06-OCT-1993.
PF 31-MAR-1992; 400902.
PR 31-MAR-1992; EP-400902.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG;
DR WPI: 93-312951/40.
DR P-PSDB: R42635.
PT Monoclonal antibody to human interferon type-I receptor - having
PT neutralising activity against human type I interferon, used for
PT therapy and diagnosis
PS Disclosure: Fig.3; 21pp; English.
CC Monoclonal antibodies produced against soluble forms of the human
CC interferon alpha-beta receptor based on the full-length human IFN-R
CC sequence are claimed. The antibodies are useful for treatment and
CC prophylaxis of disorders involving cell proliferation and/or viral
CC infection.
SQ Sequence 557 AA;

```

alignment_scores:

Quality: 340.00 Length: 67
 Ratio: 5.075 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R42635 ..

Align seg 1/1 to: R42635 from: 1 to: 557

```

1 ATGATGCTGCTCTCTGGGCGCGAGCACTAGTGTCTGCTGCGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValAlaValAlG1 17
51 CCCATGGGTGTTCGCCGAGCCGAGTGAATAATCTAAATCTCC 100
17 yProTriPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAAGTAGAGGTGACATCATAGATGACACTTATCTGAGTGAAC 150
34 InLysValGluValAspIleIleAspAspAsnPhelIleuArgTriPasn 50
151 AGGACCGATGACTGTCTGGGAAATGTACTTTTCATTGATTACAAA 200

```

seq_name: A_Geneseq_36:R75356

seq_documentation_block:

ID R75356 standard: Protein: 557 AA.

```

AC R75356;
DT 16-OCT-1995 (first entry)
DE Human IFN receptor.
KW IFN receptor; interferon receptor; interferon-alpha;
KW interferon-beta; monoclonal antibody; immunomodulator; AIDS.
OS Homo sapiens.
FH key Location/Qualifiers
FT domain 1..436
FT /label= Extracellular_domain
FT MO507716-A.
PD 23-MAR-1995.
PF 16-SEP-1994; E03114.
PR 17-SEP-1993; EP-402279.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Beniziri EJ, Tovey MG;
DR WPI: 95-131187/17.
DR N-PSDB: 086458.
PT Compsn. of monoclonal antibodies against interferon receptor -
PT useful as immunomodulator, eg. for treating AIDS
PS Disclosure: Fig.3A-2B; 105pp; English.
CC The amino acid sequence of human interferon class I receptor is
CC given in R75356. A recombinant soluble form of the extracellular
CC domain of this receptor (R71723) has been used to raise
CC immunomodulatory monoclonal antibodies.
SQ Sequence 557 AA;

```

alignment_scores:

Quality: 340.00 Length: 67
 Ratio: 5.075 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R75356 ..

Align seg 1/1 to: R75356 from: 1 to: 557

```

1 ATGATGCTGCTCTCTGGGCGCGAGCACTAGTGTCTGCTGCGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValAlaValAlG1 17
51 CCCATGGGTGTTCGCCGAGCCGAGTGAATAATCTAAATCTCTC 100
17 yProTriPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAAGTAGAGGTGACATCATAGATGACAACTTATCTGAGTGAAC 150
34 InLysValGluValAspIleIleAspAspAsnPhelIleuArgTriPasn 50
151 AGGACCGATGACTGTCTGGGAAATGTACTTTTCATTGATTACAAA 200

```

51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67

201 A 201

67 s 67

seq_name: A_Geneseq_36:W21804

seq_documentation_block:

ID W21804 standard; Protein: 557 AA.

AC W21804;

DE 23-SEP-1997 (first entry)

DE Transmembranal interferon alpha-receptor.

KW Interferon alpha-receptor; IFNAR.

OS Homo sapiens.

FS Key

FT domain

FT domain

FT domain

FT domain

FT domain

FT domain

FT domain

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CC Human transmembranal interferon alpha receptor (IFNAR) (W21804)
CC includes a 21-amino acid transmembrane region. Novel, splice-
deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected
CC that lack this transmembrane domain. These, soluble non-membrane
CC bound polypeptides can be expressed in host cells and used to
CC inhibit, modulate or modify the activities of interferons alpha
CC and beta in cells, tissues and organisms, or for diagnostic
CC purposes.
CC Sequence 557 AA:

alignment_scores:

Quality: 340.00

Ratio: 5.075

Percent Similarity: 100.000

Percent Identity: 100.000

Length: 67

Gaps: 0

Align seg 1/1 to: W21804 from: 1 to: 557

US-09-240-675-1_COPY_27_229 x W21804

..

1 ATGATGCTGCTCTCTGCGGCGAGACCCCTAGTCTGCTGCGCGGCGG 50

1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG 17

51 CCCATGGGTCTTCCGACGCCGAGGTGAAAAATCTAAATCTCTCTC 100

17 YPRTPTValLeuSerAlaAlaGlyGlyLysAsnLeuLysSerProG 34

101 AAAAAGAGAGTCTGACATCATGATGACAACTTATCCAGAGTGAAC 150

34 InlySValGluValAspIleIleAspAspAsnPhelleLeuAlaGlyTPrAsn 50

151 AGAGGAGTCTGCTGCGGAAATGCACTTTTCATTCGATTATCAAAA 200

51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67

201 A 201

67 s 67

seq_name: A_Geneseq_36:W93941

seq_documentation_block:

ID W93941 standard; Protein: 1429 AA.

AC W93941;

DE 30-JUN-1999 (first entry)

DE Human bix protein.

KW Bix protein; breast cancer; nuclear receptor-binding auxiliary protein;

KW anti-cancer; anti-proliferative; mitogen; transcription factor; human;

KW tumour suppressor; ovarian cancer; proliferative disorder; treatment;

KW immune tissue; prevention; reproductive tissue.

OS Homo sapiens.

PN W0991554-A1.

PD 01-APR-1999.

PE 23-SEP-1998; U19782.

PR 23-SEP-1997; US-059621.

PA (DRIG/) DRIGERS P H.

PA (RUBI/) RUBINO D M.

PA (SEGE/) SEGERS J.

PI Driggers PH, Rubino DM, Segers J;

DR WPI: 99-254688/21.

DR N-PSDB: X24044.

PT Breast cancer gene encoding a nuclear receptor-binding auxiliary

PT protein, bix

PS Claim 1b: Page 58-62; 69pp; English.

CC This invention describes a novel human breast cancer gene encoding a

CC nuclear receptor-binding auxiliary protein, bix. The bix encoded protein

CC has anti-cancer, anti-proliferative and mitogenic activity and acts as a

CC transcription factor and tumour suppressor. Levels of expression of Bix

CC can be detected using the primers, probes and antibodies (contained in

CC the kit) to determine a predisposition to breast and ovarian cancer and

CC other proliferative disorders of immune tissues. Vectors containing the

CC Bix gene can be used for prevention and treatment of cancers and

CC proliferative diseases of mammalian reproductive and immune tissues.

CC Sequence 1429 AA:

SO

alignment_scores:

Quality: 75.00

Ratio: 1.923

Percent Similarity: 52.703

Percent Identity: 41.892

Length: 74

Gaps: 5

Align seg 1/1 to: W93941 from: 1 to: 1429

US-09-240-675-1_COPY_27_229 x W93941

..

3 GATGTCGTCCTCTGCGGCGAGACCCCTAGTCTGCTGCGCGGCGGCC 52

1230 AspGlyArgProSerTrp.....ProSerAlaArgArgArgCysE 1243

53 CATGGGTCTTCCGACGCCGAGGTGAAAAATCTAAATCTCTCTCA 102

1243 rArgGly.....SerArgThrTrpLysArgSerGlyArgSerSers 1257

103 AAAGTAGAGAGTGCACATCATAGATGACAACT..... 134

1257 eArgArgArgAlaHisSerGlnTrpAspLeuGluArgLeuArgAla 1273

135TATCTGAGGTGAGAACAGAGGAGTCTGCTGCGGAATGGA 178

1274 GlnLysGlnLeuGluArgGlnGlnHis...ValArgArgGluAlaG 1289

179 CTTTTCATTGATTCATTCAAAA 200

1289 u.....ArgLeuSerGln 1293

seq_name: A_Geneseq_36:W93962

seq_documentation_block:

ID W93962 standard; Protein: 30 AA.

AC W93962;

seq_name: A_Geneseq_36:W93962

seq_documentation_block:

ID W93962 standard; Protein: 30 AA.

AC W93962;

DT 30-JUN-1999 (first entry)
DE Human brx immunogenic peptide 1.
KW Bx protein; breast cancer; nuclear receptor-binding auxiliary protein;
KW anti-cancer; anti-proliferative; mitogen; transcription factor; human;
KW tumour suppressor; ovarian cancer; proliferative disorder; treatment;
KW immune tissue; prevention; reproductive tissue; immunogenic.
OS Homo sapiens.
PN WO915344-A1.
PD 01-APR-1999.
PF 23-SEP-1998; U19782.
PR 23-SEP-1997; US-059621.
PA (DRIC/) DRIGERS P H.
PI (RUBI/) RUBINO D M.
PI Driggers PH, Rubino DM, Segers J;
DR MPI: 99-254688/21.
PT Breast cancer gene encoding a nuclear receptor-binding auxiliary
PT protein, brx
PS Disclosure: Page 29; 69pp; English.
CC This invention describes a novel human breast cancer gene encoding a
CC nuclear receptor-binding auxiliary protein, brx. The brx encoded protein
CC has anti-cancer, anti-proliferative and mitogenic activity and acts as a
CC transcription factor and tumour suppressor. Levels of expression of brx
CC can be detected using the primers, probes and antibodies (contained in
CC the kit) to determine a predisposition to breast and ovarian cancer and
CC other proliferative disorders of immune tissues. Vectors containing the
CC brx gene can be used for prevention and treatment of cancers and
CC proliferative diseases of mammalian reproductive and immune tissues.
SQ Sequence 30 AA:

alignment_scores:
Quality: 62.00 Length: 33
Ratio: 3.263 Gaps: 2
Percent Similarity: 57.576 Percent Identity: 54.545

alignment_block:

US-09-240-675-1_COPY_27_229 x W93962 ..

Align seg 1/1 to: W93962 from: 1 to: 30

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3 CATGTCCTCTCTCGGCGGACACACCTAGTCTGCTCCGCGGCGCC 52
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3 AspGlyArgProSerTrp.....ProSerAlaArgArgArgCysSe 16
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53 CATGGGTGTGTCCGCGAGCGAGTGAATAAATCTAAATCTGCTCA 101
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16 rArgGly.....SerArgThrTrpLysArgSerGlyArgSerSer 29
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seq_name: A_Geneseq_36:W52296

seq_documentation_block:

ID W52296 standard; Protein; 325 AA.

AC W52296: (first entry)
DT 23-JUN-1998
DE CRFB4 protein.
KW CRFB4; Interleukin-10; IL-10; IL-10 receptor; allograft rejection;
KW vaccine; photosensitivity; inflammation; autoimmune disease;
KW septic shock; immune response; organ rejection; gene therapy.
OS Homo sapiens.
PN WO9802342-A1.
PD 22-JAN-1998.
PF 17-JUL-1997; U12455.
PR 17-JUL-1996; US-683743.
PA (UYNE-) UNIV NEW JERSEY.
PI Kotenko SV, Pestka S;
DR MPI: 98-110590/10.
PT New recombinant DNA - comprises sequences encoding Interleukin-10
PT and CRFB4 linked to operator, useful, e.g. preventing allograft
PT rejection
PS Claim 2: Page -: 79pp; English.
CC This sequence is the human CRFB4 sequence, DNA encoding it is used in the

CC recombinant DNA (I) of the invention. (I) comprises a sequence (S1)
CC encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2)
CC encoding CRFB4, both operably linked to expression control sequences.
CC Cells containing (I) may be used to identify agonists/antagonist of
CC IL-10. Agonists are potentially useful, e.g. for preventing allograft
CC rejection, as vaccine adjuvants, for treatment of photosensitivity,
CC inflammation, autoimmune disease and septic shock, while antagonists are
CC potentially useful for increasing immune responses against tumours,
CC viruses, bacteria and parasites (especially intracellular pathogens) and
CC for preventing organ rejection. A vector containing (I) is used to
CC restore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses
CC a dysfunctional IL10R and is able to bind IL-10 but not to transduce a
CC signal. Antisense CRFB4 sequences (especially ribozymes), can inhibit
CC IL-10 activity in cells. Antibodies specific for CRFB4 are used to
CC measure and localise CRFB4, for diagnosis of defective IL-10 activity.
CC Fragments of (I) are used as primers or probes to assay CRFB4-specific
CC RNA. Agonists/antagonists may be administered parenterally, orally or
CC rectally especially by intravenous injection or directly into a tumour or
CC allograft.
SQ Sequence 325 AA:

alignment_scores:
Quality: 61.50 Length: 54
Ratio: 1.922 Gaps: 1
Percent Similarity: 59.259 Percent Identity: 29.630

alignment_block:

US-09-240-675-1_COPY_27_229 x W52296 ..

Align seg 1/1 to: W52296 from: 1 to: 325

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3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuG1 19
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97 .....CTCAAAAGTAGAGTGCACATCATGATGACAACT 133
|||||
19 YmetValProProGluAsnValArgmetAsnSerValAsnPhelysA 36
|||||
134 TTATCTGAGGTGGAACAGAGCGATGAGTCTCGGGAATGATCTTT 183
|||||
36 snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
|||||
184 TCATTCGATTAAT 195
|||
53 ThrAlaGlnTyr 56
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seq_name: A_Geneseq_36:W07702

seq_documentation_block:

ID W07702 standard; Protein; 543 AA.

AC W07702:
DT 06-APR-1997 (first entry)
DE Mouse ETS2 repressor factor (ERF).
DE ETS2 repressor factor; ERF; transcriptional repressor;
KW tumour suppressor; tumour; cancer; oncoprotein; therapy.
OS Mus sp.
FH Key Location/Qualifiers
FT domain 21..98
FT /label= DNA_binding_domain
FT /note= "ets-like DNA binding domain"
FT domain 466..525
FT /label= Active_repressor_domain
PN WO9639517-A1.
PD 12-DEC-1996.
PF 04-JUN-1996; U010177.
PR 05-JUN-1995; US-469412.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Athanasiou MA, Beal GJ, Blair DG, Fisher RJ, Mavrothalassitis GJ;
DR MPI: 97-043139/04.
DR N-PSDB; T47200.

PT New DNA encoding ERS2 repressor factor - useful for reducing
PT tumorigenicity, esp. oncogene associated tumour cells
PS Disclosure, Page 70-72, 101p: English.
CC Murine ERS2 repressor factor (ERF) (W07702) is a member of the ERS2
CC family and acts as a transcriptional repressor in mammalian cells.
CC Its amino acid sequence was deduced from the murine ERF gene
CC (147198). Human ERF (see also W07700) has also been identified.
CC ERF has tumour suppressor activity. Chimeric molecules comprising
CC the ERF repressor domain in combination with a heterologous
CC transcription factor having a binding domain can be used to reduce
CC tumorigenicity associated with inappropriate expression of
CC transcription factors.
Sequence 543 AA;
50

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alignment_scores:
  Quality: 61.00      Length: 24
  Ratio: 3.389      Gaps: 0
Percent Similarity: 75.000      Percent Identity: 45.833
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alignment_block:
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US-09-240-675-1_COPY_27_229/rev x W07702 . .

Align seg 1/1 to: W07702 from: 1 to: 543

82 TTCACCTGGGGCTGGCGGCAACACACATGGGCCCGCCAGCAGACACT 33
 ||| ::::||||:| ||||:||||| ||||:|||||
 367 PhelysPhelysPseudInProProProlenGlyArgArgGlnArgAlaAl 383
 32 AGGCTCGTCGCGCCCGCAGAGGA 11
 ||||:|||||
 383 aglyGlnlySalProGly 390

34 InlysvaIGluValAspIleIleAspAspAsnPhelIleuArgTrpAsn 50
151 AGACGAGTGTCTGCGGAGATGATGATTTTCATTGATTCACAA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
201 A 201
67 s 67
seq_name: /cgn2_6/prodata/1/1aa/5B-COMB.pep:US-08-307-588-2
seq_documentation_block:
; Sequence 2, Application US/08307588
; Patent No. 5919453
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MACUIRE, Deborah
; APPLICANT: PLAVEC, Ivan
; APPLICANT: TOVEY, Michael G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; TITLE OF INVENTION: RECEPTOR WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,588
; FILING DATE: 05-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00770
; FILING DATE: 30-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92400902.0
; FILING DATE: 31-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 436 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-307-588-2
alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-307-588-2 ..
Align seg 1/1 to: US-08-307-588-2 from: 1 to: 436
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1 MetheValValLeuLeuGlyAlaThrThrLeuValValAlaValGI 17
51 CCCATGGGTGTTGCCGAGCCGAGGTGGAATAATCTAAATCTCTC 100
17 yPrtIrrAlIeuserAlaAlaAlaGlyGlyAsnLeuYsserProG 34
101 AAAAGTAGAGTCGACATCATAGATGACAATTATCTGAGGTGGAAC 150
34 InlysvaIGluValAspIleIleAspAspAsnPhelIleuArgTrpAsn 50
151 AGACGAGTGTCTGCGGAGATGATGATTTTCATTGATTCACAA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
201 A 201
67 s 67
seq_name: /cgn2_6/prodata/1/1aa/5A-COMB.pep:US-08-328-256-12
seq_documentation_block:
; Sequence 12, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: ABRAMOVICH, Carolina
; APPLICANT: RATOVIJSKI, Edward
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,256
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107378
; FILING DATE: 24-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: REVEL-13
; REFERENCE/DOCKET NUMBER: 25,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-328-256-12
alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-328-256-12 ..
1 ATGATGTCCTCTCTGCGGCGGAGACCTAGTGTCTGCGCGG 50
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Align seg 1/1 to: US-08-328-256-12 from: 1 to: 496

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1 ATGATGTCCTCTCTGCGCGCAGACCTAGTCTGTCGCGCGTGG 50
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1 MetcervallaleuLeuGlYAlaThrThrleuValleuValAlaValGl 17
17 yProTPrValleuSerAlaAlaAlaGlYGlYAsnleuYSerProG 34
101 AAAAGTAGAGTGCACATCATAGTACAACTTATCTGAGTGGAC 150
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34 InLysValIGluValAspIleIleAspAsnPhelIleuAgtTPrasn 50
151 AGGAGCGATGAGTCTGTCGGAATGTGACTTTTCATTCGATTATCAAAA 200
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51 ArgSerAspGluSerValIGlyAsnValThrPheSerPheAspTyrGlnly 67
201 A 201
67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-10

seq_documentation_block:

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; Sequence 10, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: ABRAMOVICH, Carolina
; APPLICANT: RAVOVITSKI, Edward
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,256
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107378
; FILING DATE: 24-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: REVEL-13
; REFERENCE/DOCKET NUMBER: 25,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-328-256-10
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alignment_scores: Quality: 340.00

Length: 67

Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x US-08-328-256-10 ..

Align seg 1/1 to: US-08-328-256-10 from: 1 to: 557

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17 yProTPrValleuSerAlaAlaAlaGlYGlYAsnleuYSerProG 34
101 AAAAGTAGAGTGCACATCATAGTACAACTTATCTGAGTGGAC 150
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34 InLysValIGluValAspIleIleAspAsnPhelIleuAgtTPrasn 50
151 AGGAGCGATGAGTCTGTCGGAATGTGACTTTTCATTCGATTATCAAAA 200
|||||
51 ArgSerAspGluSerValIGlyAsnValThrPheSerPheAspTyrGlnly 67
201 A 201
67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-471-454-2

seq_documentation_block:

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; Sequence 2, Application US/08471454
; Patent No. 5731169
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LOTFALFA, Georges
; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P. C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,454
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-454-2

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x US-08-471-454-2 ..

Align seg 1/1 to: US-08-471-454-2 from: 1 to: 557

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|||||
17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTAGAGTGCATCATGATGACAACTTATCTGAGGTGGAAC 150
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34 IntyValGluValAspIleIleAspAspAsnPhelleuAlaGTrpAsn 50
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51 ArgSerAspGluSerValGlyAsnValThrPheserPhesAspTyrGlnly 67
201 A 201
67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-466-974-2

seq_documentation_block:

Sequence 2, Application US/08466974
Patent No. 5861258
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,974
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/300,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-974-2

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x US-08-466-974-2 ..

Align seg 1/1 to: US-08-466-974-2 from: 1 to: 557

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51 CCCATGGGTCTTGTCCGCGACCCGAGGTGAAAAATCTAAATCTCTTC 100
|||||
17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTAGAGTGCATCATGATGACAACTTATCTGAGGTGGAAC 150
|||||
34 IntyValGluValAspIleIleAspAspAsnPhelleuAlaGTrpAsn 50
151 AGGACGATGAGTCTGTGGGAATGTGACTTTTTCATTTCGATTATCAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheserPhesAspTyrGlnly 67
201 A 201
67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-471-453-2

seq_documentation_block:

Sequence 2, Application US/08471453
Patent No. 586153
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,453
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-453-2

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_copy_27_229 x US-08-471-453-2 ..

Align seg 1/1 to: US-08-471-453-2 from: 1 to: 557

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1 ATGATGTCCTCTCTCGGCGGCGAGACCTAGTGTCTGCGCCGTGGG 50
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAla 17
51 CCCATGGGTGTTCGCCGACGCCGAGGTGGAATAAATCTAAATCTCTC 100
|||||
17 yProTrrValLeuSerAlaAlaAlaGlyGlyAsnLeuLysSerProG 34
101 AAAAGTAGAGTCGACATCATAGATGACACTTATCTGAGGTGGAAC 150
|||||
34 InLysValGluValAlaSpIleIleAspAspAsnPhelLeuArgTrrpsn 50
151 AGGAGCGATGAGTCTGTGCGGAGATGTGACTTTTCATTCGATTATCAAA 200
|||||
51 ArgSerAspGlnSerValGlyAsnValThrPheSerPheAspTrrGlnLys 67
201 A 201
|
67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-307-588-4

seq_documentation_block:

; Sequence 4, Application US/08307588
; Patent No. 5919453
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MAGUIRE, Deborah
; APPLICANT: PLAVEC, Ivan
; APPLICANT: TOVEY, Michael G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/GUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEFAX: (202)672-5300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-588-4

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_copy_27_229 x US-08-307-588-4 ..

Align seg 1/1 to: US-08-307-588-4 from: 1 to: 557

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1 ATGATGTCCTCTCTCGGCGGCGAGACCTAGTGTCTGCGCCGTGGG 50
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1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAla 17
51 CCCATGGGTGTTCGCCGACGCCGAGGTGGAATAAATCTAAATCTCTC 100
|||||
17 yProTrrValLeuSerAlaAlaAlaGlyGlyAsnLeuLysSerProG 34
101 AAAAGTAGAGTCGACATCATAGATGACACTTATCTGAGGTGGAAC 150
|||||
34 InLysValGluValAlaSpIleIleAspAspAsnPhelLeuArgTrrpsn 50
151 AGGAGCGATGAGTCTGTGCGGAGATGTGACTTTTCATTCGATTATCAAA 200
|||||
51 ArgSerAspGlnSerValGlyAsnValThrPheSerPheAspTrrGlnLys 67
201 A 201
|
67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/PC/TUS.COMB.pep:PCT-US94-14277-3

seq_documentation_block:

; Sequence 3, Application PC/TUS9414277
; GENERAL INFORMATION:
; APPLICANT: Agnet, Michel
; APPLICANT: Bohnl, Ruth

```

; APPLICANT: Hemmi, Silvio
; TITLE OF INVENTION: Receptor Subunit Polypeptides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14277
; FILING DATE: 07-DEC-1994
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/164596
; FILING DATE: 09-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 866PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELETYPE: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 202 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US94-14277-3

Alignment_scores:
  Quality: 112.00      Length: 39
  Ratio: 3.613         Gaps: 0
  Percent Similarity: 79.487   Percent Identity: 48.718

Alignment_block:
US-09-240-675-1_COPY_27_229 x PCT-US94-14277-3 ..
Align seg 1/1 to: PCT-US94-14277-3 from: 1 to: 202

      82 AAAAATCTAAATCTCTCAAAAGTAGAGTCGACATCATAGATGACAA 131
      ::::::::::::::::::::| | | | | | | | | | | | | | | | | |
      1 GUASnLeuLysProProGluAsnValArgMetAsnSerValAsnPhelysa 17
      132 CTTTATCTGAGGTGAGACAGAGCGATGCTGTGCGGAATGTGACTT 181
      1:::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
      17 nYrTrLLeuLysTrpSerSerHisGlyLysSerMetGlySerValThrhp 34
      182 TTTTCATTCGATATCA 198
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      34 heserLaGluTrpArg 39

seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-683-743-4

seq_documentation_block:
; Sequence 4, Application US/08683743
; Patent No. 5843697
; GENERAL INFORMATION:
; APPLICANT: Pestka, Sidney
; APPLICANT: Kotenko, Serguei
; TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
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; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,743
; FILING DATE: 17-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 601-1-050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; FRAGMENT TYPE:
; US-08-683-743-4

Alignment_scores:
  Quality: 61.50      Length: 54
  Ratio: 1.922         Gaps: 1
  Percent Similarity: 59.259   Percent Identity: 29.630

Alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-683-743-4 ..
Align seg 1/1 to: US-08-683-743-4 from: 1 to: 325

      55 TGGCGTGTGTCGCCAGCCGAGTCGNAAAAATCTAAATCT..... 96
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
      3 TrpSerLeuGlySerTrpLeuGlyLysLeuValSerAlaLeuGl 19
      97 .....CCTCAAAAGTAGAGTCGACATCATAGATGACAACT 133
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
      19 yMetValProProGluAsnValArgMetAsnSerValAsnPhelysa 36
      134 TTTATCTGAGGTGAGACAGAGCGATGCTGTGCGGAATGTGACTTT 183
      || | | | | | | | | | | | | | | | | | | | | | | | | | | |
      36 snLeuGlnTrpLysProAlaPheAlaLysGlyAsnLeuThrph 52
      184 TCATTCGATAT 195
      ::::::::::::::::::::| | | | | | | | | | | | | | | | | |
      53 ThrAlaGlnTyr 56

seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-469-412A-7

seq_documentation_block:
; Sequence 7, Application US/08469412A
; Patent No. 5856125
; GENERAL INFORMATION:
; APPLICANT: Mavrothalassitis, George J.
; APPLICANT: Blair, Donald G.
; APPLICANT: Fisher, Robert J.
; APPLICANT: Beal Jr., Gregory J.
; APPLICANT: Athanasiou, Meropi A.
; APPLICANT: Sgouras, Dionyssios N.
; TITLE OF INVENTION: The ERF Genetic Locus and Its Products
```


NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,412A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugene A
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 015280-229000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..543
OTHER INFORMATION: /note= "murine ERF amino acid sequence
OTHER INFORMATION: (first 8 amino acids from first exon not
included)"
US-08-469-412A-7

Alignment_scores:
Quality: 61.00 Length: 24
Ratio: 3.389 Gaps: 0
Percent Similarity: 75.000 Percent Identity: 45.833

Alignment_block:
US-09-240-675-1_COPY_27_229/rev x US-08-469-412A-7 ..
Align seg 1/1 to: US-08-469-412A-7 from: 1 to: 543

seq_documentation_block:
; Sequence 64, Application US/08317310A
; Patent No. 5858701
; GENERAL INFORMATION:
; APPLICANT: WHITE, Morris F.
; APPLICANT: SUN, Xiao Jian
; APPLICANT: PIERCE, Jacalyn H.
; TITLE OF INVENTION: THE IRS FAMILY OF GENES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston

82 TTCACCTGCGGCTGCGACACACCATGGCCGCGGAGAGGAGCACT 33
||| :|||:||||| :|||:|||||
367 PhelypheyleysleuglnProProleuGlyArgArglnrGlnrGlnr 383
|||:||||| :|||:|||||
32 AGGCTGCTGCGCGCCGAGAGGA 11
|||:||||| :|||:|||||
383 aglyglulysAlaProGlyGly 390

seq_name: /sgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-317-310A-64

STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,310A
FILING DATE: 03-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: JDP-022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 1321 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-317-310A-64

Alignment_scores:
Quality: 61.00 Length: 29
Ratio: 2.652 Gaps: 1
Percent Similarity: 79.310 Percent Identity: 51.724

Alignment_block:
US-09-240-675-1_COPY_27_229/rev x US-08-317-310A-64 ..
Align seg 1/1 to: US-08-317-310A-64 from: 1 to: 1321

98 GGAGATTTAGATTTTTCACCTGCGGCTGCGGAGACACCATGGGCC 49
|||:||||| :|||:||||| :|||:|||||
1029 GlyAspleuYrArgleuProProAlaSerAlaAlaThrSerGlnGlyr 1045
|||:||||| :|||:||||| :|||:|||||
48 CACGGCGAGACGACTAGGCTGCTGCGGCCAGGA 14
|||:||||| :|||:||||| :|||:|||||
1045 orhrAlaGlySerSerMet.SerSerGluProGly 1056

seq_name: /sgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-323-170B-2

seq_documentation_block:
; Sequence 2, Application US/08323170B
; Patent No. 5733772
; GENERAL INFORMATION:
; APPLICANT: Williamson, Kim C.
; APPLICANT: Kaslow, David C.
; TITLE OF INVENTION: Cloning and Expression of Plasmidium
; TITLE OF INVENTION: falcliparum Transmision-Blocking Target Antigen, Pfs230
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,170B
; FILING DATE: 13-OCT-1994
; CLASSIFICATION: 424

REFERENCE/DOCKET NUMBER: 1169-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 684-1111
TELEFAX: (703) 684-1124
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-505-218-4

alignment_scores:
Quality: 57.50 Length: 74
Ratio: 1.438 Gaps: 3
Percent Similarity: 54.054 Percent Identity: 29.730

alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-505-218-4 ..

Align seg 1/1 to: US-08-505-218-4 from: 1 to: 335

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   |||||
103 ValLeuTyrMetLeuLeuThrValValLeuValPheLeuPhePheVal 119
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60 GTGTCCGACGCGCAGGTGAGAAATCTTAATCTCTCAAAAGTAG 109
   |||||
119 ValThrLysLysGlyGlyLysSerValProAsnAlaTrpGlnSerL 136
   |||||
110 AGGTGACATCATAGATGACAACTTATCTGAGGTGGAACGAGCGCAT 159
   |||||
136 euValGluLeuIleTyrAsp...PheValLeu...AsnLeuValAsn 149
   |||||
160 GAGTCTGTCCGG..... 171
   |||||
150 GluGlnIleGlyGlyLeuSerGlyAsnValLysGlnLysPhePheProAr 166
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172 ....AATGACTTTTCATTC 189
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166 GluSerValThrPheThrPhe 173

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Date: Jun 1, 2000 12:36 AM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:
-MODEL=frame+asp.model -DEV=xlp
-O=/cgn2.1/USPTO.spool/US09240675/runat.30052000.164312.24623/app-query.fasta.1
-DB=PIR_63 -QFMT=fastan -SUFFIX=modif.rpr -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPECL=0.000 -LOOPEXT=0.000
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELDP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blomsam62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US09240675 -NCPD=6 -ICPD=3 -NO_XLPHY -WAIT
-THREADS=1

Search information block:

Query: US-09-240-675-1_COPY_27_229
Query length: 203
Database: PIR_63: +
Database sequences: 168808
Database length: 58629743
Search time (sec): 85.570000

score_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
PIR2:A32694	+	340.00	768.66	1.e-35	557 Interferon alpha/beta receptor
PIR2:S27387	+	209.00	464.26	9.e-19	560 Interferon alpha receptor type
PIR2:A45283	+	198.00	438.27	2.6e-17	590 Interferon alpha/beta receptor
PIR2:T09357	+	71.00	148.71	0.5876	304 Hypothetical protein F23K16.40
PIR2:CS807	+	71.00	140.36	0.7362	828 ttp3 protein - rat
PIR2:T26391	+	68.50	146.64	1.40	194 Hypothetical protein Y105C5B.0
PIR2:T00405	-	67.00	128.66	2.47	1106 Hypothetical 119.5K protein (u
PIR2:S42718	-	65.00	121.61	4.58	1475 nuclear pore complex protein n
PIR2:T08930	+	63.00	124.87	7.79	571 Hypothetical protein T15N24.90
PIR2:A45731	+	62.50	135.36	8.22	141 conc alpha protein - phase 14
PIR2:154418	+	62.50	127.53	8.76	361 MHC class I histocompatibility
PIR2:A26391	+	62.00	120.50	10.67	730 phospholipase C (EC 3.1.4.3) -
PIR2:501418	+	61.50	127.53	11.58	273 cytokine receptor family II, me
PIR2:A47003	+	61.50	126.08	11.72	325 cytokine receptor family class
PIR2:T25677	+	60.50	123.38	15.83	340 Hypothetical protein F08D12.9
PIR2:S42701	+	60.00	125.81	17.84	221 PR64 protein - chicken
PIR2:T02955	-	60.00	124.14	18.09	270 probable cytochrome P450 monoox
PIR2:T29518	+	60.00	121.31	18.51	379 Hypothetical protein T25F10.2 -
PIR2:146276	+	60.00	113.28	19.77	994 c-met tyrosine kinase receptor
PIR2:146480	+	60.00	105.86	21.01	2424 calcium channel Br-2 - rabbit
PIR2:T46479	+	60.00	105.86	21.01	2424 calcium channel Br-2 - rabbit
PIR2:T72653	+	59.50	130.61	19.72	108 Hypothetical protein APE058 -
PIR2:S11143	-	59.50	121.06	21.33	340 class I histocompatibility anti
PIR2:A44831	-	59.50	112.22	22.93	982 phosphoenolpyruvate carboxylase
PIR2:A42701	+	59.00	123.48	24.04	221 PR64/SC35 protein - human
PIR2:A42634	+	59.00	123.48	24.04	221 splicing factor SC35 - human
PIR2:S24169	-	59.00	121.16	24.50	292 mucin - rat
PIR2:T01773	+	59.00	117.65	25.21	445 self-incompatibility locus gly
PIR2:S42281	+	59.00	117.65	25.21	445 S-locus glycoprotein type II pr
PIR2:S26402	+	59.00	116.75	25.40	496 homeotic protein Hox A10 - huma
PIR2:T25131	+	59.00	116.25	25.51	527 Hypothetical protein T22H2.2 -
PIR2:A48584	-	59.00	101.39	28.81	3135 transmission blocking target a
PIR2:T35558	+	58.50	118.73	28.73	340 DNA-directed RNA polymerase alp
PIR2:A38885	+	58.00	124.96	31.39	140 flagellar protein required for
PIR2:A64336	+	58.00	122.96	31.91	178 Hypothetical protein M0288 - M
PIR2:S08459	-	58.00	117.65	33.33	37 Hypothetical protein 2 - spiro
PIR2:T14516	+	58.00	114.46	34.21	494 S-locus-specific glycoprotein S
PIR2:D75627	+	58.00	113.30	34.54	568 potassium-transporting ATPase -
PIR2:T38547	+	58.00	108.60	35.89	999 novel cellular proto-oncogene
PIR2:T05823	-	57.50	122.59	36.80	162 Hypothetical protein T5K18.160
PIR2:T24003	+	57.50	116.66	38.63	330 Hypothetical protein R07B5.3 -

PIR1:PWMT6	+	57.50	115.35	39.04	386	+	H+-transporting ATP synth
PIR2:JC2100	+	57.50	115.35	39.04	386	+	H+-transporting ATP synth
PIR2:A69763	-	57.50	114.00	39.48	454	+	homoserine dehydrogenase 1
PIR2:T34338	-	57.50	113.57	39.62	478	+	hypothetical protein M030-

seq_name: PIR2:A32694

seq_documentation_block:

Interferon alpha/beta receptor precursor - human
C.Species: Homo sapiens (map)
C.Date: 22-Jun-1998 #sequence_revision 22-Jun-1990 #text_change 22-Oct-1999
C.Accession: A32694; S17112
R.Uze, G.: Lutfalla, G.; Greaser, I.
Cell 60, 225-234, 1990
A.Title: Genetic transfer of a functional human Interferon alpha receptor into mou
A.Reference number: A32694; MUID:90124632
A.Accession: A32694
A.Molecule type: mRNA
A.Residues: 1-557 <U>Z>
A.Cross-references: GB:J03171; NID:9184645; PIDN:AAA52730.1; PID:9306914
R.Lutfalla, G.
Submitted to the EMBL Data Library, July 1991
A.Description: The structure of the human Interferon alpha/beta receptor gene.
A.Reference number: S17112
A.Accession: S17112
A.Molecule type: DNA
A.Residues: 1-16, 'A', '18-329, 'V', '343-557 <U>Z>
A.Cross-references: EMBL:X60459; NID:932671
C.Genetics:
A.Gene: GDB:IFNAR1, IFNAR, IFRC
A.Cross-references: GDB:120078; OMIM:107450
A.Map position: 21q22.1-21q22.1
A.Intons: 26/1, 67/2, 136/1, 177/3, 225/1, 263/2, 342/1, 381/3, 432/1, 480/3
E.1-2/Domain: transmembrane #status predicted <R>N2>
F.437-455/Domain: transmembrane #status predicted <R>N2>
F.50, 58, 81, 88, 110, 172, 254, 313, 314, 376, 416, 433, 507, 518, 537/Binding site: carbohydra

alignment_scores:

Quality:	Ratio:	Length:
340.00	5.075	67
Percent Similarity: 100.000	Percent Identity: 100.000	

alignment_block:

US-09-240-675-1_COPY_27_229 x A32694 ..

Align seg 1/1 to: A32694 from: 1 to: 557

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|||||
1 Methevalvalleuenglalathrthlevallevalalavalgl 17
51 CCCATGGCTGTGTCGCGACCCGAGGTGGAATAATCTAATTCCTC 100
|||||
17 yppotrpvalleuseralalalaaglyglylvasnleuylsesserprog 34
101 AAAAAGAGAGGTCGACATAGATGACAACCTTATTCGAGGTGGAAC 150
|||||
34 lnyvalgluvalaspilietleppaspasnheilleuvalaagtrpasm 50
151 AGGAGCATGAGTCTGCGGAAATGACTTTTCATTCGATTATCAAAA 200
|||||
51 ArgserpsluuseralglasnavaltthPheserPhespsyrgrlnly 67
201 A 201
67 s 67
seq_name: PIR2:S27387
```

seq_documentation_block:
Interferon alpha receptor type 1 precursor - bovine

C:Species: Bos primigenius taurus (cattle)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S27387; S37770
 R:Kouchel-Viehn, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
 FEBS Lett. 313, 255-259, 1992
 A:Title: Specific antiviral activities of the human alpha interferons are determined at
 A:Reference number: S27387; MUID:93076908
 A:Accession: S27387
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-560 <MOU>
 A:Cross-references: EMBL:X68443; NID:g431; PIDN:CAA48484.1; PID:g432
 A:Experimental source: MDBK cells
 R:Lim, J.K.; Langer, J.A.
 Biochim. Biophys. Acta 1173, 314-319, 1993
 A:Title: Cloning and characterization of a bovine alpha interferon receptor.
 A:Reference number: S33770; MUID:93305725
 A:Accession: S33770
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-421, 'V', 423-560 <LIM>
 A:Cross-references: EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PID:g163188
 A:Experimental source: Lung
 C:Keywords: antiviral; cytokine receptor; transmembrane protein
 F:1.24/Domain: signal sequence #status predicted <SIG>
 F:25-560/Product: Interferon alpha receptor type 1 #status predicted <MAT>

Alignment_scores:
 Quality: 209.00 Length: 65
 Ratio: 3.800 Gaps: 2
 Percent Similarity: 84.615 Percent Identity: 69.231

Alignment_block:
 US-09-240-675-1_copy_27_229 x S27387

Align seg 1/1 to: S27387 from: 1 to: 560

```

4 ATGGTCGCTCTCTGGCGCGAGACCCCTAGTCTGCGCGCGCCGCCCC 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MetLeuAlaLeuLeuLysValaThrLeuMetLeuValaAla...GlyIyr 16

54 ATGGGCTGTCTCCGACGCGAGGTGGAATAAATCTAAATCTCTCAAA 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
16 GtrPValleuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA 32

104 AAGTAGAGTCGACATCATAGATGACAACTTATCTGAGTGGAACAGC 153
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
32 snValGluLeuLeuIleLeuAspAsnPhaPheLeuLysTrpSer 48

154 AGCGATGAGTCTGCGGGAATGTGACTTTTTCATTGATATCAAA 198
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
49 SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGln 63

```

seq_name: p1r2:A45283

seq_documentation_block:

Interferon alpha/beta receptor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C:Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429
 R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudmon, D.; Mogensen, K.E.
 Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
 A:Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homosp
 A:Reference number: A45283; MUID:92262522
 A:Accession: A45283
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-590 <UZE>
 A:Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1; PID:g194112
 A:Note: sequence extracted from NCBI Backbone (NCBIN:102354, NCBI:P:102357)
 R:Lutfalla, G.; Uze, G.
 Gene 148, 343-346, 1994

A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-

A:Reference number: I48423; MUID:95047447
 A:Accession: I48423
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 118-125 <RES>
 A:Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1; PID:g755810
 A:Accession: I48424
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 127-224 <RE2>
 A:Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1; PID:g755811
 A:Accession: I48425
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 243-264 <RE3>
 A:Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1; PID:g510261
 A:Accession: I48426
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 265-375 <RE4>
 A:Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1; PID:g510262
 A:Accession: I48427
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 397-424 <RE5>
 A:Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.1; PID:g755812
 A:Accession: I48428
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 426-445 <RE6>
 A:Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1; PID:g755813
 A:Accession: I48429
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 473-590 <RE7>
 A:Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA65008.1; PID:g510265
 C:Genetics:
 A:Gene: IFNAR
 A:Insertions: 177/3; 331/1
 C:Keywords: cytokine receptor; transmembrane protein

Alignment_scores:
 Quality: 198.00 Length: 65
 Ratio: 3.536 Gaps: 0
 Percent Similarity: 86.154 Percent Identity: 55.385

Alignment_block:
 US-09-240-675-1_copy_27_229 x A45283

Align seg 1/1 to: A45283 from: 1 to: 590

```

4 ATGGTCGCTCTCTGGCGCGAGACCCCTAGTCTGCGCGCGCCGCCCC 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MetLeuAlaValAlaGlyAlaAlaLeuValLeuValAlaGlyAlaIyr 17

54 ATGGGCTGTCTCCGACGCGAGGTGGAATAAATCTAAATCTCTCAAA 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 GtrPValleuProSerAlaAlaGlyGlyGluAlaAsnLeuLysTrpProGluA 34

104 AAGTAGAGTCGACATCATAGATGACAACTTATCTGAGTGGAACAGC 153
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 snIleAspValTyrIleLeuAspAsnTrpIleLeuLysTrpSerSer 50

154 AGCGATGAGTCTGCGGGAATGTGACTTTTTCATTGATATCAAA 198
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 HisGlyGluSerMetGlySerValThrPheSerAlaGlyTyrArg 65

```

seq_name: p1r2:T09357

seq_documentation_block:

hypothetical protein F23K16.40 - Arabidopsis thaliana

C.Species: Arabidopsis thaliana (mouse-ear cress)
 C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
 C.Accession: T09357
 R.Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
 submitted to the Protein Sequence Database, June 1999
 A.Reference number: 216652
 A.Accession: T09357
 A.Molecule type: DNA
 A.Residues: 1-304 <BEV>
 A.Cross-References: EMBL:AL078620; GSPDB:GN0062; ATSP:F23K16.40
 A.Experimental source: cultivar Columbia; BAC clone F23K16
 C.Genetics:
 A.Gene: ATSP:F23K16.40
 A.Map position: 4
 A.Introns: 129/2; 243/2

alignment_scores:
 Quality: 71.00 Length: 70
 Ratio: 1.775 Gaps: 4
 Percent Similarity: 57.143 Percent Identity: 32.857

alignment_block:
 US-09-240-675-1_COPY_27_229 x T09357 ..

Align seg 1/1 to: T09357 from: 1 to: 304

```

3 GATGTCGTCCTCCTCGGCGCAGACCTAGTCGTGCGCGT..... 47
   :::::||||| :::::||||| :::::||||| :::::|||||
169 ASNGLYARGHSHSHSHSHSHSPTHPROSERARGHSHSPLYSHSAS 185
   :::::GGGCCCCATGGGTGTGTGCGCAGCCGACGTGAAAAATCTAAAA 93
   :::::||||| :::::||||| :::::||||| :::::|||||
185 nTHRALSerLeuGlyValAlaSerSerLeuLysMetLysLysLeuLys 201
   :::::TCCTCTAAAAAGTA.....GA 110
   :::::|||||
202 ThnArgTrpLysValArgGluProArgPheCysPheLysThrLeuSerGI 218
111 GGTGCAATAGATGACAACTTATCTCGAGGTGGAACAGCAGCATG 160
   ||||| :::::||||| :::::||||| :::::|||||
218 uValAspValLeuAspAspGlyTyr.....ArgTrpArgLysTyrGly 233
161 AGTCTGTC 168
   :::::|||||
233 InLysVal 235

seq_name: p1r2:JC5807

seq_documentation_block:
trp3 protein - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 07-May-1999
C.Accession: JC5807
R.Pretz, K.D.; Noeller, J.K.; Krause, E.; Goebel, A.; Schulz, I.
Biochem. Biophys. Res. Commun. 240, 167-172, 1997
A.Title: Expression and characterization of a trp1 homolog from rat.
A.Reference number: JC5807; MUID:98042538
A.Accession: JC5807
A.Status: nucleic acid sequence not shown
A.Molecule type: mRNA
A.Residues: 1-828 <PRE>
A.Experimental source: brain
C.Comment: This protein participates in store-operated Ca2+ entry into cells.
C.Superfamily: TRP3 protein

alignment_scores:
Quality: 71.00 Length: 73
Ratio: 1.614 Gaps: 3
Percent Similarity: 60.274 Percent Identity: 34.247

alignment_block:

```

US-09-240-675-1_COPY_27_229 x JC5807 ..

Align seg 1/1 to: JC5807 from: 1 to: 828

```

4 ATGTCGTCTCCTCGGCGCAGACCTAGTCGTGCGCGCGCC 53
   :::::||||| :::::||||| :::::||||| :::::|||||
338 LeuValValLeuValAlaLeuAlaLeuProPheLeuAlaLeuGly 354
54 ATGCGTGTTCCTCGGCGCAGACCTAGTGAATAATCTTCCT 99
   ||||| :::::||||| :::::||||| :::::|||||
354 rTTPleAlaProCysSerArgLeuGlyLysLeuAlaGserProPheM 371
   :::::||||| :::::||||| :::::|||||
100 ..CAAAAGTAGAGTCGACATCATGACAACTTATCTCGAGGTG 147
   :::::||||| :::::||||| :::::|||||
371 etLysPheValAlaAlaSerPheLeuLeuPheLeuValPhe 387
148 AACAGAGCGATGATGTCGCGG.....AATGACTTT 182
   ||| ||||| :::::|||||
388 AsnAlaSerAspArgPheGluGlyIleThrLeuProAsnIleThrVa 404
183 TTCATTCGATTATCAAAA 201
   :::::||||| |||
404 L...IleAspTyrProLys 409

seq_name: p1r2:T26391

seq_documentation_block:
hypothetical protein Y105C5B.o - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T26391
R.McMurray, A.
submitted to the EMBL Data Library, September 1999
A.Reference number: Z20208
A.Accession: T26391
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-194 <WII>
A.Cross-References: EMBL:AL110479; NID:e1542153; PIDN:CAB54363.1; CESP:Y105C5B.o
A.Experimental source: clone Y105C5B
C.Genetics:
A.Gene: CESP:Y105C5B.o
A.Introns: 13/1; 56/3; 155/2

alignment_scores:
Quality: 68.50 Length: 56
Ratio: 1.756 Gaps: 2
Percent Similarity: 69.643 Percent Identity: 32.143

alignment_block:
US-09-240-675-1_COPY_27_229 x T26391 ..


Align seg 1/1 to: T26391 from: 1 to: 194



```

10 GTCTCTCTGGGCGCAGACCTAGTCGTGTCGCGCGCCCATGGGT 59
 :::::||||| ||| :::::||||| :::::|||||
1 MetLeuLeuArgAlaIleLeuLeuIlePheIleSer...AlaProTrpVa 16
60 GTTGTCGCGCAGCGCAGGTGGAATAATCTTAATCTCTCAAAAGTAG 109
 ||||| :::::||||| :::::||||| :::::|||||
16 IleuSerValThrValLysArgAsnMetThrGluTyrGluGlnLysIleH 33
110 AGGTGCAATCATGATGACAACTTATCTCGAGGTGGAACAGCAGCAT 159
 :::::||||| :::::||||| :::::|||||
33 ISleAsnLeuLeu.....AsnGlyIleArgGlnLysAsnAlaIleAsp 47
160 GAGCTGTGCGGAAATGTG 177
 ||| :::::||||| :::::|||||
48 GluGlnValAlaAsnMet 53

seq_name: p1r2:J00405

```


```

seq_documentation_block:

hypothetical 119.5K protein (uvrA region) - Micrococcus luteus
N:Alternate names: ORF 1 protein
C:Species: Micrococcus luteus, Micrococcus lysodeikticus
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1993
C:Accession: J00405
R:Shiota, S.; Nakayama, H.
Mol. Gen. Genet. 217, 332-340, 1989
A:Title: Micrococcus luteus homolog of the Escherichia coli uvrA gene: identification of
A:Reference number: S04781; MUID:89364717
A:Accession: J00405
A:Molecule type: DNA
A:Residues: 1-1106 <SH1>
A:Cross-references: EMBL:X15867
A:Note: All the codons between two in-frame stop codons are translated; the translations
A:Note: the gene encoding this protein overlaps uvrA gene

alignment_scores:

Quality: 67.00 Length: 65
Ratio: 2.233 Gaps: 2
Percent Similarity: 46.154 Percent Identity: 32.308

alignment_block:

US-09-240-675-1_COPY_27_229/rev x J00405 ..

Align seg 1/1 to: J00405 from: 1 to: 1106

```
178 TCACATCCCGACAGATCATCGCTGTCACCTGACAGATAAGTTG 129
    |||  ::::|  |||  |||  |||  |||  |||  |||  |||  |||
36 SerProthiylglutThiProvalSerGlyPro..... 46
128 TCATGTATGATGTCACCTGTCATCTTTTGAGAGATTTAGTTTTC 79
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
47 .....CysProProLeuGlyCysTyrProAlaGlnGluLeuH 60
78 ACCTGCGGCTG.....CGGACAAACCCATGGGC 50
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
60 LSHLSHrGleuLeuAlaGlyArgGlyProAlaGlyArgProAlaGly 76
49 CCACGGCGACGACACTAGAGTGTGCGGCCGACGAGACGACCA 5
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
77 ProAlaGlyArgGlyAlaGlyArgGlyAlaGlyProHISArgArgPro 91
```

seq_name: p1r2:S42718

seq_documentation_block:

nuclear pore complex protein nup153 - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S42718; S37477
R:Memorow, I.; Bastos, R.; Horton, H.; Burke, B.
Biochim. Biophys. Acta 1211, 219-223, 1994
A:Title: Sequence analysis of a cDNA encoding a human nuclear pore complex protein, nup153
A:Reference number: S42718; MUID:94154002
A:Accession: S42718
A:Molecule type: mRNA
A:Residues: 1-1475 <WCM>
A:Cross-references: EMBL:Z25353; NID:9406224; PIDN:CAA80982.1; PID:9406225

alignment_scores:

Quality: 65.00 Length: 51
Ratio: 2.167 Gaps: 1
Percent Similarity: 58.824 Percent Identity: 39.216

alignment_block:

US-09-240-675-1_COPY_27_229/rev x S42718 ..

Align seg 1/1 to: S42718 from: 1 to: 1475

```
167 ACAGACTATCGCTCTGTCACCTGACAGATAAAGTTGATATGAT 118
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
```

1248 ThrSerInSerLeuLeuPheSerGlnAspSerLysLeuAlaThrThr 1264

117 GTGACCTCTACTTTTGGAGAGATTGATTTTCCACCTGCGGCTG 68

1264 rSerThiGlyThrAlaValThrProPheValPheGlyProGlyAlaSer 1281

67 CGGACACAC.....CATGGCCACGGGAGAGAGC 36

1281 eRNAaThrThrThrSerGlyPheGlyPheGlyAlaThrThrThrSer 1297

35 ACT 33

1298 Ser 1298

seq_name: p1r2:T08930

seq_documentation_block:

hypothetical protein T15N24.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
C:Accession: T08930
R:Bevan, M.; Zimmermann, W.; Gruenewald, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.;
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16518
A:Accession: T08930
A:Molecule type: DNA
A:Residues: 1-571 <BEV>
A:Cross-references: EMBL:AL078465; GSPDB:GN00062; ATSP:T15N24.90
A:Experimental source: cultivar Columbia; BAC clone T15N24
A:Gene: ATSP:T15N24.90
A:Map position: 4
A:Introns: 76/3; 90/3; 142/3; 311/1; 363/2; 415/2

alignment_scores:

Quality: 63.00 Length: 62
Ratio: 1.750 Gaps: 4
Percent Similarity: 58.065 Percent Identity: 33.871

alignment_block:

US-09-240-675-1_COPY_27_229 x T08930 ..

Align seg 1/1 to: T08930 from: 1 to: 571

```
15 CCTGGCGCGACGACCTAGTGTGCTGCGCGGCGCCATGGGT.... 59
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
353 ProAspAspAspAspAspProPheSerLysArgArgGlyMetGluGlyAla 369
60 .....GTGTCCGACGCGCAGTGGGAAAAAATCTAAATCT 96
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
369 tGluThrProLeuValLysProIleArgGluProArgValValValG 386
97 CCTGAAAAAGTAGAGTGCATCATATGATGACAACTTATCTGAGGTG 146
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
386 InThrLeuSer.GluValAspIleLeuAspAspGlyTyr.....ArgTr 400
147 GAACAGAGCGCATGAGTGTGTC.....GGGAT 174
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
400 pArgLysTyrGlyGlnLysValValAlaArgGlyAsn 411
```

seq_name: p1r2:A45731

seq_documentation_block:

comc-alpha protein - phage T4
N:Alternate names: gp comc alpha
C:Species: phage T4
A:Note: host Escherichia coli
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Oct-1999
C:Accession: A45731
R:Sanson, B.; Uzan, M.
J. Bacteriol. 174, 6539-6547, 1992
A:Title: Sequence and characterization of the bacteriophage T4 comcAlpha gene product

A:Reference number: A45731; MUID:93015705
 A:Accession: A45731
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-141 <SAN>
 A:Cross-references: GB:M89919; NID:9215829; PIDN:AAA32485.1; PID:9215832
 C:Genetics:
 A:Gene: comC alpha
 A:Map position: 5,848-6,274
 C:Superfamily: phage T4 comC-alpha protein
 C:Keywords: transcription regulation

alignment_scores:
 Quality: 62.50 Length: 50
 Ratio: 2.155 Gaps: 3
 Percent Similarity: 58.000 Percent Identity: 34.000

alignment_block:
 US-09-240-675-1_COPY_27_229 x A45731 ..

Align seg 1/1 to: A45731 from: 1 to: 141

```

16 CTGGGGCGCGACGACCTAGTCGTCGCGCGCCGATGCGTCTGC 65
||||| ||| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
49 LeuGlyArgProThrLysIleMetThrSerIleGly.....ValLeuLys 63
66 CGAGCCGCGAGTGTGAAAAAATCTAAATCTCCCAAAAAGTAGAGTCG 115
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
63 sarGcysAlaGlyGly.....A 69
116 ACATCATAGATGACAACTTATCTCGATGAGAAACAGAGCGATGACTCT 165
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
69 spleLeuAspGluAsnPheIle.....TrpLeuSerThrAsnGluAla 83

```

seq_name: p1r2:154418

seq_documentation_block:
 MHC class I histocompatibility antigen HLA-B7 alpha chain precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
 C:Accession: I54418
 R:SOOT, A.K.: Pan, J.; Biro, P.A.; Pereira, D.; Sriyastava, R.; Reddy, V.B.; Duceaman, B.
 Immunogenetics 22, 101-121, 1985
 A:Title: Structure and polymorphism of class I MHC antigen mRNA.
 A:Reference number: I54418; MUID:85287366
 A:Accession: I54418
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-361 <SOO>
 A:Cross-references: GB:M16102; NID:9187693; PIDN:AAA59622.1; PID:9307217
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

alignment_scores:
 Quality: 62.50 Length: 61
 Ratio: 1.645 Gaps: 2
 Percent Similarity: 62.295 Percent Identity: 24.590

alignment_block:
 US-09-240-675-1_COPY_27_229 x I54418 ..

Align seg 1/1 to: I54418 from: 1 to: 361

```

4 ATGGTCGCTCTCTGGCGGCGACGACCTAGTCGTCGCGCGCCGAGGCC 53
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1 MetLeuValMetAlaProArgThrValLeuLeuLeuLeuSer...GlyPr 16
54 ATGGGCTGTTCGCGACCGCAGGTGAAAAAATCTAAAA.....93
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
16 ofTrpLeuThrGluThrTrpAlaGlySerHisSerMetAlaGlyTrpPheTyrT 33
94 .....TCTCTCAAAAAGTAGAGGTGCAC 117

```

```

33 htrSerValSerArgPro*****GlyGluProArgPheIleSerValGly 49
118 ATCATGATGACACTTATCTCGAGCGTGAAC 150
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
50 TyrValAspAspThrGlnPheValArgPheAsp 60

```

seq_name: p1r2:A26391

seq_documentation_block:
 Phospholipase C (EC 3.1.4.3) - Pseudomonas aeruginosa
 N:Alternate names: lecithinase C; lipophospholipase I
 C:Species: Pseudomonas aeruginosa
 C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 08-Oct-1999
 C:Accession: A26391
 R:Pritchard, A.E.; Vasili, M.L.
 J. Bacteriol. 167, 291-298, 1986
 A:Title: Nucleotide sequence and expression of a phosphate-regulated gene encoding
 A:Reference number: A26391; MUID:86250607
 A:Accession: A26391
 A:Molecule type: DNA
 A:Residues: 1-730 <PRI>
 A:Cross-references: GB:M13047; NID:9151492; PIDN:AAA25966.1; PID:9151493
 C:Keywords: phosphoric diester hydrolase

alignment_scores:
 Quality: 62.00 Length: 69
 Ratio: 1.824 Gaps: 4
 Percent Similarity: 49.275 Percent Identity: 26.087

alignment_block:
 US-09-240-675-1_COPY_27_229 x A26391 ..

Align seg 1/1 to: A26391 from: 1 to: 730

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37 CTCTGCGCGGTGGCGCCATGGGTGTTCGCGACCGCAGTGTGAAAAA 86
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
404 LeuIleAlaIleSerProTrp.....SerLysGlyGly.....414
87 TCTAAATCTCTCCCAAAAAGTAGAGTCGACATCATAGATGACACTTAA 136
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
415 .....LysValSerAlaGluValPheAspHisThrSerV 426
137 TCCTGAGG.....144
426 alleuArgPheLeuGluArgArgPheGlyLeuValGluGluAsnIleSer 442
145 ....TGGACAGAGCGAGTGTCTGTGCGGAATGTGACTTTTTCATTGCA 191
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
443 ProTrpArgArgAla.....ValCysGlyAspLeuThrSerLeuPheAs 457
192 TTATCAA 198
|:|:|:|:|:|
457 pPheGln 459

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seq_name: p1r2:G01418

seq_documentation_block:
 cytokine receptor family II, member 4 - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
 C:Accession: G01418
 R:Lutfailla, G.
 submitted to the EMBL Data Library, April 1994
 A:Reference number: G06935
 A:Accession: G01418
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-273 <LUT>
 A:Cross-references: EMBL:U08988; NID:9571295; PID:9571296
 C:Genetics:
 A:Gene: GDB:CRFB4; CRF2-4

OM of: US-09-240-675-1_COPY_27_229 to: SwissProt_38.* out_format : pfs
Date: Jun 1, 2000 12:37 AM

About: Results were produced by the GenCore software, version 4.5.
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:
-MODEL-frame+asp_model -DEV-xip
-O-Copy2_1/USPRO.spool/US09240675/runat_30052000_16433_24686/app_query.fasta.1
-DB-SwissProt_38 -QFMT-fastan -SUFFIX-modif.rsp -GAPOP=12.000
-GAPEXT=4.000 -MIMATCH=0.100 -LOOCL=0.000 -LOOEXT=0.000
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX-Dlosum62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pcr
-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NOM-ext -MILEN=0
-MALEN=1000000 -USER=US09240675 -NCPU=6 -ICPU=3 -NO_XLPHY -WAIT
-THREADS=1

Search information block:

Query: US-09-240-675-1_COPY_27_229

Query length: 203

Database: SwissProt_38.*

Database sequences: 83857

Database length: 30454973

Search time (sec): 45.030000

Score list:

Sequence	Strd Orig	Zscore	Escore	Len	Documentation
SwissProt_38:INRL_HUMAN	340.00	743.63	1.4e-14	557	P17181 homo sapiens (human)
SwissProt_38:INRL_BOVIN	209.00	449.62	3.4e-18	560	P04790 bos taurus (bovine)
SwissProt_38:INRL_SHEEP	204.00	438.40	1.4e-17	560	P28588 ovis aries (sheep)
SwissProt_38:INRL_MOUSE	168.00	424.50	8.0e-17	590	P33896 mus musculus (mouse)
SwissProt_38:IN53_HUMAN	155.00	118.37	3.61	1475	P49790 homo sapiens (human)
SwissProt_38:COMA_BPT4	62.50	132.43	6.21	141	P01438 bacteriophage t4, comc
SwissProt_38:PHGC_PSEAE	62.00	117.53	8.12	730	P06200 pseudomonas aeruginosa
SwissProt_38:CRP4_HUMAN	61.50	123.19	8.82	325	P00834 homo sapiens (human)
SwissProt_38:ERF_MOUSE	61.00	117.64	10.60	551	P70459 mus musculus (mouse)
SwissProt_38:IRK2_MOUSE	61.00	110.31	11.31	1321	P81122 mus musculus (mouse)
SwissProt_38:SPF2_CHICK	60.00	123.05	13.20	221	P30352 gallus gallus (chicken)
SwissProt_38:SCCA_RABIT	60.00	102.98	15.79	2424	P27884 oryctolagus cuniculus
SwissProt_38:CAPR_HUMAN	59.50	109.43	17.04	982	P28594 anabena sp. (strain)
SwissProt_38:SPF2_HUMAN	59.00	120.81	17.60	221	P01130 homo sapiens (human)
SwissProt_38:HXMA_HUMAN	59.00	114.03	18.70	496	P31260 homo sapiens (human)
SwissProt_38:S230_PLAFO	58.50	98.58	21.46	315	P008372 plasmodium falciparum
SwissProt_38:RPOA_STRCO	58.50	116.10	20.98	339	P23404 streptomyces coelicolor
SwissProt_38:FLTL_BACSU	58.00	122.39	22.68	140	P23452 bacillus subtilis, fl
SwissProt_38:Y288_METJA	58.00	120.38	23.09	178	P05736 methanococcus jannasch
SwissProt_38:VE2_SPVIR	58.00	115.03	24.22	337	P15893 spiroplasma virus spv1
SwissProt_38:ATP6_WHEAT	57.50	112.77	28.25	386	P20359 tritium aestivum (wheat)
SwissProt_38:TAP6_DROME	57.50	112.51	28.32	398	P01687 drosophila melanogaster
SwissProt_38:TP6_BACSU	57.50	111.41	28.60	454	P94417 bacillus subtilis, ptc
SwissProt_38:PEHX_ERMCH	57.50	109.05	29.21	602	P15922 ewingia chrysanthemi
SwissProt_38:DNJ1_ZYMMO	57.00	107.42	29.64	731	P28719 zymomonas mobilis, dr
SwissProt_38:DEAD_KLEPN	57.00	107.17	33.96	659	P33906 klebsiella pneumoniae
SwissProt_38:RE_BACSU	56.50	115.35	36.09	217	P03457 bacillus subtilis, rld
SwissProt_38:RRL_RVYZ	56.50	108.41	38.40	497	P50766 human papillomavirus v1
SwissProt_38:VE2_HPV20	56.50	96.14	42.84	219	P27316 rift valley fever v1
SwissProt_38:SPF3_HUMAN	56.00	116.58	40.81	164	P23152 homo sapiens (human)
SwissProt_38:GTR1_RAT	56.00	107.37	44.31	492	P11677 rattus norvegicus (rat)
SwissProt_38:SEXY_MYCGA	56.00	107.27	44.35	498	P03235 mycoplasma gallisepti
SwissProt_38:IRK_CAVPO	55.00	99.33	47.64	1300	P14671 canis familiaris (guinea)
SwissProt_38:ET2_HUMAN	55.00	114.77	47.42	178	P20800 homo sapiens (human)
SwissProt_38:AMFN_LALIC	55.50	101.72	53.27	845	P37897 lactococcus lactis (s)
SwissProt_38:IF2_ECOLI	55.50	101.81	53.48	890	P02995 escherichia coli, tran
SwissProt_38:GUND_CLOSR	55.50	100.42	53.89	986	P23659 clostridium stercoar
SwissProt_38:RHSD_ECOLI	55.00	97.32	55.40	1466	P16919 escherichia coli, rh
SwissProt_38:MOVP_TMVT0	55.00	110.34	56.39	264	P03588 tobacco mosaic virus
SwissProt_38:MOVP_TOMVA	55.00	110.34	56.39	264	P28799 tobacco mosaic virus
SwissProt_38:WNTA_ALOVO	54.50	115.83	61.40	120	P28099 atopias vulpinus (th

seq_name: SwissProt_38:INRL_HUMAN

seq_documentation_block:	ID	INRL_HUMAN	STANDARD:	PRT:	557 AA.
AC	P17181				
DT	01-AUG-1990	(Rel. 15, Created)			
DT	01-AUG-1990	(Rel. 15, Last sequence update)			
DT	15-FEB-2000	(Rel. 39, Last annotation update)			
DE	INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).				
GN	IFNAR1 OR IFNAR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 90124632.				
RA	Uze G., Lutfalla G., Gresser I.;				
RT	"Genetic transfer of a functional human interferon alpha receptor				
RT	into mouse cells: cloning and expression of its cDNA."				
RL	Cell 60:225-234(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 92129376.				
RA	Lutfalla G., Gardiner K., Proudhon D., Vleth E., Uze G.;				
RT	"The structure of the human interferon alpha/beta receptor gene."				
RL	J. Biol. Chem. 267:2802-2809(1992).				
RN	[3]				
RP	PHOSPHORYLATION BY TYR2.				
RX	MEDLINE: 95059042.				
RA	Colamonicl O., Yan H., Domanski P., Handa R., Smalley D.,				
RA	Waltersman J., Witte K., Krishnan K., Krolewski J.;				
RT	"Direct binding to and tyrosine phosphorylation of the alpha subunit				
RT	of the type I interferon receptor by p135tyk2 tyrosine kinase."				
RL	Mol. Cell. Biol. 14:8133-8142(1994).				
CC	- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE				
CC	I IFN- TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS				
CC	INCLUDING JAKS, TYR2, STAT PROTEINS AND IFN- R ALPHA- AND BETA-				
CC	SUBUNTS THEMSELVES.				
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND				
CC	EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.				
CC	- PFM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYR2 TYROSINE KINASE.				
CC	- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL: J03171; AA5230.1; -				
DR	EMBL: X60459; CA44292.1; -				
DR	PIR: A32694; A32694.				
DR	PIR: S17112; S17112.				
DR	MIM: 107450; -				
KW	Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;				
KW	Phosphorylation.				
FT	SIGNAL	1	27	POTENTIAL.	
FT	CHAIN	28	557	INTERFERON-ALPHA/BETA RECEPTOR ALPHA	
FT	DOMAIN	28	436	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	437	457	POTENTIAL.	
FT	DOMAIN	458	557	CYTOPLASMIC (POTENTIAL).	
FT	DISULFD	79	87	BY SIMILARITY.	
FT	DISULFD	199	220	BY SIMILARITY.	

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FT MOD RES 466 466 PHOSPHORYLATION (BY TYR2) (PROBABLE).
FT MOD RES 481 481 PHOSPHORYLATION (BY TYR2) (PROBABLE).
FT CARBOHYD 50 50 POTENTIAL.
FT CARBOHYD 58 58 POTENTIAL.
FT CARBOHYD 81 81 POTENTIAL.
FT CARBOHYD 88 88 POTENTIAL.
FT CARBOHYD 110 110 POTENTIAL.
FT CARBOHYD 172 172 POTENTIAL.
FT CARBOHYD 254 254 POTENTIAL.
FT CARBOHYD 313 313 POTENTIAL.
FT CARBOHYD 314 314 POTENTIAL.
FT CARBOHYD 376 376 POTENTIAL.
FT CARBOHYD 416 416 POTENTIAL.
FT CARBOHYD 433 433 POTENTIAL.
FT VARIANT 168 168 POTENTIAL.
FT CONFLICT 17 17 /FTID-VAR_002717.
SQ SEQUENCE 557 AA; 63525 MW; 0F674C8A1ADB73 CRC64;

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alignment_scores:
  Quality: 340.00 Length: 67
  Ratio: 5.075 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000

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alignment_block:

US-09-240-675-1_COPY_27_229 x INRL_HUMAN ..

Align seg 1/1 to: INRL_HUMAN from: 1 to: 557

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1 ATGATGTCCTCTCTCTGCGCGACGACCTAGTCGTCGCGGCGG 50
1 MethetvalvalleuLeuGlYAlathrLeuvalleuValalaValaGI 17
51 CCCATGGGTGTGCCGCGCGAGGTGGAATAATCTAAATCTCCCTC 100
17 yprotprvalleuseralalaalaglyGlyshnleuLysserProG 34
101 AAAAGTAGAGTCGACATCATAGTGAACCTTATCTGAGGCGAAC 150
34 InLysvalGluvalaspIleleaspaspaspheileLeuArgTyrpsh 50
151 AGGAGCGATGAGTCGTGCGGGAATGCTTTTCATTCGATTACAAA 200
51 ArgseraspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
201 A 201
67 s 67

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seq_name: SwissProt_38:INRL_BOVIN

seq_documentation_block: ID INRL_BOVIN STANDARD; PRT; 560 AA.

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AC 004790;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
GN IFNARI OR IFNAR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN 11;
RP SEQUENCE FROM N.A.
RC TISSUE-LUNG;
RX MEDLINE: 93076908.
RA Mouchel-Vieilh E., Lutfalla G., Mogensen K.E., Uze G.;
RT "Specific antiviral activities of the human alpha Interferons are
RL determined at the level of receptor (IFNAR) structure.";
RL FDBS Lett. 313:255-259(1992).
RN [2]

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RP SEQUENCE FROM N.A.
RX MEDLINE: 93305725.
RA Lim J.-K., Langer J.A.;
RT "Cloning and characterization of a bovine alpha Interferon receptor.";
RL Biochim. Biophys. Acta 1173:314-319(1993).
CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYR2, STAT PROTEINS AND IFN-ALPHA AND BETA-
CC SUBUNITS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC This swiss-prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X68443; CAA48484.1; -.
CC EMBL: L06320; AAA02571.1; -.
CC PIR: S33770; S33770.
CC PIR: S27387; S27387.
CC PIR: PF00041; fn3; 1.
CC Receptor; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 24 BY SIMILARITY.
CC CHAIN 25 560 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
CC CHAIN.
CC DOMAIN 25 437 EXTRACELLULAR (POTENTIAL).
CC DOMAIN 438 458 POTENTIAL.
CC DOMAIN 459 560 CYTOPLASMIC (POTENTIAL).
CC DISULFID 76 84 BY SIMILARITY.
CC DISULFID 199 220 BY SIMILARITY.
CC CARBOHYD 47 47 POTENTIAL.
CC CARBOHYD 55 55 POTENTIAL.
CC CARBOHYD 85 85 POTENTIAL.
CC CARBOHYD 109 109 POTENTIAL.
CC CARBOHYD 172 172 POTENTIAL.
CC CARBOHYD 254 254 POTENTIAL.
CC CARBOHYD 313 313 POTENTIAL.
CC CARBOHYD 377 377 POTENTIAL.
CC CARBOHYD 434 434 POTENTIAL.
CC CONFLICT 422 422 F->V (IN REF. 2).
SQ SEQUENCE 560 AA; 63818 MW; 66D76B72861E1D11 CRC64;

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alignment_scores:
  Quality: 209.00 Length: 65
  Ratio: 3.800 Gaps: 2
  Percent Similarity: 84.615 Percent Identity: 69.231

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alignment_block:

US-09-240-675-1_COPY_27_229 x INRL_BOVIN ..

Align seg 1/1 to: INRL_BOVIN from: 1 to: 560

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4 ATGTCGTCCTCTCTGCGCGACGACCTAGTCGTCGCGGCGGCC 53
||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 MetleuAlaLeuLeuGlYAlathrThrLeuMetleuValala...GlyAr 16
54 ATGGGTGTTCGCGCGAGCGCGAGTGAATAATCTAAATCTCCCAAA 103
||||:||||:||||:||||:||||:||||:||||:||||:||||:
16 gtrpvalleuProAlaIleSerGlyAlaIleAsnLeuLys...ProGluu 32
104 AAGTAGAGTCGACATCATAGTGAACCTTATCTGAGGCGAAGG 153
||||:||||:||||:||||:||||:||||:||||:||||:||||:
32 snValGluIleHisIleIleaspaspaspheheleuLysTyrpanser 48
154 AGCGATGAGTCGTGCGGGAATGACTTTTCATTCGATTACAA 198
||||:||||:||||:||||:||||:||||:||||:||||:||||:
49 SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGln 63

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seq_name: SwissProt_38:INR1_SHEEP
seq_documentation_block:
ID INR1_SHEEP STANDARD: PRT: 560 AA.
AC 028569: 095205:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
GN (INTERFERON ALPHA/BETA RECEPTOR-1).
OS IFNARI OR IFNAR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM;
RX MEDLINE: 97135690.
RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
RT *Structure of an ovine interferon receptor and its expression in
RT endometrium.*
RL J. Mol. Endocrinol. 17:207-215(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM;
RX MEDLINE: 98006426.
RA Han C.-S., Mathalagan N., Klemann S.W., Roberts R.M.;
RT *Molecular cloning of ovine and bovine type I interferon receptor
RT subunits from uteri, and endometrial expression of messenger
RT ribonucleic acid for ovine receptors during the estrous cycle and
RT pregnancy.*
RL Endocrinology 138:4757-4767(1997).
CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I FENS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
CC CONCEPTUS AT DAY 15 OF PREGNANCY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X95939: CAA65183.1: -
DR EMBL: U65978: AAB84231.1: -
DR PRAM: PF00041: fn3: 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 560
FT DOMAIN 25 437 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 438 458 POTENTIAL.
FT DOMAIN 459 560 CYTOPLASMIC (POTENTIAL).
FT DISULFID 76 84 BY SIMILARITY.
FT DISULFID 199 220 BY SIMILARITY.
FT CARBOHYD 47 47 POTENTIAL.
FT CARBOHYD 55 55 POTENTIAL.
FT CARBOHYD 85 85 POTENTIAL.
FT CARBOHYD 108 108 POTENTIAL.
FT CARBOHYD 109 109 POTENTIAL.
FT CARBOHYD 172 172 POTENTIAL.
FT CARBOHYD 222 222 POTENTIAL.
FT CARBOHYD 285 285 POTENTIAL.
FT CARBOHYD 313 313 POTENTIAL.

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FT CARBOHYD 359 359 POTENTIAL.
FT CARBOHYD 377 377 POTENTIAL.
FT CARBOHYD 434 434 POTENTIAL.
FT CONFLICT 352 352 S -> G (IN REF. 2).
FT CONFLICT 522 522 A -> D (IN REF. 2).
SQ SEQUENCE 560 AA: 63918 MW: 67198A1905D4805C CXC64:

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alignment_scores:
Quality: 204.00 Length: 65
Ratio: 3.778 Gaps: 2
Percent Similarity: 83.077 Percent Identity: 69.231

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alignment_block:

US-09-240-675-1_COPY_27_229 x INR1_SHEEP ..

Align seg 1/1 to: INR1_SHEEP from: 1 to: 560

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4 ATGGTCGCTCCTCGGGCGGACGACCTAGTCTGTCGCGCGCCG 53
|||||: |||||||: |||||||: |||||||: |||||||: ||
1 MetLeuSerLeuLeuGlyAlaThrThrLeuMetLeuValAla... Glyar 16
54 ATGGCTGTCTCGCGACGCGCAGGTGGAATAATCTAAATCTCCCA 103
|||||: |||||||: |||||||: |||||||: |||||||: ||
16 gtrpValLeuProAlaAlaSerGlyAlaAlaSerLeuLysSer... Glua 32
104 AAGTAGAGCTGACATCATGATGACAACTTTATCTGAGTGGAACAG 153
|||||: |||||||: |||||||: |||||||: |||||||: ||
32 snValGluIleHisIleIleAspAspAspAspAspAspAspAsp 48
154 AGCGATGATGCTGTGGGAAATGTGACTTTTTCATTCGATTATCAA 198
|||||: |||||||: |||||||: |||||||: |||||||: ||
49 SerSerGluSerValArgAsnValThrPheSerAlaAspPyroGln 63
seq_name: SwissProt_38:INR1_MOUSE
seq_documentation_block:
ID INR1_MOUSE STANDARD: PRT: 590 AA.
AC P33896:
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
GN IFNARI OR IFNAR OR IFAR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92262522.
RA Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogenssen K.E.;
RT *Behavior of a cloned murine interferon alpha/beta receptor expressed
RT in homospicific or heterospicific background.*
RT Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).
CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I FENS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M89641: AAA37890.1: -
DR PIR: A45283; A45283.
DR MGD: MGI:107658; IFNAR.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M89919; AAA32485.1; -
DR PIR: A45731; A45731.
KW Transcription regulation.
SQ SEQUENCE 141 AA; 16682 MW; 96C9EFA8C673C479 CRC64;

alignment_scores:
    Quality: 62.50      Length: 50
    Ratio: 2.155      Gaps: 3
    Percent Similarity: 58.000      Percent Identity: 34.000

alignment_block:
US-09-240-675-1_COPY_27_229 x COMA_BPT4 ..
Align seg 1/1 to: COMA_BPT4 from: 1 to: 141

16 CTGGGCGCGAGACCTGCTGCTGCGCGCGCCGATGGCTGCTGTC 65
   |||||      ||      ||      ||      ||      ||      ||      ||
49 Leu1y1gpr0th1y1s1le1m1et1h1s1er1l1e1c1y1.....Val1e1u1y1 63
66 CGCAGCGCGAGCGTGAATAATCTAAATCTCCCAAAAGTAGAGTCG 115
   :      |||||      ||      ||      ||      ||      ||      ||
63 s1a1r1g1c1y1a1g1c1y1.....A 69

116 ACATCATAGATGACACTTATCTCTGAGTGAACAGAGGAGTACT 165
   |||||      ||      ||      ||      ||      ||      ||      ||
69 sple1e1u1a1s1p1g1u1a1s1p1h1e1l1e1.....Tri1p1e1u1s1e1r1h1a1s1g1u1a1 83

seq_name: SwissProt_38:PHLC_PSEAE

seq_documentation_block:
ID PHLC_PSEAE STANDARD; PRT; 730 AA.
AC P06200;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE HEMOLYTIC PHOSPHOLIPASE C PRECURSOR (EC 3.1.4.3) (HEAT LABILE-
GN HEMOLYSIN) (PHOSPHATIDYLCHOLINE CHOLINEPHOSPHODIOLASE).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
OC Pseudomonas.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 86250607.
RA Pritchard A.E., Vasil M.L.;
RT "Nucleotide sequence and expression of a phosphate-regulated gene
RT encoding a secreted hemolysin of Pseudomonas aeruginosa.";
RL J. Bacteriol. 167:291-298(1986).
RN [2]
RP REVISIONS.
RA Pritchard A.E.;
RL Submitted (AUG-1986) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: HYDROLYZES SPHINGOMYELIN IN ADDITION TO
CC PHOSPHATIDYLCHOLINE.
CC -1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O -> 1,2-
CC DIACYLGLYCEROL + CHOLINE PHOSPHATE.
CC -1- SIMILARITY: 40% IDENTITY TO NON-HEMOLYTIC PHOSPHOLIPASE C.
CC -----
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CC -----
DR EMBL: M13047; AAA25966.1; -
DR PIR: A26391; A26391.
KW Hemolysis; Toxin; Hydrolyase; Signal.
FT SIGNAL 1
FT CHAIN 39
SQ SEQUENCE 730 AA; 82655 MW; F1D3695824445FBF CRC64;

alignment_scores:
    Quality: 62.00      Length: 69
    Ratio: 1.824      Gaps: 4
    Percent Similarity: 49.275      Percent Identity: 26.087

alignment_block:
US-09-240-675-1_COPY_27_229 x PHLC_PSEAE ..
Align seg 1/1 to: PHLC_PSEAE from: 1 to: 730

37 CTGTCGCGCGTGGCGCCATGGGTGTTGTCGCGAGCGGAGTGAATAA 86
   |||||      ||      ||      ||      ||      ||      ||      ||
404 Leu1l1a1l1e1s1e1r1p1r1p1.....Ser1y1g1l1y1g1..... 414
87 TCTAAATCTCTCAAAAGTAGAGTCGACATCATGATGACACTTAA 136
   |||||      ||      ||      ||      ||      ||      ||      ||
415 .....Lys1v1a1s1e1r1a1g1u1v1a1l1p1h1e1a1s1h1s1e1r1v 426
137 TCCTGAGG..... 144
426 al1e1u1a1r1p1h1e1u1a1r1g1a1r1p1h1e1g1l1y1e1u1a1l1u1e1n1l1e1s1e1r 442
145 ...TGGACAGGAGCGATGATGCTGCGGAATGACTTTTCATTGCA 191
   |||||      ||      ||      ||      ||      ||      ||      ||
443 p1r1t1r1p1a1r1g1a1r1a1.....Val1c1y1s1g1l1y1a1s1p1h1e1r1h1s1e1r1u1p1h1e1a1s 457

192 TTAACA 198
   |||||
457 p1p1h1e1n1 459

seq_name: SwissProt_38:CRF4_HUMAN

seq_documentation_block:
ID CRF4_HUMAN STANDARD; PRT; 325 AA.
AC Q08334;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.
GN CRFB4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93300510.
RA Lutfalla G., Gardiner K., Uze G.;
RT "A new member of the cytokine receptor gene family maps on chromosome
RT 21 at less than 35 kb from IFNAR.";
RL Genomics 16:366-373(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96054036.
RA Lutfalla G., McInnis M.G., Antonarakis S.E., Uze G.;
RT "Structure of the human CRFB4 gene: comparison with its IFNAR
RT neighbor.";
RL J. Mol. Evol. 41:338-344(1995).
CC -1- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
```

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DR EMBL: Z17227; CAA78933.1; -
 DR EMBL: U08988; AAA86872.1; -
 DR PIR: A47003; A47003.
 DR HSSP: P13726; IDAN.
 DR MIM: 123889; -
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 325 CYTOKINE RECEPTOR CLASS-II CRF2-4.
 FT DOMAIN 20 220 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 221 249 POTENTIAL.
 FT DOMAIN 250 325 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 66 74 BY SIMILARITY.
 FT DISULFID 188 209 BY SIMILARITY.
 FT CARBOHYD 49 49 POTENTIAL.
 FT CARBOHYD 68 68 POTENTIAL.
 FT CARBOHYD 102 102 POTENTIAL.
 FT CARBOHYD 161 161 POTENTIAL.
 FT CONFLICT 124 124 A -> D (IN REF. 2).
 FT CONFLICT 269 273 FLAGHP -> VGRME (IN REF. 2).
 FT CONFLICT 274 325 MISSING (IN REF. 2).
 SQ SEQUENCE 325 AA; 37011 MW; 66706C79F8514B23 CRC64;

alignment_scores:
 Quality: 61.50 Length: 54
 Ratio: 1.922 Gaps: 1
 Percent Similarity: 59.259 Percent Identity: 29.630

alignment_block:
 US-09-240-675-1_COPY_27_229 x CRF4_HUMAN ..
 Align seg 1/1 to: CRF4_HUMAN from: 1 to: 325

```

55 TGGGTGTGTCGCGAGCCGAGTGGAAAAATCTAATAATC..... 96
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   3 TTPSerLeuGlySerTrieuGlyGlyCysLeuValSerAlaLeuG1 19
   97 ..... CCTCAAAAGTAGAGTGGACATCATAGTGCACACT 133
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   19 YMeTAlProProGluAsnValArgMetAsnSerValAsnPhelysa 36
   134 TTATCCTGAGGTGAACAGAGCAGTGTCTGTGCGGAATGTGACTTT 183
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   36 snlleLeuGlnTrieuSerProAlaPheAlaIalysGlyAsnLeuThrPhe 52
   184 TCATTGCATTAT 195
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   53 ThrAlaGlnTyr 56

```

seq_name: SwisProt_38:ERF_MOUSE
 seq_documentation_block:
 ID ERF_MOUSE STANDARD; PRT; 551 AA.
 AC P70459;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ERF-DOMAIN TRANSCRIPTION FACTOR ERF.
 GN ERF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129/SVJ;

RX MEDLINE: 97282708.
 RA Liu D., Pavlopoulos E., Modi W., Moschonas N., Mayrothalassitis G.J.:
 RT "ERF: genomic organization, chromosomal localization and promoter
 RT analysis of the human and mouse genes.";
 RL Oncogene 14:1445-1451(1997).
 CC -1- FUNCTION: POTENT TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE H1
 CC ELEMENT OF THE ETS2 PROMOTER. MAY REGULATE OTHER GENES INVOLVED
 CC IN CELLULAR PROLIFERATION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- PTM: PHOSPHORYLATED BY MULTIPLE KINASES INCLUDING PROBABLY ERK2.
 CC PHOSPHORYLATION REGULATES THE ACTIVITY OF ERF (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
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DR EMBL: U58533; AAC09474.1; -
 DR EMBL: U58534; AAC09474.1; JOINED.
 DR HSSP: 001543; 1FLI.
 DR MGD: MGI:109637; ERF.
 DR PRINTS: PR00454; ETSDOMAIN.
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
 DR PFAM: PF00178; Ets; 1.
 KW Transcription regulation; Repressor; DNA-binding; Nuclear protein;
 KW Phosphorylation.
 FT DNA_BIND 27 107 ETS-DOMAIN.
 FT DOMAIN 166 171 POLY-SER.
 FT DOMAIN 280 293 POLY-GLY.
 FT DOMAIN 362 373 POLY-SER.
 FT DOMAIN 420 425 POLY-PRO.
 FT MOD_RES 529 529 PHOSPHORYLATION (BY ERK2) (BY
 FT SIMILARITY).
 SQ SEQUENCE 551 AA; 59050 MW; 5AC1B72FB2743FE5 CRC64;

alignment_scores:
 Quality: 61.00 Length: 24
 Ratio: 3.389 Gaps: 0
 Percent Similarity: 75.000 Percent Identity: 45.833

alignment_block:
 US-09-240-675-1_COPY_27_229/rev x ERF_MOUSE ..
 Align seg 1/1 to: ERF_MOUSE from: 1 to: 551

```

82 TTCACCTGCGGCTGCGACACACCCATGGCCGACGGGAGCAGCACT 33
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   375 PhelysPheLysLeuGlnProProLeuGlyArgArgGlnArgAlaAl 391
   32 AGGCTGTCGCGCCGAGGAGA 11
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   391 AGlyGluLysAlaProGlyGly 398

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seq_name: SwisProt_38:IRS2_MOUSE
 seq_documentation_block:
 ID IRS2_MOUSE STANDARD; PRT; 1321 AA.
 AC P81122;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS).
 GN IRS2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE VOLTAGE-DEPENDENT P/Q-TYPE CALCIUM CHANNEL ALPHA-1A SUBUNIT (CALCIUM
 CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 4) (BRAIN CALCIUM CHANNEL
 DE 1) (B1).
 GN CACNA1A OR CACNA1A4 OR CACNA4 OR CACNA3.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN:
 RX MEDLINE; 91187110.
 RA Mori Y., Friedrich T., Kim M.-S., Mikami A., Nakai J., Ruth P.,
 RA Imoto K., Tanabe T., Numa S.,
 RT "Primary structure and functional expression from complementary DNA
 RT of a brain calcium channel.";
 RL Nature 350:398-402(1991).
 RN [2]
 RP BETA-SUBUNIT BINDING DOMAIN, AND MUTAGENESIS.
 RX MEDLINE; 94150724.
 RA Pragnell M., de Waard M., Mori Y., Tanabe T., Sutch T.P.,
 RA Campbell K.P.,
 RT "Calcium channel beta-subunit binds to a conserved motif in the I-II
 RT cytoplasmic linker of the alpha 1-subunit.";
 RL Nature 368:67-70(1994).
 CC -I- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIANE THE
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1A
 CC GIVES RISE TO P AND/OR Q-TYPE CALCIUM CURRENTS. P/Q-TYPE CALCIUM
 CC CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND
 CC ARE BLOCKED BY THE FUNNEL TOXIN (FTX) AND BY THE OMEGA-AGAOTOXIN-
 CC IYA (OMEGA-AGA-IYA). THEY ARE HOWEVER INSENSITIVE TO
 CC DIHYDROPYRIDINES (DHP), AND OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-
 CC GVIA).
 CC -I- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
 CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
 CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
 CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
 CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
 CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -I- ALTERNATIVE PRODUCTS: IN THE BRAIN, A SHORT ISOFORM BI-1/IA-1 AND
 CC A LONG ISOFORM BI-2/IA-2 (SHOWN HERE), ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -I- TISSUE SPECIFICITY: BRAIN-SPECIFIC. PURKINJE CELLS CONTAIN
 CC PREDOMINANTLY P-TYPE VSCC, THE Q-TYPE BEING A PROMINENT CALCIUM
 CC CURRENT IN CEREBELLAR GRANULE CELLS.
 CC -I- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -I- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL: X57477; CAA40715.1; -;
 DR EMBL: X57689; CAA40872.1; -;
 DR EMBL: X57476; CAA40714.1; -;
 DR EMBL: X57688; CAA40871.1; -;

DR PF00520; Ion_trans; 4.
 DR PRINTS: PRO0167; CACCHANNEL.
 DR PRINTS: PRO0170; NACCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation; Alternative splicing.
 FT REPEAT 85
 FT REPEAT 473 717
 FT REPEAT 1240 1523
 FT REPEAT 1560 1823
 FT DOMAIN 1 98
 FT TRANSMEM 99 117
 FT DOMAIN 118 135
 FT TRANSMEM 136 155
 FT DOMAIN 156 167
 FT TRANSMEM 168 185
 FT DOMAIN 186 190
 FT TRANSMEM 191 209
 FT DOMAIN 210 228
 FT TRANSMEM 229 248
 FT TRANSMEM 249 268
 FT TRANSMEM 326 335
 FT TRANSMEM 336 360
 FT DOMAIN 361 487
 FT TRANSMEM 488 506
 FT DOMAIN 507 521
 FT TRANSMEM 522 541
 FT DOMAIN 542 549
 FT TRANSMEM 550 568
 FT DOMAIN 569 578
 FT TRANSMEM 579 597
 FT DOMAIN 598 616
 FT TRANSMEM 617 636
 FT DOMAIN 637 689
 FT TRANSMEM 690 714
 FT DOMAIN 715 1253
 FT TRANSMEM 1254 1272
 FT DOMAIN 1273 1288
 FT TRANSMEM 1289 1308
 FT DOMAIN 1309 1320
 FT TRANSMEM 1321 1338
 FT DOMAIN 1340 1350
 FT TRANSMEM 1351 1369
 FT DOMAIN 1370 1388
 FT TRANSMEM 1389 1408
 FT DOMAIN 1409 1495
 FT TRANSMEM 1496 1520
 FT DOMAIN 1521 1575
 FT TRANSMEM 1576 1604
 FT DOMAIN 1605 1609
 FT TRANSMEM 1610 1629
 FT DOMAIN 1630 1637
 FT TRANSMEM 1638 1656
 FT TRANSMEM 1657 1665
 FT TRANSMEM 1666 1684
 FT DOMAIN 1685 1703
 FT TRANSMEM 1704 1723
 FT DOMAIN 1724 1795
 FT TRANSMEM 1796 1820
 FT DOMAIN 1821 2424
 FT DOMAIN 18 18
 FT TRANSMEM 727 732
 FT DOMAIN 1004 1010
 FT TRANSMEM 1012 1017
 FT DOMAIN 2219 2227
 FT TRANSMEM 2242 2246
 FT DOMAIN 2288 2297
 FT TRANSMEM 2298 2301
 FT DOMAIN 2377 2377
 FT TRANSMEM 2411 2416
 FT DOMAIN 383 400
 FT TRANSMEM 318 318
 FT SITE 668 668
 FT SITE 668 668
 I.
 II.
 III.
 IV.
 CYTOPLASMIC (POTENTIAL).
 S1 OF REPEAT I (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S2 OF REPEAT I (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S3 OF REPEAT I (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S4 OF REPEAT I (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S5 OF REPEAT I (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S6 OF REPEAT I (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S1 OF REPEAT II (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S2 OF REPEAT II (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S3 OF REPEAT II (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S4 OF REPEAT II (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S5 OF REPEAT II (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S6 OF REPEAT II (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S1 OF REPEAT III (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S2 OF REPEAT III (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S3 OF REPEAT III (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S4 OF REPEAT III (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S5 OF REPEAT III (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S6 OF REPEAT III (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S1 OF REPEAT IV (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S2 OF REPEAT IV (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S3 OF REPEAT IV (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S4 OF REPEAT IV (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S5 OF REPEAT IV (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S6 OF REPEAT IV (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 POLY-GLY.
 POLY-GLU.
 POLY-GLY.
 POLY-ARG.
 POLY-HIS.
 POLY-ARG.
 POLY-ARG.
 POLY-GLY.
 POLY-PRO.
 POLY-GLY.
 BINDING TO THE BETA SUBUNIT.
 CALCIUM ION SELECTIVITY AND PERMEABILITY
 (BY SIMILARITY).
 CALCIUM ION SELECTIVITY AND PERMEABILITY

FT SITE 1469 1469 (BY SIMILARITY).
FT SITE 1765 1765 (BY SIMILARITY).
FT MOD_RES 1831 1831 (BY SIMILARITY).
FT CA_BIND 1849 1860 (BY SIMILARITY).
FT CARBOHYD 283 283 (BY SIMILARITY).
FT CARBOHYD 1665 1665 (BY SIMILARITY).
FT VARSPLIC 772 1051 (BY SIMILARITY).
FT VARSPLIC 1857 1884 (BY SIMILARITY).
FT VARSPLIC 2230 2273 (BY SIMILARITY).
FT VARSPLIC 2274 2424 (BY SIMILARITY).
FT VARSPLIC 419 419 (BY SIMILARITY).
FT VARSPLIC 877 877 (BY SIMILARITY).
FT VARSPLIC 1104 1104 (BY SIMILARITY).
FT VARSPLIC 386 386 (BY SIMILARITY).
FT VARSPLIC 389 389 (BY SIMILARITY).
FT VARSPLIC 392 392 (BY SIMILARITY).
FT VARSPLIC 400 400 (BY SIMILARITY).
FT VARSPLIC 2424 AA: 273228 MM: F7CC4D0AB4B45604 CRC64;
FT VARSPLIC 2230 2273 (BY SIMILARITY).
FT VARSPLIC 2274 2424 (BY SIMILARITY).
FT VARSPLIC 419 419 (BY SIMILARITY).
FT VARSPLIC 877 877 (BY SIMILARITY).
FT VARSPLIC 1104 1104 (BY SIMILARITY).
FT VARSPLIC 386 386 (BY SIMILARITY).
FT VARSPLIC 389 389 (BY SIMILARITY).
FT VARSPLIC 392 392 (BY SIMILARITY).
FT VARSPLIC 400 400 (BY SIMILARITY).
FT VARSPLIC 2424 AA: 273228 MM: F7CC4D0AB4B45604 CRC64;

alignment_scores:
Quality: 60.00 Length: 55
Ratio: 1.765 Gaps: 3
Percent Similarity: 61.818 Percent Identity: 36.364

alignment_block:

US-09-240-675-1_COPY_27_229 x CCAA_RABIT

Align seg 1/1 to: CCAA_RABIT from: 1 to: 2424

6 GGTCTCTCTCTGCGGAGACCCCTAGTCT.....CGTGC 43
||||| ||||||| ||||||| ||||||| ||||||| |||||||
2229 GGTCTCTCTCTGCGGAGACCCCTAGTCT.....CGTGC 43
2245 GGTCTCTCTCTGCGGAGACCCCTAGTCT.....CGTGC 43
44 CCGTCTCTCTCTGCGGAGACCCCTAGTCT.....CGTGC 43
2245 GGTCTCTCTCTGCGGAGACCCCTAGTCT.....CGTGC 43
94 TCTCTCTCTCTGCGGAGACCCCTAGTCT.....CGTGC 43
2261 TCTCTCTCTCTGCGGAGACCCCTAGTCT.....CGTGC 43
144 GTGGAACAGGACGCA 158
2277 LeuArgLeuArgArg 2281

seq_name: SwissProt_38:CAP_PANASP

seq_documentation_block:

ID CAP_PANASP STANDARD: PRT: 982 AA.
AC P28594
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31) (PEPCASE) (PEPC).
GN PC.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
RN [1]
RP MEDLINE: 92268848.
RA Luebenburg J., Coleman J.R.;
RT "Identification, characterization and sequence analysis of the gene
RT encoding phosphoenolpyruvate carboxylase in Anabaena sp. PCC 7120";

RL J. Gen. Microbiol. 138:685-691(1992).
CC -1- FUNCTION: TO FORM OXALACETATE, A FOUR-CARBON DICARBOXYLIC ACID
CC SOURCE FOR THE TRICARBOXYLIC ACID CYCLE.
CC -1- CATALYTIC ACTIVITY: ORTHOPHOSPHATE + OXALACETATE -> H(2)O +
CC PHOSPHOENOLPYRUVATE + CO(2).
CC -1- PATHWAY: TRICARBOXYLIC ACID CYCLE.
CC -1- SIMILARITY: BELONGS TO THE PEPCASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M80541; AAA22023.1; -
CC
CC PIR: A44831; A44831.
CC PRINTS: P00150; PEPCARBYLASE.
CC PROSITE: P500393; PEPCASE_2; 1.
CC DR PROSITE: P500781; PEPCASE_1; 1.
CC PFAM: PF00311; PEPCASE; 3.
CC KM Lyase: Carbon dioxide fixation; Allosteric enzyme;
FT Tricarboxylic acid cycle.
FT ACT_SITE 155 155 BY SIMILARITY.
FT ACT_SITE 628 628 BY SIMILARITY.
FT ACT_SITE 982 AA: 112679 MM: 250621FFAFC8BDE CRC64;
SQ SEQUENCE 982 AA: 112679 MM: 250621FFAFC8BDE CRC64;

alignment_scores:
Quality: 59.50 Length: 40
Ratio: 2.288 Gaps: 2
Percent Similarity: 65.000 Percent Identity: 40.000

alignment_block:

US-09-240-675-1_COPY_27_229/rev x CAP_PANASP

Align seg 1/1 to: CAP_PANASP from: 1 to: 982

115 GAGCTCTCTCTCTGAG.....GAGATTTAGATTTTCCAGCTGCG 72
||||| ||||||| ||||||| ||||||| ||||||| |||||||
752 ArgGlyLeuIleTyrGluGlnProAspHeLeuSpherHeLeuS... 766
71 GGTCTCTCTCTCTGAG.....GAGATTTAGATTTTCCAGCTGCG 72
767 ...GlnValThrProIleGluGlnIleSerGlnLeuGlnIleSerSera 782
21 GCCCAGGAGGACGACATCA 2
782 rGProAlaArgArgProSer 788

seq_name: SwissProt_38:SFR2_HUMAN

seq_documentation_block:

ID SFR2_HUMAN STANDARD: PRT: 221 AA.
AC Q01130;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35)
GN SFRS2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP MEDLINE: 92237694.
RA Fu X.-D., Maniatis T.;
RT "Isolation of a complementary DNA that encodes the mammalian splicing
RT factor SC35";
RT Science 256:535-538(1992).
RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE-BONE MARROW;
 RX MEDLINE: 92212859.
 RA Veillard M., Sureau A., Soret J., Martinerie C., Perbal B.;
 RT "A potential splicing factor is encoded by the opposite strand of the
 RL trans-spliced c-myc exon.";
 RN Proc. Natl. Acad. Sci. U.S.A. 89:2511-2515(1992).
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94134745.
 RA Sureau A., Perbal B.;
 RT "Several mRNAs with variable 3' untranslated regions and different
 RL stability encode the human PR264/SC35 splicing factor.";
 RN Proc. Natl. Acad. Sci. U.S.A. 91:932-936(1994).
 RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE: 93101590.
 RA Sureau A., Soret J., Veillard M., Crochet J., Perbal B.;
 RT "The PR264/c-myc connection: expression of a splicing factor
 RL modulated by a nuclear protooncogene.";
 RN Proc. Natl. Acad. Sci. U.S.A. 89:11683-11687(1992).
 RP SEQUENCE OF 67-83.
 RX MEDLINE: 92249775.
 RA Zahler A.M., Lane W.S., Stolk J.A., Roth M.B.;
 RT "SR proteins: a conserved family of pre-mRNA splicing factors.";
 RN Genes Dev. 6:837-847(1992).
 RP PROTEIN INTERACTIONS IN SPliceOSOME ASSEMBLY.
 RX MEDLINE: 94084782.
 RA Wu J.Y., Maniatis T.;
 RT "Specific interactions between proteins implicated in splice site
 RL selection and regulated alternative splicing.";
 RN Cell 75:1061-1070(1993).
 RP BINDING TO U1-70K.
 RX MEDLINE: 94187841.
 RA Korte J.D., Jamison S.F., Will C.L., Luo P., Luhrmann R.;
 RT "Protein-protein interactions and 5'-splice-site recognition in
 RL mammalian mRNA precursors.";
 RN Nature 368:119-124(1994).
 RP RNA BINDING SPECIFICITY.
 RX MEDLINE: 95354672.
 RA Tacke R., Manley J.L.;
 RT "The human splicing factors ASF/SF2 and SC35 possess distinct,
 RL functionally significant RNA binding specificities.";
 RN EMBO J. 14:3540-3551(1995).
 RP SPECIFICITY FOR BETA-GLOBIN MRNA.
 RX MEDLINE: 93368668.
 RA Fu X.-D.;
 RT "Specific commitment of different pre-mRNAs to splicing by single SR
 RL proteins.";
 RN Nature 365:82-85(1993).
 RP FUNCTION: NECESSARY FOR THE SPLICING OF PRE-MRNA. IT IS REQUIRED
 CC FOR FORMATION OF THE EARLIEST ATP-DEPENDENT SPLICING COMPLEX AND
 CC INTERACTS WITH SPliceOSOMAL COMPONENTS BOUND TO BOTH THE 5' AND 3'
 CC SPLICING SITES DURING SPliceOSOME ASSEMBLY. IT ALSO IS REQUIRED FOR
 CC ATP-DEPENDENT INTERACTIONS OF BOTH U1 AND U2 SNRNPs WITH PRE-
 CC MRNA. INTERACTS WITH OTHER SPliceOSOMAL COMPONENTS, VIA THE RS
 CC DOMAINS, TO FORM A BRIDGE BETWEEN THE 5' AND 3' SPLICING SITE
 CC BINDING COMPONENTS, U1 SNRNP AND U2AF. IN VITRO, BINDS SF2/ASF,
 CC U1-70K AND THE 35 KD BUT NOT THE 65 KD SUBUNIT OF U2AF. BINDS TO
 CC PURINE-RICH RNA SEQUENCES, EITHER 5'-AGAGAGTA-3' (S-C OR G) OR
 CC 5'-GTTCGAGTA-3'. CAN BIND TO BETA-GLOBIN MRNA AND COMMIT IT TO THE
 CC SPLICING PATHWAY.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- ALTERNATIVE PRODUCTS: DIFFERENT FORMS OF THE PROTEIN MAY BE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- PTM: EXTENSIVELY PHOSPHORYLATED ON SERINE RESIDUES IN THE RS
 CC DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RNP).
 CC -1- SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
 CC -----
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 CC or send an email to license@isb-sdb.ch).
 CC -----
 DR EMBL: M90104; AAA60306.1; -
 DR EMBL: X62447; CAA44307.1; -
 DR EMBL: X75755; CAA53383.1; -
 DR EMBL: L03693; AAA60162.1; -
 DR PIR: S17328; S17328.
 DR PIR: A42634; A42634.
 DR HSP: P19339; ISXL.
 DR MIM: 600813; -
 DR PROSITE: PS00030; RNP_L; 1.
 DR PRAM: PF00076; rtm_1.
 DR Nuclear protein; RNA-binding; mRNA splicing; Alternative splicing;
 KW Phosphorylation.
 FT DOMAIN 16 21 RNA-BINDING (RNP2) (BY SIMILARITY).
 FT DOMAIN 55 62 RNA-BINDING (RNP1) (BY SIMILARITY).
 FT DOMAIN 111 116 GLY-RICH (HINGE REGION).
 FT DOMAIN 117 221 ARG/SER-RICH (RS DOMAIN).
 FT CONFLICT 38 38 R -> G (IN REF. 2 AND 3).
 SQ SEQUENCE 221 AA; 25575 MW; 9D1B76DB85701F5 CRC64;
 alignment_scores:
 Quality: 59.00 Length: 54
 Percent Similarity: 2.185 Gaps: 2
 Percent Identity: 50.000 Percent Identity: 35.185
 alignment_block:
 US-09-240-675-1_COPY_27_229 x SFR2_HUMAN ..
 Align seg 1/1 to: SFR2_HUMAN from: 1 to: 221
 6 GGTGCTGCTCTCT.....GGCGGCGAGCAGCCTAGTGTCTGTCG 43
 |||||
 93 GYArgProPoaSpSerHisSerArgArgGlyProProPoaArg 109
 44 C.....CGTGGCCCATGGGTGTC 63
 |
 109 GYArgGlyGlyGlyGlyArgArgSerArgSerProArgArgArg 126
 64 TCCGAGCGCGAGCGTGAATAATCTCTCAAAAGTAGAGCT 113
 |||||
 126 rGArgSerArgSerArgSerArgSerArgSerArgSer 142
 114 CGACATCATAGA 125
 |||||
 143 ArgTYrSerArg 146
 seq_name: SwissProt_38:HXAA_HUMAN
 seq_documentation_block:
 ID HXAA_HUMAN STANDARD; PRT; 496 AA.
 AC P31260; O15949;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE HOMOEOBOX PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL).
 OS HOXA10 OR HOX1H.
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91288229.

RA RUBINO D., DRIGERS P., ARBIT D., KEMP L., MILLER B., COSO O.,
 RA PAGLIAI K., GRAY K., GUTKIND S., SEGARS J.;
 RT "Characterization of Brx, a novel DBI family member that modulates
 RT estrogen receptor action."
 RL Oncogene 16:2513-2526(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RA RUBINO D.M., DRIGERS P.H., MILLER B., SEGARS J.H.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF126008; AAD21311.1;
 KW Receptor.
 SQ SEQUENCE 1429 AA; 161033 MW; 542B8C25 CRC32;

alignment_scores:
 Quality: 75.00 Length: 74
 Ratio: 1.923 Gaps: 5
 Percent Similarity: 52.703 Percent Identity: 41.892

alignment_block:
 US-09-240-675-1_COPY_27_229 x Q9Y5T6 ..

Align seg 1/1 to: Q9Y5T6 from: 1 to: 1429

```

3 GATGTCGCTCTGCGCGCAGACCCCTAGTCTGTCGTCGCGCGGCC 52
|||||
1230 AspGlyArgProSerTrp.....ProSerAlaArgArgCysSe 1243
53 CATGGGTGTGTCGCCAGCCGAGGTGGAATAATCTAATCTCTCAA 102
|||||
1243 rArggly.....SerArgThrTrpLysArgSerGlyArgSerSers 1257
103 AAAGTAGAGGTGCACATCATATGACAACCT..... 134
::|||
1257 eArgArgArgAlaHisSerGlnTrpAspLeuGluArgLeuArgAla 1273
135 .....TATCCTAGGTGAGACAGACGATGATGCTGCGGAGTGTGA 178
|||||
1274 GlnLysGlnLeuGluArgGluGlnGlnHis...ValArgArgGluAla 1289
179 CTTTTCATTCGATTATCAAAA 200
:|||||
1289 u.....ArgLeuSerGln 1293

```

seq_name: sp_invertebrate:076514

seq_documentation_block:
 ID 076514 PRELIMINARY; PRT; 365 AA.

AC 076514;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE CEF-1.
 GN CEF-1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 OC Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-N2;
 RA MORITA K., CHOW K.L., UENO N.;
 RT "Body Length and Male Tail Ray Pattern Formation of C. elegans are
 RT Regulated by a Member of TGF β Family."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF074395; AAC26791.1;
 DR HSP; P18075; IBM.
 DR PFAM; PF00019; TGF-beta; 1.
 DR PRINTS; PR00438; GFCYSNOT.
 SQ SEQUENCE 365 AA; 41781 MW; 54051BEE CRC32;

alignment_scores:

Quality: 66.00 Length: 54
 Ratio: 1.941 Gaps: 2
 Percent Similarity: 62.963 Percent Identity: 31.481

alignment_block:
 US-09-240-675-1_COPY_27_229 x 076514 ..

Align seg 1/1 to: 076514 from: 1 to: 365

```

27 GACCCTAGTGTCTGTCGCCGCGGCCCATGATGCTGTCGCCAGCCGAC 76
:::|||||
228 GluProSerSerValArgArg.....LysArgSerArgG1 239
77 GTGAAAAAATCTAAATCTCTCTCAAAAAGTAGAGTCGACATCATGAT 126
:::|||||
239 nThrGlyAsnSerGlnArgLysAsnArgLysGlyArgLysHis. 255
127 GACAACCTTATCCCTGAGTGAACAGACGATGATGCTGTCGCGAATGT 176
256 .....AsnThrGluAlaGluSerAsnLeuCysArgArgThr 267
177 GACTTTTCAT 188
|||||
268 AspPheTyVal 271

```

seq_name: sp_human:Q13507

seq_documentation_block:
 ID Q13507 PRELIMINARY; PRT; 848 AA.

AC Q13507; 000593;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE TRANSIENT RECEPTOR POTENTIAL RELATED CHANNEL 3 PROTEIN.
 GN TRPC3 OR HTRP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96234226.
 RA ZHU X., JIANG M., PEYTON M., BOULAY G., HURST R., STEFANI E.,
 RA BIRNBAUMER L.;
 RT "Trp, a novel mammalian gene family essential for agonist-activated
 RT capacitative Ca²⁺ entry."
 RL Cell 85:661-671(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97358541.
 RA XU X.Z.S., LI H.S., GUGGINO W.B., MONTPELL C.;
 RT "Coassembly of TRP and TRPL produces a distinct store-operated
 RT conductance."
 RL Cell 89:1155-1164(1997).
 DR EMBL; U47050; AAC51653.1;
 DR EMBL; Y13758; CAA74083.1;
 DR PFAM; PF00023; ank; 2.
 DR PRINTS; PR01097; TRNSRCEPTRP.
 SQ SEQUENCE 848 AA; 97354 MW; 78AC2E9D CRC32;

alignment_scores:
 Quality: 63.00 Length: 75
 Ratio: 1.537 Gaps: 3
 Percent Similarity: 54.667 Percent Identity: 33.333

alignment_block:
 US-09-240-675-1_COPY_27_229 x Q13507 ..

Align seg 1/1 to: Q13507 from: 1 to: 848

```

4 ATGTCGTCCTCTGCGCGCAGACCCCTAGTCTGTCGTCGCGGCC 53
:::|||||
351 LeuValValLeuValValAlaLeuGlyLeuProPheLeuAlaIleGly 367

```

```

54 ATGGGTGTTCCCGACCCGAGTGGAAAAATCTAAATCTCTCAAA 103
   |||||  |||||  |||||  |||||  |||||  |||||
367 rtrpillealprocyserrargluegylsileleuargserprohem 384
   |||||  |||||  |||||  |||||  |||||  |||||
104 AAGTAGAGCNC.....GACATCATAGATGCAACTTATCCCTG 141
   |||||  |||||  |||||  |||||  |||||  |||||
384 eltyshpvalalahlalalaserphellellepheleuglyleu 400
   |||||  |||||  |||||  |||||  |||||  |||||
142 AGGTGACACAGAGCAGATGATCTGTGCG.....AATG 176
   |||||  |||||  |||||  |||||  |||||  |||||
401 valpheasmlaserasparpneuglyllethrthrleuproasnll 417
   |||||  |||||  |||||  |||||  |||||  |||||
177 GACCTTTTCATTCGATTATCAAAA 201
   |||||  |||||  |||||  |||||  |||||  |||||
417 ethrvalthr...Asptryprolys 424

```

seq_name: sp_mammal:077699

```

seq_documentation_block:
ID 077699 PRELIMINARY: PRT; 117 AA.
AC 077699;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE TRP3 PROTEIN (FRAGMENT).
GN TRP3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
RN [1]
RP WISENBACH U., PHILIPP S., FLOCKERZI V.;
RA "Cloning and analysis of trp channels."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006781; CA07246.1; -.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13295 MW; B9F9B808 CRC32;

```

alignment_scores:

Quality:	62.00	Length:	75
Ratio:	1.512	Gaps:	3
Percent Similarity:	54.667	Percent Identity:	33.333

alignment_block:

US-09-240-675-1_COPY_27_229 x 077699 ..

Align seg 1/1 to: 077699 from: 1 to: 117

```

4 ATGTGCTGCTCCTGGCGGACGACCTAGTGTCTGCGCGGAGCC 53
   |||||  |||||  |||||  |||||  |||||  |||||
25 leuvalvalleuvalalalaleuuglyleupropheulalieglyt 41
   |||||  |||||  |||||  |||||  |||||  |||||
54 ATGGGTGTTCCCGACCCGAGTGGAAAAATCTAAATCTCTCAAA 103
   |||||  |||||  |||||  |||||  |||||  |||||
41 rtrpillealprocyserrargluegylsileleuargserprohem 58
   |||||  |||||  |||||  |||||  |||||  |||||
104 AAGTAGAGCNC.....GACATCATAGATGCAACTTATCCCTG 141
   |||||  |||||  |||||  |||||  |||||  |||||
58 eltyshpvalalahlalalaserphellellepheleuglyleu 74
   |||||  |||||  |||||  |||||  |||||  |||||
142 AGGTGACACAGAGCAGATGATCTGTGCG.....AATG 176
   |||||  |||||  |||||  |||||  |||||  |||||
75 valpheasmlaserasparpneuglyllethrthrleuproasnll 91
   |||||  |||||  |||||  |||||  |||||  |||||
177 GACCTTTTCATTCGATTATCAAAA 201
   |||||  |||||  |||||  |||||  |||||  |||||
91 ethrvalthr...ileasptyprolys 98

```

seq_name: sp_human:095927

```

seq_documentation_block:
ID 095927 PRELIMINARY: PRT; 290 AA.
AC 095927;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE D465N24.2.1 (PUTATIVE NOVEL PROTEIN) (ISOFORM 1).
GN D465N24.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA WILSON S.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031432; CAB37992.1; -.
SQ SEQUENCE 290 AA; 33613 MW; B59E0C18 CRC32;

```

alignment_scores:

Quality:	62.00	Length:	62
Ratio:	2.296 <td>Gaps:</td> <td>1 </td>	Gaps:	1
Percent Similarity:	43.548 <td>Percent Identity:</td> <td>29.032</td>	Percent Identity:	29.032

alignment_block:

US-09-240-675-1_COPY_27_229 x 095927 ..

Align seg 1/1 to: 095927 from: 1 to: 290

```

6 GGTGTCCTCTGCGGCGGACGACCTAGTGTCTGCGCGGACCAT 55
   |||||  |||||  |||||  |||||  |||||  |||||
11 glyserproglnglulysaspserserthrserargserglyse 27
   |||||  |||||  |||||  |||||  |||||  |||||
56 GGGTGTGTCGCGGACGCGC.....
   |||||  |||||  |||||  |||||  |||||  |||||
27 reerargleuserargserargserargserpheserargsera 44
   |||||  |||||  |||||  |||||  |||||  |||||
75 .....AGGTGCAAAAAATCT 89
   |||||  |||||  |||||  |||||  |||||  |||||
44 rgerhlseserargvalserargpheserargserargser 60
   |||||  |||||  |||||  |||||  |||||  |||||
90 AAAATCTCTCAAAAAGTAGAGTGCACATCTACA 125
   |||||  |||||  |||||  |||||  |||||  |||||
61 lyserserargserargserargserargserargser 72

```

seq_name: sp_rodent:088970

seq_documentation_block:

ID 088970 PRELIMINARY: PRT; 734 AA.

```

AC 088970;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE INSULIN RECEPTOR SUBSTRATE-2 (FRAGMENT).
GN IRS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA XU G., ULMER W.T., WOLF B.A.;
RA "Partial genomic DNA sequence of mouse beta-cell IRS-2."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090738; AAC61743.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 734 AA; 75251 MW; B3410CAF CRC32;

```

alignment_scores:

Quality:	61.00	Length:	29
Ratio:	2.652 <td>Gaps:</td> <td>1 </td>	Gaps:	1
Percent Similarity:	79.310 <td>Percent Identity:</td> <td>51.724</td>	Percent Identity:	51.724


```

228 GluProSerSerValArgArg.....LysArgSerAlaG1 239
77 GTGGAAAAATCTTAATCTCTCAAAAGTAGAGTGCATCATGAT 126
   :|||||: :|||||: :|||||: :|||||: :|||||:
239 nThGlyAsnSerGluArgLysAsnArgLysGlyArgLysHis. 255
127 GACAACCTTATCCAGAGTGACAGAGCATGATCTGTGGGAATG 176
   :|||||: :|||||: :|||||: :|||||: :|||||:
256 .....AsnThrGluAlaGluSerAsnLeuGlyArgArgThr 267
177 GACTTTTCAT 188
   :|||||: :|||||: :|||||: :|||||: :|||||:
268 AspHeterVal 271
seq_name: sp_rodent:Q60805
seq_documentation_block:
ID Q60805 PRELIMINARY: PRT: 994 AA.
AC Q60805;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE C-MER PROTOONCOGENE PRECURSOR (C-MER TYROSINE KINASE RECEPTOR).
GN MER.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE OF 1-315 FROM N.A.
RC STRAIN-B6; TISSUE-SPLEEN;
RC MEDLINE: 95303502.
RA GRAHAM D.K., BOWMAN G.W., DAMSON T.L., STANFORD W.L., EARP H.S.,
RA SNOODGRASS H.R.;
RT "Cloning and developmental expression analysis of the murine c-mer
RT tyrosine kinase."
RL Oncogene 10:2349-2359(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-B6; TISSUE-SPLEEN;
RC SNOODGRASS H.R.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U21301; AAA80222.1; -.
DR HSSP: P06213; 1TRK.
DR WGD: MGI:96965; Mer.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00047; 1g; 2.
DR PFAM: PF00069; pkinase; 1.
KW signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 994 C-MER TYROSINE KINASE RECEPTOR.
SQ SEQUENCE 994 AA; 110156 MW; 3C2F429D CRC32;
alignment_scores:
Quality: 60.00 Length: 39
Ratio: 2.222 Gaps: 1
Percent Similarity: 69.231 Percent Identity: 33.333
alignment_block:
US-09-240-675-1_COPY_27_229 x Q60805
Align seg 1/1 to: Q60805 from: 1 to: 994
43 GCCGTGGCCCATGGTGTCTCCACGCCGACGAGTGGAAAAATCTTAA 92
   :|||||: :|||||: :|||||: :|||||: :|||||:
364 AlaValSerProThrPheLeuAlaSerThrThrGluAlaProSerVal 380
93 ATCTCCTCAAAAAGTAGAGTGCATCATGATCTGTGGGAATG 141
   :|||||: :|||||: :|||||: :|||||: :|||||:
380 lAlaProLeuAsnIleThrValPheLeuAsnGluSerAsnAsnIleLeuA 397
142 .....AGGTGACACAG 153
   :|||||: :|||||: :|||||: :|||||: :|||||:

```

```

397 spIleArgTrpThrLys 402
seq_name: sp_human:Q9Y5L9
seq_documentation_block:
ID Q9Y5L9 PRELIMINARY: PRT: 2971 AA.
AC Q9Y5L9;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE TRANSCRIPTIONAL ACTIVATOR SRCAP.
GN SRCAP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 99278407.
RA JOHNSTON H., KNEER J., CHACKALAPARAMPIL I., YACIOUR P., CHIRIVIA J.;
RT "Identification of a novel SNF2/SWI2 protein family member, SRCAP,
RT which interacts with CREB-binding protein."
RL J. Biol. Chem. 274:16370-16376(1999).
DR EMBL: AF143946; AAD39760.1; -.
SQ SEQUENCE 2971 AA; 315639 MW; 1C7B94CB CRC32;
alignment_scores:
Quality: 60.00 Length: 25
Ratio: 3.333 Gaps: 0
Percent Similarity: 72.000 Percent Identity: 52.000
alignment_block:
US-09-240-675-1_COPY_27_229/rev x Q9Y5L9
Align seg 1/1 to: Q9Y5L9 from: 1 to: 2971
83 TTTCACACTGCGGCTCGGACCAACCCATGGCCCGGACGACGAC 34
   :|||||: :|||||: :|||||: :|||||: :|||||:
942 PheProProAlaAlaAlaThrThrThrThrThrThrThrAlaThrAlaThrAlaThr 958
33 TAGGTCGTGCGCGCCGACGAGACG 9
   :|||||: :|||||: :|||||: :|||||: :|||||:
958 TrThrAlaValProAlaProThr 966
seq_name: sp_archaea:Q9YEB6
seq_documentation_block:
ID Q9YEB6 PRELIMINARY: PRT: 108 AA.
AC Q9YEB6;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE 108AA LONG HYPOTHETICAL PROTEIN.
GN APE0658.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Aeropyrum.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K1;
RC MEDLINE: 99310339.
RA KAKARABAYASI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y.,
RA JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H.,
RA HOSOTYAMA A., FUKUI S., NAGAI Y., NISHIJIMA K., NAKAZAWA H.,
RA TAKAMIZU M., MASUDA S., FUNAHASHI T., TANAKA T., KUDOH Y.,
RA YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y.,
RA NOMURA N., SAKO Y., KIKUCHI H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1."
RL DNA Res. 6:83-101(1999).
DR EMBL: AP000060; BAA79630.1; -.
SQ SEQUENCE 108 AA; 11371 MW; BCB1E741 CRC32;

```

alignment_scores:
 Quality: 59.50 Length: 35
 Ratio: 2.705 Gaps: 1
 Percent Similarity: 62.857 Percent Identity: 42.857

alignment_block:
 US-09-240-675-1_COPY_27_229 x Q9YEB6 ..

Align seg 1/1 to: Q9YEB6 from: 1 to: 108

```

12 CCGCTGGGGCGGCGACACCTAGTCTGCTGCGCCGCGGCGCCATGGGTCT 61
   |||||:::||||:::||||:::|||||:::|||||:::|||||
13 ProProSerArgProSerPro.....GlnArgGlyProGlnGlyVa 26
62 TGTCCGCGCGCGGCGAGTGGAAAAATCTAAATCTCCTCAAAAAGTAGAG 111
   |::: |||::: ||| |||:::|||||
26 lphneGlyAlaCysArgGlyProGlnProLeuGlnSerArgArgSerArg 43
112 GTCGA 116
   |||||
43 lYArg 44
  
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 00:40:13 ; Search time 42.08 Seconds
(without alignments)
128,900 Million cell updates/sec

Title: US-09-240-675-2_COPY_1_229

Perfect score: 1196
Sequence: 1 MMVLLGATTLVAVGPVW.....WKIGYSPVHCIKTVENEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1196	100.0	436	R14487	Soluble Interferon
2	1196	100.0	436	R28495	Sequence of a soul
3	1196	100.0	436	R17173	IFN receptor extra
4	1196	100.0	557	R11958	Human alpha-interf
5	1196	100.0	557	R14488	Complete Interfero
6	1196	100.0	557	R28496	Sequence of a soul
7	1196	100.0	557	R42635	Human Interferon r
8	1196	100.0	557	R75356	Human IFN receptor
9	1191	99.6	434	R21805	Spliced-deleted in
10	1191	99.6	496	R21806	Transmembranal int
11	1191	99.6	557	R21804	CRFB4 protein. New
12	222.5	18.6	325	W52296	IFN-gamma receptor
13	203	17.0	332	R75782	Zcyto7 cytokine r
14	184.5	15.4	553	R79159	Human IFN-gamma ac
15	151.5	12.7	337	R71035	Human IFN-gamma rec
16	149.5	12.5	337	R75783	Human IFN-gamma ac
17	140.5	11.7	574	R97861	Human cytokine rec
18	131.5	11.0	211	R97864	Human cytokine rec
19	117	9.8	227	R14642	Gamma interferon r
20	117	9.8	231	R14641	Gamma interferon r
21	117	9.8	473	R55749	Extremolular doma
22	117	9.8	489	R07469	Plasmd pBABE hu
23	117	9.8	942	R70113	Gamma-IFN-R-GPB 13
24	114.5	9.6	245	R62023	Soluble human inte
25	111	9.3	210	R14643	Gamma interferon r
26	95.5	8.0	575	W41803	Mouse IL-10 recept
27	95	7.9	578	R57138	Interleukin-10 rec
28	95	7.9	578	W41804	Human IL-10 recept
29	94.5	7.9	575	R57139	Interleukin-10 rec
30	93.5	7.8	219	W17734	Human truncated t1
31	93.5	7.8	263	W17725	Human tissue facto
32	92	7.7	251	R28067	Sequence encoded b
33	92	7.7	251	R42463	Truncated tissue f
34	92	7.7	251	W17746	Human truncated t1

35	92	7.7	251	W55781	Truncated tissue f
36	92	7.7	265	R80063	Human IFNAB-BPI en
37	92	7.7	295	P81503	Human tissue facto
38	92	7.7	295	P80504	Sequence encoded b
39	92	7.7	295	P80713	Complete sequence
40	92	7.7	295	R55178	Pre-hurph. Inhibit
41	92	7.7	295	W17716	Human tissue facto
42	92	7.7	295	W31532	Human tissue facto
43	92	7.7	295	W55780	Full length tissue
44	92	7.7	295	W59047	Human thymoplast
45	92	7.7	295	W98950	Human tissue facto

ALIGNMENTS

RESULT	ID	Query Match	Score	DB 1	Length	436
R14487	R14487	Standard: Protein: 436 AA.	100.0%	DB 1: Length 436		
AC	R14487	16-JAN-1992 (first entry)				
DE	DE	Soluble Interferon-alpha/beta receptor.				
KM	KM	IFN: autoimmune disease; graft rejection; histocompatibility.				
OS	OS	Homo sapiens.				
PN	PN	FR2657881-A.				
PD	PD	09-AUG-1991.				
PF	PF	05-FEB-1990; 001298.				
PA	PA	(FUBI-) LAB EURO BIOTECHNO.				
PI	PI	Eld P. Gresser I, Lutfalla G, Meyer F, Mogensen KE;				
PI	PI	tovey MG, Dze G.				
DR	DR	WPI: 91-319778/44.				
DR	DR	N-PSDB: Q14239.				
PT	PT	New water-soluble polypeptide(s) with affinity for IFN-alpha and				
PT	PT	beta - used to treat e.g. lupus erythematosus, Behcet's disease,				
PT	PT	aplastic anemia, diabetes mellitus, rheumatoid arthritis, etc.				
PS	PS	Claim 2: Page 45; 52pp: French.				
CC	CC	The transmembrane and cytoplasmic domains of the native IFN receptor				
CC	CC	have been deleted to obtain a soluble, circulating form of the				
CC	CC	receptor. Potentially immunogenic epitopes have thus been eliminated.				
CC	CC	Derivatives obtained by substitution or deletion of this sequence				
CC	CC	are also claimed as are hybrid molecules comprising the soluble				
CC	CC	receptor (or deriv.) and an immunoglobulin such as IgG1.				
CC	CC	See also Q14240.				
SQ	SQ	Sequence 436 AA;				
Query Match		100.0%: Score 1196: DB 1: Length 436;				
Best Local Similarity		100.0%: Pred. No. 2.6e-115.				
Matches 229; Conservative		0; Mismatches 0; Indels 0; Gaps 0;				
OY	OY	1 MMVLLGATTLVAVGPVWLSAAGGKNLSPKQVEVDIIDNFIIRNRSDESVGNVT 60				
DB	DB	1 MMVLLGATTLVAVGPVWLSAAGGKNLSPKQVEVDIIDNFIIRNRSDESVGNVT 60				
OY	OY	61 FSPFYQGTGMDNWKLSGCONITSTKCNFSSKLINVEEIKLRARAKENTSSYEVDSF 120				
DB	DB	61 FSPFYQGTGMDNWKLSGCONITSTKCNFSSKLINVEEIKLRARAKENTSSYEVDSF 120				
OY	OY	121 TPEPKAIGPPEVLEADKAIVHISPGTKDSVMALDGLSFYSLLIKNSSGVPERI 180				
DB	DB	121 TPEPKAIGPPEVLEADKAIVHISPGTKDSVMALDGLSFYSLLIKNSSGVPERI 180				
OY	OY	181 ENISRKRRIYKLSPEITTCVKVKAALTSWKIGYSPVHCIKTVENEL 229				
DB	DB	181 ENISRKRRIYKLSPEITTCVKVKAALTSWKIGYSPVHCIKTVENEL 229				
RESULT		2				
ID	ID	R28495 standard: Protein: 436 AA.				
AC	AC	R28495:				
DT	DT	31-MAR-1993 (first entry)				

DE Sequence of a soluble form of the interferon (IFN) receptor
 DE with a high affinity for IFN-alpha and -beta.
 KW Interferon receptor; alpha-interferon; beta-interferon.
 OS Synthetic.
 PN WO9218626-A.
 PD 29-OCT-1992.
 PF 17-APR-1991; F00318.
 PR 17-APR-1991; WO-F00318.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
 PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
 PI Tovey M, Uze G;
 DR MPI: 92-382110/46.
 DR N-PSDB: Q30532.
 PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
 PT and beta - useful as immunosuppressants, for treating autoimmune
 PT diseases and transplant rejection
 PT Claim 2: Fig 1: 58pp: English.
 CC DNA encoding the water-soluble polypeptide with a high affinity for
 CC IFN-alpha and -beta is isolated by PCR, using appropriate
 CC oligonucleotides as primers and cloned cDNA as template. For example,
 CC bacteriophage lambda ZAP, containing the entire coding sequence of
 CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
 CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
 CC lacks the transmembrane and cytoplasmic domains. Both forms bind
 CC IFN in the same way as antibodies so are immunosuppressants e.g. for
 CC treating autoimmune diseases and graft rejection. They lack the
 CC toxic side-effects of known immunosuppressants such as steroids.
 SQ Sequence 436 AA;

Query Match 100.0%; Score 1196; DB 1; Length 436;
 Best Local Similarity 100.0%; Pred. No. 2.6e-115;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYVLLGATTLVAVGPMWLSAAGGNLSPKQVEVDIIDDFILRMNSDSVGNVT 60
 DB 1 MMYVLLGATTLVAVGPMWLSAAGGNLSPKQVEVDIIDDFILRMNSDSVGNVT 60
 QY 61 FSEDYQKTGMNDWIKLSGCONITSTKCNFSSKLNYEEIKLRIRAEKENTSSWYEDSF 120
 DB 61 FSEDYQKTGMNDWIKLSGCONITSTKCNFSSKLNYEEIKLRIRAEKENTSSWYEDSF 120
 QY 121 TPFRAQIGPPEVHLAEADKAIVIHISPGTDSVMALDGLSFTYSLLIMKSSGVEERI 180
 DB 121 TPFRAQIGPPEVHLAEADKAIVIHISPGTDSVMALDGLSFTYSLLIMKSSGVEERI 180
 QY 181 ENYSRHKIYKLSPTTYCLVKAKALLSMKIGVSPVHCITTYENEL 229
 DB 181 ENYSRHKIYKLSPTTYCLVKAKALLSMKIGVSPVHCITTYENEL 229

RESULT 3
 R1723
 ID R1723 standard; Protein: 436 AA.
 AC R1723
 DT 16-OCT-1995 (first entry)
 DE IFN receptor extracellular domain.
 KW IFN receptor; interferon receptor; interferon-alpha;
 KW interferon-beta; monoclonal antibody; immunomodulator; AIDS.
 OS Homo sapiens.
 PN MO9507716-A.
 PD 23-MAR-1995.
 PF 16-SEP-1994; E03114.
 PR 17-SEP-1993; EP-402279.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benizri EJ, Tovey MG;
 DR MPI: 95-131187/17.
 DR N-PSDB: Q86457.
 PT Compn. of monoclonal antibodies against interferon receptor -
 PT useful as immuno:modulator, eg. for treating AIDS
 CC Disclosure: Fig.2A-2B: 105pp: English.
 CC A recombinant soluble form of the human interferon class I receptor
 CC protein extracellular domain, given in R1723, was expressed in

CC either E. coli or COS cell hosts. The protein was used to raise
 CC immunomodulatory monoclonal antibodies.
 SQ Sequence 436 AA;

Query Match 100.0%; Score 1196; DB 1; Length 436;
 Best Local Similarity 100.0%; Pred. No. 2.6e-115;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYVLLGATTLVAVGPMWLSAAGGNLSPKQVEVDIIDDFILRMNSDSVGNVT 60
 DB 1 MMYVLLGATTLVAVGPMWLSAAGGNLSPKQVEVDIIDDFILRMNSDSVGNVT 60
 QY 61 FSEDYQKTGMNDWIKLSGCONITSTKCNFSSKLNYEEIKLRIRAEKENTSSWYEDSF 120
 DB 61 FSEDYQKTGMNDWIKLSGCONITSTKCNFSSKLNYEEIKLRIRAEKENTSSWYEDSF 120
 QY 121 TPFRAQIGPPEVHLAEADKAIVIHISPGTDSVMALDGLSFTYSLLIMKSSGVEERI 180
 DB 121 TPFRAQIGPPEVHLAEADKAIVIHISPGTDSVMALDGLSFTYSLLIMKSSGVEERI 180
 QY 181 ENYSRHKIYKLSPTTYCLVKAKALLSMKIGVSPVHCITTYENEL 229
 DB 181 ENYSRHKIYKLSPTTYCLVKAKALLSMKIGVSPVHCITTYENEL 229

RESULT 4
 R1958
 ID R1958 standard; Protein: 557 AA.
 AC R1958
 DT 18-JUL-1991 (first entry)
 DE Human alpha-interferon receptor protein.
 KW Human alpha IFN; IFN agonists; antiviral; anti tumour agent;
 KW drug targeting.
 OS Homo sapiens.
 PN Key
 FT peptide
 FT 1.27
 PN WO9105862-A.
 PD 02-MAY-1991.
 PF 19-OCT-1990; F00758.
 PR 20-OCT-1989; FR-013770.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PI Mogensen KE, Uze G, Lutfalla G, Gresser I;
 DR MPI: 91-148740/20.
 DR N-PSDB: Q11701.
 PT New human alpha-interferon receptor protein - useful for testing
 PT interferon agonists and in treatment or diagnosis
 PS Disclosure: Fig 4; 30pp; French.
 CC This recombinant human alpha interferon (IFN) receptor protein is
 CC useful for the testing of IFN agonists and for treatment and diag-
 CC nosis of viral diseases and tumours. Antibodies raised against
 CC this protein can be used for blocking the receptor when required,
 CC eg where overexpression of alpha-IFN is harmful. The Abs are
 CC also useful for eg drug targeting. Variants of the protein,
 CC having residue 164 (Thr) replaced by Arg and an Asp inserted
 CC between residues 479 and 480, are also useful.
 SQ Sequence 557 AA;

Query Match 100.0%; Score 1196; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 3.7e-115;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYVLLGATTLVAVGPMWLSAAGGNLSPKQVEVDIIDDFILRMNSDSVGNVT 60
 DB 1 MMYVLLGATTLVAVGPMWLSAAGGNLSPKQVEVDIIDDFILRMNSDSVGNVT 60
 QY 61 FSEDYQKTGMNDWIKLSGCONITSTKCNFSSKLNYEEIKLRIRAEKENTSSWYEDSF 120
 DB 61 FSEDYQKTGMNDWIKLSGCONITSTKCNFSSKLNYEEIKLRIRAEKENTSSWYEDSF 120
 QY 121 TPFRAQIGPPEVHLAEADKAIVIHISPGTDSVMALDGLSFTYSLLIMKSSGVEERI 180

```
Db 121 TPFKKAQIGPPEVHLEADKAIVIHISPTKDSVMALDGLSFTYSLIKMNSGVEERI 180
|||||
Qy 181 ENISRRIKIKLSPETTYCLKVKAKALLTSWKIGVSPVHCIKITVENEL 229
|||||
Db 181 ENISRRIKIKLSPETTYCLKVKAKALLTSWKIGVSPVHCIKITVENEL 229

RESULT 5
R14488
ID R14488 standard; Protein: 557 AA.
AC R14488:
DE 16-JAN-1992 (first entry)
KM Complete Interferon-alpha/beta receptor.
OS Homo sapiens.
FH key location/Qualifiers
FT domain 437..457
FT /label= transmembrane
FT domain 458..557
FT /label= cytoplasmic
FR2657881-A.
PN 09-AUG-1991.
PF 05-FEB-1990: 001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Tovey MG, Uze G;
PI WPI: 91-319778/44.
DR N-PSDB: Q14240.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Disclosure: Page 47; 52pp; French.
CC The invention covers derivatives of the interferon-alpha and/or beta
CC receptor obtained by deleting the transmembrane and cytoplasmic domains
CC of the native receptor or by substitution. Potentially immunogenic
CC epitopes are eliminated and the deriv. can be secreted from
CC transformed cells. Soluble deriv.s block the activity of IFN alpha/beta
CC and can be used to treat autoimmune diseases or to inhibit graft
CC rejection. See also Q14239.
SQ Sequence 557 AA.

Query Match 100.0%; Score 1196; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.7e-115;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMYVLLGATTLVAVGPMWLSAAGGNLKSPOKVEVDIIDNFIIRNRSDESGVNT 60
|||||
Db 1 MMYVLLGATTLVAVGPMWLSAAGGNLKSPOKVEVDIIDNFIIRNRSDESGVNT 60

Qy 61 FSPDYQKGMNWKILSGCONITSTKCNFSSKLNYEELKIRAKENNTSSWEVDSE 120
|||||
Db 61 FSPDYQKGMNWKILSGCONITSTKCNFSSKLNYEELKIRAKENNTSSWEVDSE 120

Qy 121 TPFKKAQIGPPEVHLEADKAIVIHISPTKDSVMALDGLSFTYSLIKMNSGVEERI 180
|||||
Db 121 TPFKKAQIGPPEVHLEADKAIVIHISPTKDSVMALDGLSFTYSLIKMNSGVEERI 180

Qy 181 ENISRRIKIKLSPETTYCLKVKAKALLTSWKIGVSPVHCIKITVENEL 229
|||||
Db 181 ENISRRIKIKLSPETTYCLKVKAKALLTSWKIGVSPVHCIKITVENEL 229

RESULT 6
R28496
ID R28496 standard; Protein: 557 AA.
AC R28496:
DE 31-MAR-1993 (first entry)
KM Sequence of a soluble form of the interferon (IFN) receptor
KM with a high affinity for IFN-alpha and -beta.
KM Interferon receptor; alpha-interferon; beta-interferon.
```

```
OS Synthetic.
PN W09218626-A.
PD 29-OCT-1992.
PF 17-APR-1991: F00318.
PR 17-APR-1991: WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PI Tovey M, Uze G;
PI WPI: 92-382110/46.
DR N-PSDB: Q30533.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
PT and beta - useful as immunosuppressants, for treating auto-immune
PT diseases and transplant rejection
PS Claim 3; Fig 2; 50pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
CC IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template. For example,
CC bacteriophage lambda ZAP, containing the entire coding sequence of
CC the IFN-alpha and -beta receptor (Q30533), was incubated with Q11905
CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
CC lacks the transmembrane and cytoplasmic domains. Both forms bind
CC IFN in the same way as antibodies so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 557 AA.

Query Match 100.0%; Score 1196; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.7e-115;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMYVLLGATTLVAVGPMWLSAAGGNLKSPOKVEVDIIDNFIIRNRSDESGVNT 60
|||||
Db 1 MMYVLLGATTLVAVGPMWLSAAGGNLKSPOKVEVDIIDNFIIRNRSDESGVNT 60

Qy 61 FSPDYQKGMNWKILSGCONITSTKCNFSSKLNYEELKIRAKENNTSSWEVDSE 120
|||||
Db 61 FSPDYQKGMNWKILSGCONITSTKCNFSSKLNYEELKIRAKENNTSSWEVDSE 120

Qy 121 TPFKKAQIGPPEVHLEADKAIVIHISPTKDSVMALDGLSFTYSLIKMNSGVEERI 180
|||||
Db 121 TPFKKAQIGPPEVHLEADKAIVIHISPTKDSVMALDGLSFTYSLIKMNSGVEERI 180

Qy 181 ENISRRIKIKLSPETTYCLKVKAKALLTSWKIGVSPVHCIKITVENEL 229
|||||
Db 181 ENISRRIKIKLSPETTYCLKVKAKALLTSWKIGVSPVHCIKITVENEL 229

RESULT 7
R42635
ID R42635 standard; Protein: 557 AA.
AC R42635:
DE 20-APR-1994 (first entry)
KM Human Interferon receptor.
KM IFN-R; extracellular domain; monoclonal antibody; viral infection;
KM cell proliferation; allograft rejection; systemic lupus erythematosus;
KM poriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;
KM immunodeficiency; measles virus; interferon-alpha-beta.
OS Homo sapiens.
FH key location/Qualifiers
FT domain 1..436
FT /label= extracellular-domain
FT /note= "soluble, immunogenic form of IFN-R"
FR563487-A.
PN 06-OCT-1993.
PF 31-MAR-1992: 400902.
PR 31-MAR-1992: EP-400902.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG;
PI WPI: 93-312951/40.
DR P-PSDB: R42635.
PT Monoclonal antibody to human interferon type-I receptor - having
PT neutralising activity against human type I interferon, used for
```

PT therapy and diagnosis
 PS Disclosure: Fig 3: 21pp; English.
 CC Monoclonal antibodies produced against soluble forms of the human
 CC Interferon alpha-beta receptor based on the full-length human IFN-R
 CC sequence are claimed. The antibodies are useful for treatment and
 CC prophylaxis of disorders involving cell proliferation and/or viral
 CC infection.
 SQ Sequence 557 AA;

Query Match 100.0%; Score 1196; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 3.7e-115;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMVVLGATTLVAVGPNVLSAAGGNLSPQKVEVDIIDNFIIRNRSDSEGVNT 60
 DB 1 MMVVLGATTLVAVGPNVLSAAGGNLSPQKVEVDIIDNFIIRNRSDSEGVNT 60
 OY 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSLKLVYEIKLRIRAEKENTSSWYEVDSF 120
 DB 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSLKLVYEIKLRIRAEKENTSSWYEVDSF 120
 OY 121 TPFRAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLIIMKNSSGVEERI 180
 DB 121 TPFRAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLIIMKNSSGVEERI 180
 OY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTYENEL 229
 DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTYENEL 229

RESULT 8
 ID R75356 standard; Protein: 557 AA.
 AC R75356:
 DT 16-OCT-1995 (first entry)
 DE Human IFN receptor.
 KW IFN receptor; Interferon receptor; Interferon-alpha;
 KW Interferon-beta; monoclonal antibody; Immunomodulator; AIDS.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 1..436
 FT /label= Extracellular-domain
 PN WO9507716-A.
 PD 23-MAR-1995.
 PF 16-SEP-1994; E03114.
 PR 17-SEP-1993; EP-402279.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benlert EJ, Tovey MG;
 DR MPI: 95-131187/17.
 DR N-PSDB: Q86458.
 PT Compn. of monoclonal antibodies against Interferon receptor
 PT useful as immuno-modulator, eg. for treating AIDS
 PS Disclosure: Fig. 3a-2b, 105pp; English.
 CC The amino acid sequence of human Interferon class I receptor is
 CC given in R75356. A recombinant soluble form of the extracellular
 CC domain of this receptor (R71723) has been used to raise
 CC immunomodulatory monoclonal antibodies.
 SQ Sequence 557 AA;

Query Match 100.0%; Score 1196; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 3.7e-115;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMVVLGATTLVAVGPNVLSAAGGNLSPQKVEVDIIDNFIIRNRSDSEGVNT 60
 DB 1 MMVVLGATTLVAVGPNVLSAAGGNLSPQKVEVDIIDNFIIRNRSDSEGVNT 60
 OY 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSLKLVYEIKLRIRAEKENTSSWYEVDSF 120
 DB 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSLKLVYEIKLRIRAEKENTSSWYEVDSF 120

OY 121 TPFRAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLIIMKNSSGVEERI 180
 DB 121 TPFRAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLIIMKNSSGVEERI 180
 OY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTYENEL 229
 DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTYENEL 229

RESULT 9
 ID W21805 standard; Protein: 434 AA.
 AC W21805:
 DT 23-SEP-1997 (first entry)
 DE Spliced-deleted interferon alpha-receptor form 1.
 KW Interferon alpha-receptor; IFNAR.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 1..427
 FT /label= Extracellular-domain
 FT /note= "comprises amino acids 1-427 of the
 FT transmembrane IFNAR"
 FT domain 428..434
 FT /label= S-domain
 PN AU9475977-A.
 PD 11-MAY-1995.
 PF 20-OCT-1994; 075977.
 PR 24-OCT-1993; IL-107378.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (ABRAV/) ABRAMOVICH C.
 PI Abramovich C, Ratovitski E, Revel M;
 DR MPI: 95-200634/27.
 PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Example 2: Fig 7; 46pp; English.
 CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 1
 CC (W21805) is characterised by a new domain (S) which follows an
 CC end-deleted extracellular domain when compared to transmembrane
 CC IFNAR (W21804). There is no transmembrane domain. The amino acid
 CC sequence is predicted from a cDNA clone (see also R73520) obtd.
 CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
 CC splice-deleted forms 1 and 2 (see also W21806) probably regulate
 CC the response of human cells to IFNs, either by acting as IFN
 CC antagonists or by regulating the activity of the multiple IFN
 CC subtypes. They can be expressed in host cells and used to inhibit,
 CC modulate or modify the activities of IFNs alpha and beta in cells,
 CC tissues and organisms, or for diagnostic purposes.
 SQ Sequence 434 AA;

Query Match 99.6%; Score 1191; DB 1; Length 434;
 Best Local Similarity 99.6%; Pred. No. 8.4e-115;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MMVVLGATTLVAVGPNVLSAAGGNLSPQKVEVDIIDNFIIRNRSDSEGVNT 60
 DB 1 MMVVLGATTLVAVGPNVLSAAGGNLSPQKVEVDIIDNFIIRNRSDSEGVNT 60
 OY 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSLKLVYEIKLRIRAEKENTSSWYEVDSF 120
 DB 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSLKLVYEIKLRIRAEKENTSSWYEVDSF 120
 OY 121 TPFRAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLIIMKNSSGVEERI 180
 DB 121 TPFRAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLIIMKNSSGVEERI 180
 OY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTYENEL 229
 DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTYENEL 229

RESULT 10
 W21806

ID W21806 standard; Protein; 496 AA.
AC W21806;
DT 23-SEP-1997 (first entry)
DE Spliced-deleted interferon alpha-receptor form 2.
KM Interferon alpha-receptor; IFNAR.
OS Homo sapiens.
FH Key
FT domain
FT 1. .413
FT /label= Extracellular_domain
FT /note= "comprises amino acid residues 1-413 and
FT 422-427 of transmembrane IFNAR"
FT domain
FT /label= Intracellular_domain
FT /note= "comprises amino acids 481-557 of
FT transmembrane IFNAR"
PD A09475977-A.
PN 11-MAY-1995.
PR 20-OCT-1994; 075977.
PR 24-OCT-1993; IL-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (ABRA/) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M;
DR WPI: 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Example 3; Fig 7; 46pp; English.
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2
CC (W21806) is characterised by a double deletion when compared to
CC transmembrane IFNAR (W21804). The extracellular domain is
CC shortened by 6 amino acid residues and is followed by a truncated
CC intracellular domain. There is no transmembrane region. The amino
CC acid sequence is predicted from a cDNA clone (see also T73521) Obtd.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 (see also W21805) and 2 may regulate the
CC response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating IFN activities. They can be expressed
CC in host cells and used to inhibit, modulate or modify the
CC activities of IFNs alpha and beta in cells, tissues and organisms,
CC or for diagnostic purposes.
SO Sequence 496 AA;

Query Match 99.6%; Score 1191; DB 1; Length 496;
Best Local Similarity 99.6%; Pred. No. 1e-114;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMYVLLGATTLVAVGPMWLSAAGGNKLSPOKVEVDIIDDFILRMNSDESGVNT 60
DB 1 MMYVLLGATTLVAVGPMWLSAAGGNKLSPOKVEVDIIDDFILRMNSDESGVNT 60
QY 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSSLKLNVEEIKLRIRAKENTSSMYEVSDF 120
DB 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSSLKLNVEEIKLRIRAKENTSSMYEVSDF 120
QY 121 TPFKRAQIGPEVHLEADKAIVIHISGTDVMAALDGLSTFYSLLIMKNSGVEERI 180
DB 121 TPFKRAQIGPEVHLEADKAIVIHISGTDVMAALDGLSTFYSLLIMKNSGVEERI 180
QY 181 ENISYRHKIKYKLSPEPTYCCKVKKALLTSWKIGVSPVHCIKITVENEL 229
DB 181 ENISYRHKIKYKLSPEPTYCCKVKKALLTSWKIGVSPVHCIKITVENEL 229

RESULT 11
W21804
ID W21804 standard; Protein; 557 AA.
AC W21804;
DT 23-SEP-1997 (first entry)
DE Transmembrane interferon alpha-receptor.
KM Interferon alpha-receptor; IFNAR.
OS Homo sapiens.
FH Key
FT domain
FT 1. .436

FT domain
FT /label= Extracellular_domain
FT /label= Transmembrane_domain
FT domain
FT /label= Intracellular_domain
PD A09475977-A.
PN 11-MAY-1995.
PR 20-OCT-1994; 075977.
PR 24-OCT-1993; IL-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (ABRA/) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M;
DR WPI: 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Disclosure; Fig 7; 46pp; English.
CC Human transmembrane interferon alpha receptor (IFNAR) (W21804)
CC includes a 21-amino acid transmembrane region. Novel, splice-
CC deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected
CC that lack this transmembrane domain. These, soluble non-membrane
CC bound polypeptides can be expressed in host cells and used to
CC inhibit, modulate or modify the activities of interferons alpha
CC and beta in cells, tissues and organisms, or for diagnostic
CC purposes.
SO Sequence 557 AA;

Query Match 99.6%; Score 1191; DB 1; Length 557;
Best Local Similarity 99.6%; Pred. No. 1.2e-114;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMYVLLGATTLVAVGPMWLSAAGGNKLSPOKVEVDIIDDFILRMNSDESGVNT 60
DB 1 MMYVLLGATTLVAVGPMWLSAAGGNKLSPOKVEVDIIDDFILRMNSDESGVNT 60
QY 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSSLKLNVEEIKLRIRAKENTSSMYEVSDF 120
DB 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSSLKLNVEEIKLRIRAKENTSSMYEVSDF 120
QY 121 TPFKRAQIGPEVHLEADKAIVIHISGTDVMAALDGLSTFYSLLIMKNSGVEERI 180
DB 121 TPFKRAQIGPEVHLEADKAIVIHISGTDVMAALDGLSTFYSLLIMKNSGVEERI 180
QY 181 ENISYRHKIKYKLSPEPTYCCKVKKALLTSWKIGVSPVHCIKITVENEL 229
DB 181 ENISYRHKIKYKLSPEPTYCCKVKKALLTSWKIGVSPVHCIKITVENEL 229

RESULT 12
W52296
ID W52296 standard; Protein; 325 AA.
AC W52296;
DT 23-JUN-1998 (first entry)
DE CRFB4 protein.
KM CRFB4; Interleukin-10; IL-10; IL-10 receptor; allograft rejection;
KM vaccine; photosensitivity; inflammation; autoimmune disease;
KM septic shock; immune response; organ rejection; gene therapy.
OS Homo sapiens.
PN MO9802542-A1.
PD 22-JAN-1998.
PR 17-JUL-1997; U12455.
PR 17-JUL-1996; US-683743.
PA (UYNE-) UNIV NEW JERSEY.
PI Kotoenko SV, Pestka S;
DR WPI: 98-110590/10.
DR N-PSDB: V19874.
PT New recombinant DNA - comprises sequences encoding interleukin-10
PT and CRFB4 linked to operator, useful, e.g. preventing allograft
PT rejection.
PS Claim 2; Page -: 79pp; English.
CC This sequence is the human CRFB4 sequence, DNA encoding it is used in the
CC recombinant DNA (I) of the invention. (I) comprises a sequence (S1)
CC encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2)

CC encodina CRP4, both operably linked to expression control sequences.
CC Cells containing (1) may be used to identify agonists/antagonist of
CC IL-10. Agonists are potentially useful e.g. for preventing allograft
CC rejection, as vaccine adjuvants, for treatment of photo-sensitivity,
CC inflammation, autoimmune disease and septic shock, while antagonists are
CC potentially useful for increasing immune responses against tumours,
CC viruses, bacteria and parasites (especially intracellular pathogens) and
CC for preventing organ rejection. A vector containing (1) is used to
CC restore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses
CC a dysfunctional IL10R and is able to bind IL-10 but not to transduce a
CC signal. Antisense CRP4 sequences (especially ribozymes), can inhibit
CC IL-10 activity in cells. Antibodies specific for CRP4 are used to
CC measure and localise CRP4, for diagnosis of defective IL-10 activity.
CC Fragments of (1) are used as primers or probes to assay CRP4-specific
CC RNA. Agonists/antagonists may be administered parenterally, orally or
CC rectally especially by intravenous injection or directly into a tumour or
CC sequence 325 AA;
90

Query Match	18.68;	Score 222.5;	DB 1;	Length 325;
Best Local Similarity	30.38;	Pred. No. 4.7e-15;		
Matches	66;	Conservative 40;	Mismatches 93;	Indels 19;
				Gaps 8

Qy 19 WVL5AAAGKNLKS-----POKEVVIDIDNFLIRNRNDSDEGVATSEFDYKQTGCD 71
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 3 WSLSGLGGCLLYSALGMPPPEPNRBMNSVNKNKLNIOWESPAFKGNLTFTAOY----LS 58

Qy 72 NWILSGCOINITSCKNFSSLLNLNYEEIKLRIRAE-KENTS5WYEVDSEFTPEPKOIQP 13
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 59 YRIFOQCKMNTLTLEDFFS--LSKYGDHLYLRVREFADSHSDVMNI-TTCPPDITLIIP 11

Qy 131 PEWHLEA-EDKAIVIHISFGTIDSV-MMALDGL--SFTYSLLIWNKSSGYEERIEINIYSR 18
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 116 PGM0VEVLADSLMRRLAKRIENEXETJMTMKNVYSMTFYNIQYWKNCTIDEKFQITPYDF 17

Qy 187 HKIKLSPEPTYCYLKTKAALLSKAIIGVSPFHCKTT 224
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 176 EVLRNELEPWTTYCV0RGFLPDRNRAGENISEVEECOT 213

RESULT	13
ID	R75782 standard; Protein: 332 AA.
AC	R75782;
DT	13-NOV-1995 (first entry)
DE	IFN-gamma receptor beta-subunit.
KW	interferon-gamma receptor beta subunit; mufin; interferon-gamma-antagonist.
OS	Mus sp.
PT	Key
FT	peptide
FT	location/Qualifiers
FT	/label= Sig_Peptide
FT	19..242
FT	/label= Extracellular_domain
FT	243..266
FT	/label= Transmembrane_anchoring_domain
FT	267..332
FT	/label= Cytoplasmic_domain
PN	W09516036-A.
PD	15-JUN-1995.
PF	07-DEC-1994; U14277.
PR	09-DEC-1993; US-164596.
PA	(AGUE/) AGUET M.
PA	(BOEH/) BOENNI R.
PA	(HEMM/) HEMMI S.
PI	Aguet M., Boehni R., Hemmi S.; WPI: 95-224321/29.
DR	N-RSDb: Q90808.
PT	Novel Interferon gamma receptor beta chain polypeptide - for treatment of inflammatory bowel disease and liver damage
CC	Claim 3; Fig.2a; 86pp; English. The IFN-gamma receptor beta-subunit encoded by a cDNA clone derived

CC from mouse B-cells is given in R5782. Recombinant beta-subunit,
CC pref. with the transmembrane anchoring domain deleted or
CC inactivated and with the cytoplasmic domain deleted, may be
CC may be used to treat pathological conditions associated with endogenous
CC IFN-gamma production.
50 Sequence 332 AA;

Query Match	17.0%;	Score 203;	DB 1;	Length 332;
Best Local Similarity	30.1%;	Pred. NO. 4.9e-13;		
Matches 69;	Conservative 38;	Mismatches 86;	Indels 36;	Gaps 13

```

QY 21 LSAAG-----KNKSPKQVEVDIIDDFILRNKRSDS-----YGVNVEFPIYQXTGM 70
Db 16 LGAALSSPDSFSQLAALPNPLHLHNDQILTWBSPSSNDPRVYVQVESF-----I 69
QY 71 D-NWIKL--SGCONITSTKCNFSS---KLNVEE-EIKRIRAEKEN-TSSMYEVDSETP 122
Db 70 DGSWRLLLEPCTDITETKCOLDTGGGRKALPPHFTYFLVLRARAGNTISWVGLPEPQH 125
QY 123 ERKAOIGPE-VHLEAEDKAIVIHISPEKDSVMALDGLSFYSLLIMKSSGVEERIE 187
Db 130 YENVTVGPPKNISVTPGKGLVIFHSPEFD----VFHGAFQOLVHWMEKSETEQOEVE 184
QY 132 NYSRHKIY--KLSPEYYCLKYVAAL-LTSMKI---GVYSPVRCIKTT 224
Db 185 GPEKNSNLTVLGNLKPVRVYLCQDTAOLILKRNKKLRPHGLISWVSCHEPT 233

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RESULT	14
W79159	
ID	W79159 standard; Protein; 553 AA

DE	20-NOV-1998 (first entry)
DE	zcyto7 cytokine receptor polypeptide
KM	zcyto7, cytokine receptor, ligand-binding polypeptide; kidney; pancreas
KM	type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue
KM	ligand 2; cell proliferation; cell differentiation; renal disease; human;
KM	neural disease; pancreatic disease.
OS	Homo sapiens.

Key	Location/Qualifiers
Domain	30..250
Domain	/note="extracellular (ligand-binding) domain, sequence claimed in claim 1"
Domain	275..553
Domain	/note="intracellular domain"

PN MO837193-A1.
 PD 27-AUG-1998.
 PR 18-FEB-1998; U03029.
 PR 02-OCT-1997; US-943087.
 PR 20-FEB-1997; US-803305.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Farrah TM, Jelnberg AC, Kho CJ, Lok S.
 PI Whitmore TE:
 DR Whitmore TE:
 DR WPI: 98-480798/41.
 DR N-PSDS: V57515.
 PR Novel human zcytor7 DNA encodes a type 2 cytokine receptor - useful
 PR for treating zcytor7, neural, pancreatic and prostatic diseases
 PS Claim 1: Pages 55-59; 72pp: English.
 CC This represents the zcytor7 cytokine receptor. zcytor7 is a ligand-
 CC binding receptor polypeptide and is a novel member of the type 2 cytokine
 CC receptor family (CPR2). An expression vector containing the zcytor
 CC polynucleotide, operably linked to transcription promoter, a sequence
 CC encoding a transmembrane and intracellular domain, or both, and a
 CC transcriptional terminator can be used to transform host cells for the
 CC recombinant production of the polypeptide. The sequences can be used to
 CC study the zcytor7 gene and to isolate ligands binding to it. zcytor7 is
 CC preferentially expressed in the kidney, pancreas, prostate or nervous
 CC tissue. Agonists of zcytor7 can be used to stimulate proliferation and
 CC differentiation of cell in these organs. The antagonists and agonists can
 CC also be used in the treatment of renal, neural, pancreatic and prostate
 CC diseases.
 SQ Sequence 553 AA;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:17:54 ; Search time 23.82 Seconds

(Without alignments)
138,798 Million cell updates/sec

Title: US-09-240-675-2_COPY_1_229

Perfect score: 1196
Sequence: 1 MMVVLGATTLVAVGPMV.....WKIGVSPVHCITVENEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 145308 seqs, 14437401 residues

Total number of hits satisfying chosen parameters: 145308

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued_Patents_AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1196	100.0	434 1 US-08-328-256-11	Sequence 11, Appl
2	1196	100.0	436 2 US-08-307-588-2	Sequence 2, Appl
3	1196	100.0	496 1 US-08-328-256-12	Sequence 12, Appl
4	1196	100.0	557 1 US-08-328-256-10	Sequence 10, Appl
5	1196	100.0	557 2 US-08-471-454-2	Sequence 2, Appl
6	1196	100.0	557 2 US-08-466-974-2	Sequence 2, Appl
7	1196	100.0	557 2 US-08-471-453-2	Sequence 2, Appl
8	1196	100.0	557 2 US-08-307-588-4	Sequence 4, Appl
9	490.5	41.0	202 4 PCT-US84-14277-3	Sequence 3, Appl
10	222.5	18.6	325 2 US-08-683-743-4	Sequence 4, Appl
11	203	17.0	332 4 PCT-US94-14277-6	Sequence 2, Appl
12	192	16.1	223 4 PCT-US94-14277-2	Sequence 6, Appl
13	184.5	15.4	553 2 US-08-943-087-14	Sequence 14, Appl
14	184.5	15.4	553 2 US-08-943-087-12	Sequence 16, Appl
15	184.5	15.4	553 2 US-08-943-087-16	Sequence 18, Appl
16	184.5	15.4	553 2 US-08-943-087-18	Sequence 20, Appl
17	184.5	15.4	553 2 US-08-943-087-20	Sequence 22, Appl
18	184.5	15.4	553 2 US-08-943-087-22	Sequence 24, Appl
19	184.5	15.4	553 2 US-08-943-087-24	Sequence 26, Appl
20	184.5	15.4	553 2 US-08-943-087-26	Sequence 28, Appl
21	184.5	15.4	553 2 US-08-943-087-28	Sequence 30, Appl
22	184.5	15.4	553 2 US-08-943-087-30	Sequence 32, Appl
23	184.5	15.4	553 2 US-08-943-087-32	Sequence 34, Appl
24	184.5	15.4	553 2 US-08-943-087-34	Sequence 36, Appl
25	184.5	15.4	553 2 US-08-943-087-36	Sequence 38, Appl
26	184.5	15.4	553 2 US-08-943-087-38	Sequence 40, Appl
27	184.5	15.4	553 2 US-08-943-087-40	Sequence 42, Appl
28	184.5	15.4	553 2 US-08-943-087-42	Sequence 44, Appl
29	184.5	15.4	553 2 US-08-943-087-44	Sequence 46, Appl

30	184.5	15.4	553 2 US-08-943-087-46	Sequence 48, Appl
31	184.5	15.4	553 2 US-08-943-087-48	Sequence 50, Appl
32	174.5	14.6	221 2 US-08-943-087-50	Sequence 52, Appl
33	169.5	14.2	221 2 US-08-943-087-52	Sequence 54, Appl
34	168.5	14.1	221 2 US-08-943-087-54	Sequence 56, Appl
35	167.5	14.0	221 2 US-08-943-087-56	Sequence 58, Appl
36	165.5	13.8	221 2 US-08-943-087-58	Sequence 60, Appl
37	162.5	13.6	221 2 US-08-943-087-60	Sequence 62, Appl
38	149.5	12.5	337 4 PCT-US94-14277-8	Sequence 8, Appl
39	145	12.1	200 4 PCT-US94-14277-4	Sequence 4, Appl
40	140.5	11.7	574 2 US-08-906-713-2	Sequence 2, Appl
41	117.5	9.8	489 5 PCT-US93-11110-1	Sequence 1, Appl
42	117.5	9.8	489 5 PCT-US93-11110-1	Sequence 1, Appl
43	95.5	8.0	575 1 US-08-424-788-2	Sequence 2, Appl
44	95.5	8.0	575 1 US-08-110-683-4	Sequence 4, Appl
45	95.5	8.0	575 2 US-08-477-166-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-08-328-256-11

Sequence 11, Application US/08328256

Patent No. 5643749

GENERAL INFORMATION:

APPLICANT: REVEL, Michel

APPLICANT: ABRAMOVICH, Carolina

APPLICANT: RATOVITSKI, Edward

TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESS: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/328,256

FILING DATE: 24-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 107378

FILING DATE: 24-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: REVEL-13

REFERENCE/DOCKET NUMBER: 25,618

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 434 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-328-256-11

Query Match 100.0%; Score 1196; DB 1; Length 434;

Best Local Similarity 100.0%; Pred. No. 2,4e-126;

Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MMVVLGATTLVAVGPMVLSAAGKRLKSPQVEVDIIDNFIILRRNRDSGVNVT 60

|||||
Db 1 MMVLLGATTLVAVGPWVLSAAGGNLKSPOKVEVDIIDDNFIILRNRSDESGVNT 60
QY 61 FSPDYOKTGMNDWIKISGCONITSTKCNFSSLKLNVEEIKLRIRAEKENTSSWYEVDSF 120
Db 61 FSPDYOKTGMNDWIKISGCONITSTKCNFSSLKLNVEEIKLRIRAEKENTSSWYEVDSF 120
QY 121 TPRKRAOIGPEVHLEADKAIVIHISPGTKDSVMALDGLSFTYSLILMKNSSGVEERI 180
Db 121 TPRKRAOIGPEVHLEADKAIVIHISPGTKDSVMALDGLSFTYSLILMKNSSGVEERI 180
QY 181 ENIYSRHKIYKLSPEPTYCLKAKAALLTSWKIGVSPVHCIKITVENEL 229
Db 181 ENIYSRHKIYKLSPEPTYCLKAKAALLTSWKIGVSPVHCIKITVENEL 229

RESULT 2
US-08-307-588-2
; Sequence 2, Application US/08307588
; Patent No. 5919453
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MAGUIRE, Deborah
; APPLICANT: PLAVEC, Ivan
; APPLICANT: TOVEY, Michael G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307, 588
; FILING DATE: 05-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00770
; FILING DATE: 30-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92400902.0
; FILING DATE: 31-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 436 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-307-588-2

Query Match 100.0%; Score 1196; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 2,4e-126;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMVLLGATTLVAVGPWVLSAAGGNLKSPOKVEVDIIDDNFIILRNRSDESGVNT 60
Db 1 MMVLLGATTLVAVGPWVLSAAGGNLKSPOKVEVDIIDDNFIILRNRSDESGVNT 60

QY 61 FSPDYOKTGMNDWIKISGCONITSTKCNFSSLKLNVEEIKLRIRAEKENTSSWYEVDSF 120
Db 61 FSPDYOKTGMNDWIKISGCONITSTKCNFSSLKLNVEEIKLRIRAEKENTSSWYEVDSF 120
QY 121 TPRKRAOIGPEVHLEADKAIVIHISPGTKDSVMALDGLSFTYSLILMKNSSGVEERI 180
Db 121 TPRKRAOIGPEVHLEADKAIVIHISPGTKDSVMALDGLSFTYSLILMKNSSGVEERI 180
QY 181 ENIYSRHKIYKLSPEPTYCLKAKAALLTSWKIGVSPVHCIKITVENEL 229
Db 181 ENIYSRHKIYKLSPEPTYCLKAKAALLTSWKIGVSPVHCIKITVENEL 229

RESULT 3
US-08-328-256-12
; Sequence 12, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: ABRAMOVICH, Carolina
; APPLICANT: RATOVIJSKI, Edward
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328, 256
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107378
; FILING DATE: 24-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: REVEL-13
; REFERENCE/DOCKET NUMBER: 25,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-328-256-12

Query Match 100.0%; Score 1196; DB 1; Length 496;
Best Local Similarity 100.0%; Pred. No. 3e-126;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMVLLGATTLVAVGPWVLSAAGGNLKSPOKVEVDIIDDNFIILRNRSDESGVNT 60
Db 1 MMVLLGATTLVAVGPWVLSAAGGNLKSPOKVEVDIIDDNFIILRNRSDESGVNT 60
QY 61 FSPDYOKTGMNDWIKISGCONITSTKCNFSSLKLNVEEIKLRIRAEKENTSSWYEVDSF 120
Db 61 FSPDYOKTGMNDWIKISGCONITSTKCNFSSLKLNVEEIKLRIRAEKENTSSWYEVDSF 120

OY 121 TPFRAQIGPEVHLEADKAIIVHISPGTKDSVMALDGLSFTYSLIMKNSGVEERI 180
DB 121 TPFRAQIGPEVHLEADKAIIVHISPGTKDSVMALDGLSFTYSLIMKNSGVEERI 180
OY 181 ENISRHRKIYKLSPEITTCYCKVKAALLTSMKIGVSPVHCITVTENEL 229
DB 181 ENISRHRKIYKLSPEITTCYCKVKAALLTSMKIGVSPVHCITVTENEL 229

RESULT 4

US-08-328-256-10
Sequence 10 Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
NUMBER OF SEQUENCES: 12
TITLE OF INVENTION: PREPARATION AND USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328, 256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25, 618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-256-10

Query Match 100.0%; Score 1196; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3, 6e-126;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMYVLGATTLVLA VAGFWVLSAAGGNKLSPOKVEVDIIDNFI LRNRSDSVGNT 60
DB 1 MMYVLGATTLVLA VAGFWVLSAAGGNKLSPOKVEVDIIDNFI LRNRSDSVGNT 60
OY 61 FSPDOKGMNMWIKLSGCONITSTKCNFSSLKLVYEEIKLRIRAEKNTSSMYEVSF 120
DB 61 FSPDOKGMNMWIKLSGCONITSTKCNFSSLKLVYEEIKLRIRAEKNTSSMYEVSF 120
OY 121 TPFRAQIGPEVHLEADKAIIVHISPGTKDSVMALDGLSFTYSLIMKNSGVEERI 180
DB 121 TPFRAQIGPEVHLEADKAIIVHISPGTKDSVMALDGLSFTYSLIMKNSGVEERI 180
OY 181 ENISRHRKIYKLSPEITTCYCKVKAALLTSMKIGVSPVHCITVTENEL 229
DB 181 ENISRHRKIYKLSPEITTCYCKVKAALLTSMKIGVSPVHCITVTENEL 229

DB 181 ENISRHRKIYKLSPEITTCYCKVKAALLTSMKIGVSPVHCITVTENEL 229

RESULT 5

US-08-471-454-2
Sequence 2, Application US/08471454
Patent No. 5731169
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LOTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,454
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900, 642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-454-2

Query Match 100.0%; Score 1196; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3, 6e-126;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMYVLGATTLVLA VAGFWVLSAAGGNKLSPOKVEVDIIDNFI LRNRSDSVGNT 60
DB 1 MMYVLGATTLVLA VAGFWVLSAAGGNKLSPOKVEVDIIDNFI LRNRSDSVGNT 60
OY 61 FSPDOKGMNMWIKLSGCONITSTKCNFSSLKLVYEEIKLRIRAEKNTSSMYEVSF 120
DB 61 FSPDOKGMNMWIKLSGCONITSTKCNFSSLKLVYEEIKLRIRAEKNTSSMYEVSF 120
OY 121 TPFRAQIGPEVHLEADKAIIVHISPGTKDSVMALDGLSFTYSLIMKNSGVEERI 180
DB 121 TPFRAQIGPEVHLEADKAIIVHISPGTKDSVMALDGLSFTYSLIMKNSGVEERI 180
OY 181 ENISRHRKIYKLSPEITTCYCKVKAALLTSMKIGVSPVHCITVTENEL 229
DB 181 ENISRHRKIYKLSPEITTCYCKVKAALLTSMKIGVSPVHCITVTENEL 229

DB 181 ENIYSHKIKYKSPETTICLKAKAALLTSMKIGVISPVCIKTTVENEL 229

RESULT 8

US-08-307-588-4
Sequence 4, Application US/08307588

Patent No. 5919453

GENERAL INFORMATION:

APPLICANT: BENOIT, Patrick

APPLICANT: MEYER, Francois

APPLICANT: MAGUIRE, Deborah

APPLICANT: PLAVEC, Ivan

APPLICANT: TOVEY, Michael G.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

TITLE OF INVENTION: INTERFERON

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/307,588

FILING DATE: 05-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00770

FILING DATE: 30-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92400902.0

FILING DATE: 31-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Saxe, Bernhard D.

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 17283/117/GUPL

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

INFORMATION FOR SEQ. ID NO. 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-307-588-4

Query Match 100.0%; Score 1196; DB 2; Length 557;

Best Local Similarity 100.0%; Pred. No. 3,6e-126;

Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MMVVLGATTVLVANGPVLSAAGKMLKSPQKVEVDIIDNFTLRNRSDSESGVNT 60
DB 1 MMVVLGATTVLVANGPVLSAAGKMLKSPQKVEVDIIDNFTLRNRSDSESGVNT 60
DB 61 FSDYOKTGMNDWIKLSCGONITSTKCNFSLKLVYEEIKLRIRAEKENTSSWYEVDSF 120
DB 61 FSDYOKTGMNDWIKLSCGONITSTKCNFSLKLVYEEIKLRIRAEKENTSSWYEVDSF 120
DB 121 TPRKRAQIGPPEVHLAEADKAIVIHISPGTKDSVMALDGLSFTYSLLIMKNSGVEERI 180
DB 121 TPRKRAQIGPPEVHLAEADKAIVIHISPGTKDSVMALDGLSFTYSLLIMKNSGVEERI 180
DB 181 ENIYSHKIKYKSPETTICLKAKAALLTSMKIGVISPVCIKTTVENEL 229
DB 181 ENIYSHKIKYKSPETTICLKAKAALLTSMKIGVISPVCIKTTVENEL 229

RESULT 9

PCT-US94-14277-3
Sequence 3, Application PC/TUS9414277

GENERAL INFORMATION:

APPLICANT: Aguet, Michel

APPLICANT: Bohni, Ruth

APPLICANT: Hemmi, Silvio

TITLE OF INVENTION: Receptor Subunit Polypeptides

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/14277

FILING DATE: 07-DEC-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/164596

FILING DATE: 09-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: 866PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5530

TELEFAX: 415/952-9881

INFORMATION FOR SEQ. ID NO. 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 202 amino acids

TYPE: amino acid

TOPOLOGY: linear

PCT-US94-14277-3

Query Match 41.0%; Score 490.5; DB 4; Length 202;

Best Local Similarity 48.5%; Pred. No. 1.9e-47;

Matches 98; Conservative 34; Mismatches 69; Indels 1; Gaps 1;

DB 28 KNLKSPQKVEVDIIDNFTLRNRSDSESGVNTFSDYOKTGMNDWIKLSCGONITSTK 87
DB 1 ENLKRPENIDXTIIDNFTLRNRSDSESGVNTFSDYOKTGMNDWIKLSCGONITSTK 60
DB 88 NFSSKLVYEEIKLRIRAEKEN-TSSWYEVDSFTPRKRAQIGPPEVHLAEADKAIVIH 146
DB 61 EHSILDTNXXIKTQPRVRAEENSGTSMNVEDPFIPTAHMSPEVRLEREDKALIVH 120
DB 147 SPGTDVSMALDGLSFTYSLLIMKNSGVEERINISRHIIYKSPETTICLKAKAAL 206
DB 121 SPGGDGNMMALEKPSFSTIRIMQKSSDKKTINSTYVEKIPLLPBTYYCLXKAIH 180
DB 207 LPSMKIGVISPVCIKTTVENE 228
DB 181 PSLKHSNXTXQCIISTIVANK 202

RESULT 10
US-08-683-743-4
Sequence 4, Application US/08683743
Patent No. 5843697
GENERAL INFORMATION:
APPLICANT: Pestka, Sidney

APPLICANT: Kotenko, Sergei
TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,743
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FRAGMENT TYPE:
US-08-683-743-4

Query Match 18.6% Score 222.5; DB 2; Length 325;
Best Local Similarity 30.3%; Pred. No. 5.6e-17;
Matches 66; Conservative 40; Mismatches 93; Indels 19; Gaps 8;
QY 19 WVLAAAGGKRLKLS-----PKVEVDIDDFILRMNRSDSVGNVTFSPDYOKTGM 71
DB 3 WSLGSMGLGGLVLSALGMVPPENVRMNSVFNKNIQWESPAPAKGLTTTAAQY----LS 58
QY 72 NWKLGSCONITSTKCNFSSLKLVYEELKRIAE-KENTSSWYEVDSFTPRKAQIGP 130
DB 59 YRIFODKCMNTLTLEDFFSS--LSKYGDHTLRVRAEFADHSDVMNI-FTCPVDOTIIGP 115
QY 131 PEVHLEA-EDKAIVIHSPKTSV--MMALDGL--SFTYSLLLWKNSSGVEEIEINYSR 186
DB 116 PGMOVEVLADSLHMRFLAPTEIENEYETWTKNKNYNSMTYVWQYKNGDEKFIPTQYDF 175
QY 187 HKIYKLSPEPTYCLKVKAALLTSMKIGVSPVHCITKT 224
DB 176 EVLRNLEPMTTYCVYRGFLPDRNKAQEMSEPCQET 213

RESULT 11
PCT-US94-14277-2
Sequence 2, Application PC/TUS9414277
GENERAL INFORMATION:
APPLICANT: Aguet, Michel
APPLICANT: Bohni, Ruth
APPLICANT: Hemmi, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-2

Query Match 17.0% Score 203; DB 4; Length 332;
Best Local Similarity 30.1%; Pred. No. 9.1e-15;
Matches 69; Conservative 38; Mismatches 86; Indels 36; Gaps 13;
QY 21 LSAAGG---NLKSPKVEVDIDDFILRMNRSDS-----VGNVTFSPDYOKTGM 70
DB 16 LGAASSPDSFSQLAAPLNPRHLVNDQILTWEPSPSNDPRPVYQVEISF-----I 69
QY 71 D-NWIKL--SGCONITSTKCNFSS--LKNLYE-EIKRIAEKN-TSSWYEVDSFTP 122
DB 70 DQSMHRLLEPNCIDITETKCDLTGGGRKLPHPPTVFLRVAKKGNLTSKVWGLEPQH 129
QY 123 FKAQIGPE-VHLEADKAIYIHSPTKDSVMMALDGLSFTYSLLLWKNSSGVEEIE 181
DB 130 YENVYVGPKNISVTVPKGSLVIHFSPPD-----VFHGAIFQYLVHYWKSETOQEOVE 184
QY 182 NIYSRHKIY--KLSPETTYCLKVKAAL-LTSWKI--GVSPVHCITKT 224
DB 185 GPFKNSIYGLKRLKRYRYCLOTEAQLLKNKKIRPHOLLSVSCHETT 233

RESULT 12
PCT-US94-14277-6
Sequence 6, Application PC/TUS9414277
GENERAL INFORMATION:
APPLICANT: Aguet, Michel
APPLICANT: Bohni, Ruth
APPLICANT: Hemmi, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/64596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-6

Query Match 16.1%; Score 192; DB 4; Length 223;
Best Local Similarity 29.6%; Pred. No. 8.5e-14;
Matches 64; Conservative 37; Mismatches 83; Indels 32; Gaps 12;

OY 30 LKSPQKEVDIIDNFIEMNRSDS-----VGNVTFSEDTQKGM-D-NWIKL--SGGQ 80
DB 10 LARPLNRLHLNDEOILWEPSPSSNDPRVYOVESF-----IDSMHRLLEPNT 63
OY 81 NITSPKCNFS--LKLNYE-EIKLRIRAKEN-TSSWYEVDSFTPFKAQIGPE-VH 134
DB 64 DITFKCDLGGGRKLFPFTVFLVRARAKGNLTSKMGVLEPQHYENVTGSPKXNS 123
OY 135 LEAEKAIYHISPTKDSVMALDGLSTYSLIMKNSGVEERIENTYSHKTY--KL 192
DB 124 VPPGKSLVHNSPPED-----VFHGATFOYLWHYWEKSETOOEVEGPKNSIYLGNL 178
OY 193 SPETTYCLKVKAAL-LTSMKI---GVYSPVHCITTT 224
DB 179 KPRVYCIOTERQILIKKIRPHGLLSNVSCHEIT 214

RESULT 13
US-08-943-087-2
Sequence 2, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Rho, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Fairah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943.087
FILING DATE:

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-2

Query Match 15.4%; Score 184.5; DB 2; Length 553;
Best Local Similarity 26.3%; Pred. No. 2.4e-12;
Matches 55; Conservative 38; Mismatches 95; Indels 21; Gaps 7;

OY 11 LVLVAVGPM-VLSAAGKNLKSPQKEVDIIDNFIEMNRSDSEVG-NVTFSPDYQK 67
DB 18 LLLLAAPWGAIVPCVSGG--LPRKANITFSLINKKNVLTPTPEGLOGVYVTTVOYFI 75
OY 68 TGMNMIKLSGCONITSTKCNFSSIKLVYEIKLRIRAKEN-TSSWYEVDSFTPFKA 126
DB 76 YGKKWKLKSCBINNRITCDLSAETSDYEHQYAKVKAIMGTSCKMAESGRFPLET 135
OY 127 QIGPEVHLEAEKAIYHISPTK-----DSVMALDGLSTYSLIMKNSGVE 177
DB 136 QIGPEVALITDEXISVLTAPKWKRPEDLPVSMOIIYSNLKYNVSVLNTKSNRTWS 195
OY 178 ERIENTYSHKTYK--LSPETTYCLKVKA 204
DB 196 QCVTN---HTLVLTWLEPNTLYCVHVES 220

RESULT 14
US-08-943-087-14
Sequence 14, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Rho, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Fairah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943.087
FILING DATE:
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-14

Query Match 15.4%; Score 184.5; DB 2; Length 553;
Best Local Similarity 26.3%; Pred. No. 2.4e-12;
Matches 55; Conservative 38; Mismatches 95; Indels 21; Gaps 7;
OY 11 LVLVAVGPW--VLSAAGGNLKSPOKVEVDIIDNFILRMNRSDSVG-NYTFSPDYOK 67
DB 18 LLLLAAPFGRAVPCVSGG--LPKPANITFLSINKKNVLOMPPELGQVAVTVVOYFI 75
OY 68 TGMDMWIKLSCGONITSTKCNFSSILKNVEEIKLRIR-ERENTSSWEYVDSFTPRKA 126
DB 76 YGOKWLNKSECRNINRTYCDLSAETSDEHQYAKVKAIMGTKCKMAESGRFPFLET 135
OY 127 QIGPEVHLEADKAIVHISPGTK-----DSVMALDGLSTFTYSLIMKSSGVE 177
DB 136 QIGPEVALTTDEKISIVLTAPKWKRNPEDLPVSMQIYSNLKYNVSVLNTKSNRTWS 195
OY 178 ERIENIYSRHKIYK--LSPETTYCLKVKA 204
DB 196 QCVTN---HTLVLTWLEPNTLYCVHVES 220

RESULT 15
US-08-943-087-16
Sequence 16, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:
APPLICANT: Lok, SI
APPLICANT: Kho, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-16

Query Match 15.4%; Score 184.5; DB 2; Length 553;
Best Local Similarity 26.3%; Pred. No. 2.4e-12;
Matches 55; Conservative 38; Mismatches 95; Indels 21; Gaps 7;
OY 11 LVLVAVGPW--VLSAAGGNLKSPOKVEVDIIDNFILRMNRSDSVG-NYTFSPDYOK 67
DB 18 LLLLAAPFGRAVPCVSGG--LPKPANITFLSINKKNVLOMPPELGQVAVTVVOYFI 75
OY 68 TGMDMWIKLSCGONITSTKCNFSSILKNVEEIKLRIR-ERENTSSWEYVDSFTPRKA 126
DB 76 YGOKWLNKSECRNINRTYCDLSAETSDEHQYAKVKAIMGTKCKMAESGRFPFLET 135
OY 127 QIGPEVHLEADKAIVHISPGTK-----DSVMALDGLSTFTYSLIMKSSGVE 177
DB 136 QIGPEVALTTDEKISIVLTAPKWKRNPEDLPVSMQIYSNLKYNVSVLNTKSNRTWS 195
OY 178 ERIENIYSRHKIYK--LSPETTYCLKVKA 204
DB 196 QCVTN---HTLVLTWLEPNTLYCVHVES 220

Search completed: June 1, 2000, 04:17:55
Job time: 15449 sec


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RESULT 2
527387
Interferon alpha receptor type 1 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S27387; S33770
C:Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
A:Title: Specific antiviral activities of the human alpha interferons are determined at
A:Reference number: S27387; MUID:93076908
A:Accession: S27387
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-560 <M0U>
A:Cross-references: EMBL:X68443; NID:9431; PIDN:CAA48484.1; PID:9432
A:Experimental source: MDRK cells
R:Lim, J.K.; Langer, J.A.
Biochim. Biophys. Acta 1173, 314-319, 1993
A:Title: Cloning and characterization of a bovine alpha interferon receptor.
A:Reference number: S33770; MUID:93305725
A:Accession: S33770
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-421, 'V', 423-560 <LIM>
A:Cross-references: EMBL:I06320; NID:9163187; PIDN:AAA02571.1; PID:9163188
A:Experimental source: Lung
C:Keywords: antiviral; cytokine receptor; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-560/Product: Interferon alpha receptor type 1 #status predicted <MAY>

Query Match 65.4%; Score 782.5; DB 2; Length 560;
Best Local Similarity 67.1%; Pred. No. 6,5e-61;
Matches 155; Conservative 31; Mismatches 40; Indels 5; Gaps 5;

Oy 2 MVLIGATTLVAVGVWVLSAAGGNLKSPOKVEVDIIDNFIILRNKSDSGVNTF 61
Db 1 MLALIGATTLMLVA-GRWVLPASGEANIK-PENVEIHIIDNFIILRNKSSSESVKNTF 58

Oy 62 SFDOYKTMGMNWKILSGCQNTSTKCNFSSILK-LNVEEIKLRRAEK-ENTSSMYEVSF 119
Db 59 SADIQIILDTDMWKILSGCQNTSTKCNFSSVLEWVEKIEIRRAEGNNTSTWYVEP 118

Oy 120 FTFRKAOIGPPEVHLAEADKAIVIHIS-PTGKDSVMALDGLSTFYSLILKNSGVVEE 178
Db 119 FVPELEAIGPPVHLAEADKAIIISIPGKDSIMAMDRSSPRISVYIMKNSSLDE 178

Oy 179 RIENIYSRHKIYKLSPEPTYCLKVAALLTSWKIGVSPVHCITTVENEL 229
Db 179 RTEIYVPEDKIYKLSPEITYCLKVAELRLQSRVGCSPVYCINTTERHKV 229

RESULT 3
A45283
Interferon alpha/beta receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A45283; I48423; I48425; I48426; I48427; I48428; I48429
R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
A:Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homosp
A:Reference number: A45283; MUID:92262522
A:Accession: A45283
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-590 <UZE>
A:Cross-references: GB:M8961; NID:9194111; PIDN:AAA37890.1; PID:9194112
A:Note: sequence extracted from NCBI backbone (NCBIN:102354, NCBIPI:102357)
R:Lutfalla, G.; Uze, G.
Gene 148, 343-346, 1994
A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-fre
A:Reference number: I48423; MUID:95047447
```

```
A:Accession: I48423
A:Status: preliminary; translated from GB/EMBL/DBSJ
A:Molecule type: DNA
A:Residues: 118-125 <RS>
A:Cross-references: EMBL:U06237; NID:9497103; PIDN:AAA65003.1; PID:9755810
A:Accession: I48424
A:Status: preliminary; translated from GB/EMBL/DBSJ
A:Molecule type: DNA
A:Residues: 127-224 <RE2>
A:Cross-references: EMBL:U06238; NID:9497104; PIDN:AAC01749.1; PID:9755811
A:Accession: I48425
A:Status: preliminary; translated from GB/EMBL/DBSJ
A:Molecule type: DNA
A:Residues: 243-264 <RE3>
A:Cross-references: EMBL:U06239; NID:9497106; PIDN:AAA65004.1; PID:9510261
A:Accession: I48426
A:Status: preliminary; translated from GB/EMBL/DBSJ
A:Molecule type: DNA
A:Residues: 265-375 <RE4>
A:Cross-references: EMBL:U06240; NID:9497108; PIDN:AAA65005.1; PID:9510262
A:Accession: I48427
A:Status: preliminary; translated from GB/EMBL/DBSJ
A:Molecule type: DNA
A:Residues: 397-424 <RE5>
A:Cross-references: EMBL:U06241; NID:9497110; PIDN:AAA65006.1; PID:9755812
A:Accession: I48428
A:Status: preliminary; translated from GB/EMBL/DBSJ
A:Molecule type: DNA
A:Residues: 426-445 <RE6>
A:Cross-references: EMBL:U06242; NID:9497112; PIDN:AAA65007.1; PID:9755813
A:Accession: I48429
A:Status: preliminary; translated from GB/EMBL/DBSJ
A:Molecule type: DNA
A:Residues: 473-590 <RE7>
A:Cross-references: EMBL:U06244; NID:9497114; PIDN:AAA65008.1; PID:9510265
C:Genetics:
A:Gene: IFNAR
A:Introns: 177/3; 331/1
C:Keywords: cytokine receptor; transmembrane protein

Query Match 50.2%; Score 600.5; DB 2; Length 590;
Best Local Similarity 52.0%; Pred. No. 6,4e-45;
Matches 119; Conservative 40; Mismatches 69; Indels 1; Gaps 1;

Oy 2 MVLIGATTLVAVGVWVLSAAGGNLKSPOKVEVDIIDNFIILRNKSDSGVNTF 61
Db 1 MLAVGAAALVAVAGAVWVLPASAGENLKPENIDYIIDIIDNFIILRNKSSHGSGSVTF 60

Oy 62 SFDOYKTMGMNWKILSGCQNTSTKCNFSSILK-LNVEEIKLRRAEK-ENTSSMYEVSF 120
Db 61 SAERTKDEAKWLKVPQCQTTTTCFSLDINVIKIOFRABEGNNTSSMNEVDFP 120

Oy 121 TFRKAOIGPPEVHLAEADKAIVIHIS-PTGKDSVMALDGLSTFYSLILKNSGVVEE 180
Db 121 IPEYTAHMSPEVHLAEADKAIIIVHISPPGQDNNMALPEPSYIRIRWOKSSSDKTI 180

Oy 181 ENIYSRHKIYKLSPEPTYCLKVAALLTSWKIGVSPVHCITTVENEL 229
Db 181 NSTIYKIEIPELLPEPTYCLEVKAHPSLKHSHSVIVOCISTTVANKM 229

RESULT 4
G01418
Cytokine receptor family II, member 4 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C:Accession: G01418
R:Lutfalla, G.
submitted to the EMBL Data Library, April 1994
A:Reference number: G06935
A:Accession: G01418
A:Status: preliminary; translated from GB/EMBL/DBSJ
```


OY 182 NIYSRHKIY--KLSPETTYCLKVKAAL-LTSWKI--GVYSPHCITKT 224
 DB 185 GPFKNSIYLGNLKRPYVYCIQTEAQLILKNKKIRPHGLLSVSCHEET 233

RESULT 8
 138500

Interferon gamma receptor accessory factor-1 precursor - human

C:Species: Homo sapiens (man)

C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 05-Nov-1999

C:Accession: 138500; 138501

R:Son, J.; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S.

Cell 76, 793-802, 1994

A:Title: Identification and sequence of an accessory factor required for activation of

A:Reference number: A4946; MUID:941170380

A:Accession: 138500

A:Molecule type: mRNA

A:Residues: 1-337 <RES>

A:Cross-references: EMBL:U05875; NID:9463549; PIDN:AAA16955.1; PID:9463550

A:Experimental source: clone pSK1

A:Accession: 138501

A:Molecule type: mRNA

A:Residues: 1-63, 'Q', 65-337 <RES2>

A:Cross-references: EMBL:U05877; NID:9463551; PIDN:AAA16956.1; PID:9463552

A:Experimental source: clone pJS3

C:Genetics:

A:Map position: 21

C:Keywords: cytokine receptor

Query Match 12.7%; Score 151.5; DB 2; Length 337;

Best Local Similarity 24.6%; Pred. No. 7.3e-06;

Matches 61; Conservative 44; Mismatches 94; Indels 49; Gaps 13;

OY 12 VLVANGPWLAAAG---KNLSPQKVEVDIIDNFIIRW-----NRSDSVGNVTF 62

DB 9 LILLGVFAAAAPDPLSQLPAQHPIRLYNAEQVLSWBPVALNSTREVVYRVQFK 68

OY 63 FDYQKTDGMDNWKLS-----GCONITSPKCNFS-----LKLNYEEIKLRIRAEK 108

DB 69 YIDSK-----WFTADIMSGVNCOTITARECFTTASPAGPMDPNV---TLRLRAEL 119

OY 109 ENT-SSWEVDSTFPRKNAQIGPPEVHLE--AEDKAIYHISPGTKDSVMALDGLSFT 164

DB 120 GALHSAWMTMPWFQHYRNVTVGPPE-NIEVTEGEGSLIRFSSPDIDTSTAF---FC 174

OY 165 YELLIMKSSGVEERENIYSRHKIY--KLSPETTYCLKVKAALLTS---WKIGVSPV 218

DB 175 YVVAHWE--KGGIQOVKGFPRNSISLNDLKPSRYCLOVQALIMKNSNIFRVGLHSNI 232

OY 219 HCIKTIVE 226

DB 233 SCYETMAD 240

RESULT 9

A31555

Interferon gamma receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Jul-1999

C:Accession: A31555

C:Agnet, M.; Demblic, Z.; Merlin, G.

Cell 55, 273-280, 1988

A:Title: Molecular cloning and expression of the human interferon-gamma receptor.

A:Reference number: A31555; MUID:89003065

A:Accession: A31555

A:Molecule type: mRNA

A:Residues: 1-489 <AG>

A:Cross-references: GB:J03143; NID:9184650; PIDN:AAA52731.1; PID:9306915

C:Genetics:

A:Gene: GDB:IFNGR1; IFNGR

A:Cross-references: GDB:120688; OMIM:107470

A:Map position: 6q23-6q24
 C:Superfamily: Interferon gamma receptor
 C:Keywords: cytokine receptor; transmembrane protein

Query Match 9.8%; Score 117.5; DB 2; Length 489;
 Best Local Similarity 22.6%; Pred. No. 0.011;
 Matches 52; Conservative 44; Mismatches 99; Indels 35; Gaps 8;

OY 3 VILGATVILVANGPVLAA--AGCKNLKSPQKVEVDIIDNFIIRWNSDESQGVN-T 60

DB 1 MALFLPLVWQGVSRKEMGTADLGPSSVPTPIVNTIESINMFIWERY--QIMPOVPV 58

OY 61 FSPDYQKTDGMDNWKLSGCONITSPKCNFSLSKLNYEEIKLRIRAE--EKENTSSWVEY 117

DB 59 FTVEVKVYGVKNSMIDACINISHYCNINIDHGDPSNLMVRKAVGQKE--SAVAKS 116

OY 118 DSFTFPRKNAQIGPPEVHLEADKAIYHIT-----SFGTK-----DSVMW 136

DB 117 EEFAVCRDGIKGPDKLDIRKEEKOIMIDIRHPSVFNVDGEVDYDEITCYIRVNVVY 176

OY 157 ALDGLSTYSLLIMKSSGVEERENIYSRHKIYKLSPETTYCLKVKAAL 206

DB 177 RMNSSEIQYKILTK-----EDDCDEIQCOLAIPVSLNSQYCSAGCVL 221

RESULT 10

A34368

Interferon gamma receptor precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 23-Jul-1999

C:Accession: A34368; A34468; A34423; A34508; A36224; I48941

R:Kumar, C.S.; Muthukumar, G.; Frost, L.J.; Noe, M.; Ahn, Y.H.; Mariano, T.M.; Pes

J. Biol. Chem. 264, 17939-17946, 1989

A:Title: Molecular characterization of the murine interferon gamma receptor cDNA.

A:Reference number: A34368; MUID:90036866

A:Accession: A34368

A:Molecule type: mRNA

A:Status: preliminary

A:Residues: 1-477 <KMG>

A:Cross-references: GB:M25764; NID:9197962; PIDN:AAA39177.1; PID:9309393

R:Cofano, F.; Moore, S.K.; Tanaka, S.; Yuhki, N.; Landolfo, S.; Appella, E.

J. Biol. Chem. 265, 4064-4071, 1990

A:Title: Affinity purification, peptide analysis, and cDNA sequence of the mouse int.

A:Reference number: A34468; MUID:90154099

A:Accession: A34468

A:Molecule type: mRNA

A:Residues: 1-477 <COE>

A:Cross-references: GB:M26711; NID:9194126; PIDN:AAA37896.1; PID:9309330

R:Gray, P.W.; Leong, S.; Fennle, E.H.; Farrer, M.A.; Pingel, J.T.; Fernandez-Luna, J

Proc. Natl. Acad. Sci. U.S.A. 86, 8497-8501, 1989

A:Title: Cloning and expression of the cDNA for the murine interferon gamma receptor

A:Reference number: A34423; MUID:90046824

A:Accession: A34423

A:Molecule type: mRNA

A:Status: preliminary

A:Residues: 1-94, 'E', 96-477 <GRA>

A:Cross-references: GB:M28333; NID:9194131; PIDN:AAA37898.1; PID:9309331

R:Munro, S.; Maniatis, T.

Proc. Natl. Acad. Sci. U.S.A. 86, 9248-9252, 1989

A:Title: Expression cloning of the murine interferon gamma receptor cDNA.

A:Reference number: A36224; MUID:90083245

A:Accession: A36224

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 10-477 <MUN>
A:Cross-references: GB:M88995; NID:g194123; PIDN:AAA37895.1; PID:g309329
R:Raval, P.; Odick, S.; Russell, S.W.; Murphy, W.J.
Gene 154, 219-223, 1995
A:Title: Characterization of the 5' flanking region and gene encoding the mouse interferon
A:Reference number: I48941; MUID:95197006
A:Accession: I48941
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <RES>
A:Cross-references: EMBL:U05960; NID:q454092; PIDN:AAA08090.1; PID:g454093
C:Superfamily: interferon gamma receptor
C:Keywords: cytokine receptor; transmembrane protein

	Query Match	8.6%	Score 102.5	DB 2,	Length 477,
	Best Local Similarity	22.9%	Pred No. 0.23,		
	Matches	54,	Conservative	38;	Mismatches 87; Indels 57; Gaps 14.
OY	8 ATTTLVAVGPWVISAAAGKNLKS--PQKVEVDIIDNFLRNRSDSEGVNFTSFD	64			
Db	7 AGRMILTV--LMLSAKVGSGALTSTEDPEPSVPPTVLIKSYRL-----NPVVCME	58			
OY	65 YQ-----RTGMDNWIKLSGCCORITSTKGFSSLLKNVYEIR-----LRIR	105			
Db	59 YQMSQTPIFYOVVVYSSW---TDSCTNISDHC-----NTIQIMTPDVSAMARAK	109			
OY	106 AE-KENTSSWEVDSFTRPKAIGPP-EVHLAEADKAIVIHISP-----GTKDSVMA	157			
Db	110 AKVGCKEDYARKKEFLMCLKGKGGPPGLEIRRKKEQLSVLFHPDEVVANGESQGTMG	169			
OY	158 LDG---LSFTYELLIMKNSSGVEERENYSRHRIKSLSPETTYC-LTKRAALLTS	209			
Db	170 -DGSCITYTFDIYVVEHNRSQ----EIIHTHYIYEKEECNEFLTCNLINVSFTDS	219			

```

RESULT 11
T27934
hypothetical protein ZK617.1a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T27934; T28030
R:White, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20442
A:Accession: T27934
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6831 <WT>
A:Cross-references: EMBL:Z73897; PIDN:CAA98064.1; GSPDB:GN00022; CESP:ZK617.1a
A:Experimental source: clone ZK617
R:Harris, B.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20458
A:Accession: T28030
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6831 <WT>
A:Cross-references: EMBL:Z73899; PIDN:CAA98081.1; GSPDB:GN00022; CESP:ZK617.1a
A:Experimental source: clone ZK629
C:Genetics:
A:Gene: CESP:ZK617.1a
A:Map position: 4
A:Introns: 10/3; 61/3; 135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 542/3; 574/3; 581/4/3; 6683/3; 6768/1; 6800/3

```

Query Match	8.2%	Score 97.5;	DB 2;	Length 6831;
Best Local Similarity	22.8%;	Pred. No. 21;		
Matches 44;	Conservative 22;	Mismatches 74;	Indels 53;	Gaps 10

OY	30	LKSPQK----	VEV-DIIDDNFILRANNSDSDSVNMFSPFYOK--TGMDXWIKLSGONJ	82
Dd	1886	LDRSKENGPLEYSDFVEDLNLNSMKFPDDGGEPLEIYEVELKDITATGMVP----	CARY	1912
OY	83	TSTKCNFSSKLNYEEIKLRIR-	EKENTSWEYDSFTPFKAIOIGPPEVHLEADKA	141
Dd	1913	KDTAKAHIDGLKK--GYOFRVKAVNKEGASDALSTDKTKANPYDEPKT-----		1963
OY	142	IYIHISGTAKDSVMALDGLSFTYSLILW--KNSSQVEERENIYSRKHITYLSPETTY		198
Dd	1963	-----GTPYVDMDADRVS-----LEWEPKPSDG-----APITOY		1993
OY	199	CLKVKALLTSNMK	211	
Dd	1994	VIEKKGHGRDMQ	2006	

```

RESULT 12
S57242
twichln - Caenorhabditis elegans
N:Alternate names: myosin-regulating protein
N:Contains: protein kinase (EC 2.7.1.-)
C:Species: Caenorhabditis elegans
C:Date: 28-Oct-1995 #sequence-revision 24-Oct-1997 #ext-change 18-Jun-1999
C:Accession: S57242; S07571; S06797; S57218
R:Benlian, G.M.; L'Hernault, S.W.; Morris, M.E.
submitted to the EMBL Data Library, February 1993
A:Description: Additional sequence complexity within twichling of Caenorhabditis elegans
A:Reference number: S57242
A:Accession: S57242
A:Molecule type: DNA
A:Residues: 1-6839 <BEN1>
A:Cross-references: EMBL:LI0351
A:Experimental source: var. Bristol
R:Benlian, G.
submitted to the EMBL Data Library, November 1989
A:Reference number: S07571

```

A:Cross-references: EMBL:X15423; NID:g68997; PIDN:CAA33463.1; PID:68898
A:Experimental source: Var. Bristol
R:Benlian, G.M.; Kiff, J.E.; Neckelmann, N.; Moerman, D.G.; Waterston, R.H.
Nature 342, 45-50, 1989
A:Title: Sequence of an unusually large protein implicated in regulation of myosin
A:Reference number: 506797; MID:90044042
A:Accession: S06797
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 806-1175; 1178-1998, 'Y', 2000-3040, 'I', 3042-3335, 'I', 3337-5693; 5696-6359
A:Cross-references: EMBL:X15423
A:Experimental source: Var. Bristol
R:Benlian, G.M.; L'Hernault, S.W.; Morris, M.E.
Genetics 134, 1097-1104, 1993
A:Title: Additional sequence complexity in the muscle gene, unc-22, and its encoded
A:Reference number: 557218; MID:93387604
A:Accession: S57218
A:Molecule type: DNA
A:Residues: 2-99; 108-194, 'O', 196-206; 374-468; 658-753 <BEN4>
A:Experimental source: Var. Bristol
A:Comment: Lack of unc-22 leads to a constant twitching of the body muscles.
A:Genetics: unc-22
A:Gene: unc-22
A:Map position: IV
A:Intons: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/
152/3; 6691/3; 6776/1; 6808/3
A:Superfamily: twitchin, fibronectin type III repeat homology; immunoglobulin homology;
C:Keywords: ATP; autophosphorylation; duplication; muscle; phosphotransferase; ser;
E:806-888, 899-990, 991-1083, 1084-1175, 1178-1273, 1474-1567, 1770-1864, 2066-2158, 2358-
96-5790, 6283-6356, 6386-6478, 6541-6635, 6649-6742, 6745-6838/Region: motif 2
E:1274-1372, 1373-1473, 1568-1670, 1671-1769, 1865-1964, 1965-2065, 2159-2258, 2259-2357,
23, 4215-4313, 4314-4415, 4416-4516, 4612-4710, 4711-4811, 4908-5009, 5010-5109, 5110-5210/
E:3540-6197/Domains: protein kinase homology <Kin>

F:5948-5956/Region: protein kinase ATP-binding motif
F:5971/Active site: Lys #status predicted

Query Match 8.2%; Score 97.5; DB 2; Length 6839;
Best Local Similarity 22.8%; Pred. No. 21;
Matches 44; Conservative 22; Mismatches 74; Indels 53; Gaps 10;
OY 30 LKSPK-----VEV-DIIDNFIILNRNRSDESGNTFSDYOK--TGMDNWKLSGCONI 82
DB 1864 LDRPSKPNGLPEVSDVEFDNLNLSKPPDDGGEPIEYVEKLDATGRWVP---CAKV 1920
OY 83 TSTKCNFSLKLNVEEIKLRIR-A-EKENTSSMYEVDSTPPRKAQIGPVEHLAEADKA 141
DB 1921 KDTKAHIGLKKG--QYQFRKATNKEGASDALSTDKTKAKNPYDEGKT----- 1971
OY 142 IVIHISPTKDSVMALDGLSTFYSLILW--KNSSGVEERIENTYSRHKIKYLSPEPTY 198
DB 1971 -----GTPDYVDMDADNRVS-----LEWEPPKSDG-----APITQY 2001
OY 199 CLKVKAALLTSWK 211
DB 2002 VIEKKGKHGRMW 2014

RESULT 13
T27935
hypotheetical protein ZK617.1b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T27935; T28031
R:White, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20442
A:Accession: T27935
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7160 <M12>
A:Cross-references: EMBL:Z73897; PIDN:CAA98065.1; GSPDB:GN00022; CESP:ZK617.1b
A:Experimental source: clone ZK617
R:Haris, B.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20458
A:Accession: T28031
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7160 <M12>
A:Cross-references: EMBL:Z73899; PIDN:CAA98082.1; GSPDB:GN00022; CESP:ZK617.1b
A:Experimental source: clone ZK829
C:Genetics:
A:Gene: CESP:ZK617.1b
A:Map position: 4
A:Introns: 10/3; 61/3; 135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 542/3; 574/3; 59
3067/1; 3141/3; 3269/1; 6473/3; 7012/3; 7097/1; 7129/3

Query Match 8.2%; Score 97.5; DB 2; Length 7160;
Best Local Similarity 22.8%; Pred. No. 22;
Matches 44; Conservative 22; Mismatches 74; Indels 53; Gaps 10;
OY 30 LKSPK-----VEV-DIIDNFIILNRNRSDESGNTFSDYOK--TGMDNWKLSGCONI 82
DB 2185 LDRPSKPNGLPEVSDVEFDNLNLSKPPDDGGEPIEYVEKLDATGRWVP---CAKV 2241
OY 83 TSTKCNFSLKLNVEEIKLRIR-A-EKENTSSMYEVDSTPPRKAQIGPVEHLAEADKA 141
DB 2242 KDTKAHIGLKKG--QYQFRKATNKEGASDALSTDKTKAKNPYDEGKT----- 2292
OY 142 IVIHISPTKDSVMALDGLSTFYSLILW--KNSSGVEERIENTYSRHKIKYLSPEPTY 198
DB 2292 -----GTPDYVDMDADNRVS-----LEWEPPKSDG-----APITQY 2322
OY 199 CLKVKAALLTSWK 211

DB 2323 VIEKKGKHGRMW 2335

RESULT 14
A49667
Interleukin-10 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: A49667
R:Ho, A.S.; Liu, Y.; Khan, T.A.; Hsu, D.H.; Bazan, J.F.; Moore, K.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 11267-11271, 1993
A:Title: A receptor for interleukin 10 is related to interferon receptors.
A:Reference number: A49667; MUID:94068585
A:Accession: A49667
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-575 <RES>
A:Cross-references: GB:L12120; NID:g437615; PIDN:AAA16156.1; PID:g437616
C:Genetics:
A:Gene: IL10R
C:Keywords: cytokine receptor

Query Match 8.0%; Score 95.5; DB 2; Length 575;
Best Local Similarity 20.5%; Pred. No. 1.2;
Matches 51; Conservative 39; Mismatches 98; Indels 61; Gaps 10;

OY 13 LVAVGPWYLSAAGCKNKSPOKYVEDIIDNFIILRW---NRSDESGNTFSDYOKT 68
DB 9 LVITSSLSLEFIAYGTLPSPSYVWFARFQHIHMKPIPNQSESTYIEVAL----KQY 64
OY 69 GMDWMKLSGCONITSTKCNFSLKLNVEE---IKRIR-A-EKENTSSMYEVDSTPPR 123
DB 65 GNSTWMDHICRKAQALSCDITFTLDYHRSYGRARVANDSOYSNMWTTTFRFT-- 123
OY 124 RKAQIGPVEHLAEADKAIVIHISPTKDSY-VMALDGLSTFYSLILWKNSSGVEERLEN 182
DB 123 -----VDEITL-----TVDSYTLKAMGIIIGTIHPRPRTTPAGDEYEQ 162
OY 183 IYSRHKIKYLS-----PBT-----TYCLVKAALLTSKIGYSP 217
DB 163 VFKDLRYKISIRFSELSKNATKRVKQETFTLVPIGVKFCVAVLPRLSRIKAWSE 222
OY 218 VHCITTYE 226
DB 223 EQCLITTE 231

RESULT 15
T29585
hypotheetical protein F55F8.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29585
R:Gallung, S.; Scheet, P.; Kemp, K.
submitted to the EMBL Data Library, November 1996
A:Description: The sequence of C. elegans cosmid f55f8.
A:Reference number: Z20647
A:Accession: T29585
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-925 <GAT>
A:Cross-references: EMBL:U80447; PIDN:AAH37807.1; GSPDB:GN00019; CESP:F55F8.3
A:Experimental source: strain Bristol N2; clone f55f8
C:Genetics:
A:Gene: CESP:F55F8.3
A:Map position: 1
A:Introns: 6/3; 44/2; 76/1; 109/2; 159/2; 204/3; 327/1; 469/3; 617/1; 775/1; 825/3;
Query Match 8.0%; Score 95.5; DB 2; Length 925;
Best Local Similarity 25.7%; Pred. No. 2.3;

	Matches	38,	Conservative	19,	Mismatches	70,	Indels	21,	Gaps	4,
OY	70	MDNMIKLSGCONIT--	STKCNFSSLKLANYEEI--	KLRIKRAEKENTSSMYEVDSEFTPEPK	125					
Db	1	MDTNFKLSMCITGYRDGQVAFSGKGYSVIS	IGNKLSIFDRLNNTSKTLDICDYNIKR		60					
OY	126	AOIGPPEVHLAEADKAIVHI-----	SPGTDSTYMAALDGLSFTY-----	SLI	168					
Db	61	LSISPSGYHLLASDEGVVHFPVHL	SEFKIYFRSRNKPIGSLQWSPDARTVAICRENDQ	120						
OY	169	IMKNSSGVEERIEIENYSRHKIKYLSPET	196							
Db	121	IHEFGKSIENKYNPNPSSLRTYKLSDS	148							

Search completed: June 1, 2000, 04:35:19
Job time: 14299 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:38:52 ; Search time 34.71 Seconds
(without alignments)
200.927 Million cell updates/sec

Title: US-09-240-675-2_COPY_1_229

Perfect score: 1196

Sequence: 1 MMYVLLGATTLVAVGPMV.....WKIGVSPHCIKTVENEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1196	100.0	557	1 INRL_HUMAN	P17181 homo sapien
2	782.5	65.4	560	1 INRL_BOVIN	O04730 bos taurus
3	765.5	64.0	560	1 INRL_SHEEP	Q28589 ovis aries
4	600.5	50.2	590	1 INRL_MOUSE	P33836 mus musculus
5	222.5	18.6	325	1 CRF4_HUMAN	O08334 homo sapien
6	151.5	12.7	337	1 INGS_HUMAN	P3260 homo sapien
7	117.5	9.8	489	1 INGR_HUMAN	P15260 homo sapien
8	102.5	8.6	477	1 INGR_MOUSE	P15261 mus musculus
9	95.5	8.0	575	1 I10R_MOUSE	O61172 mus musculus
10	95.5	8.0	925	1 PWP2_CAEEL	P31341 caenorhabdi
11	95.5	7.9	578	1 I10R_HUMAN	Q13651 homo sapien
12	92.5	7.7	292	1 TF_BOVIN	P10931 bos taurus
13	92.5	7.7	295	1 TF_HUMAN	P13726 homo sapien
14	90.5	7.6	1304	1 CD45_HUMAN	P08575 homo sapien
15	90.5	7.5	315	1 6DCS_SOYBN	P26690 glycine max
16	89.5	7.5	530	1 INR2_BOVIN	Q55141 bos taurus
17	89.5	7.5	880	1 INR3_BOVIN	P51146 ratius norv
18	89.5	7.4	515	1 INR2_HUMAN	P48551 homo sapien
19	87.5	7.3	639	1 HS74_PARLI	O06248 paracentrot
20	86.5	7.2	2131	1 XCF2_SPIOL	P08973 spinnella ol
21	84.5	7.1	623	1 VGLR_VZVD	P09259 varicella-z
22	83.5	7.0	306	1 KI28_YEAST	P06242 saccharomyc
23	83.5	6.9	536	1 INR2_SHEEP	Q95207 ovis aries
24	83.5	6.9	335	1 CHM1_BOVIN	P17404 bos taurus
25	83.5	6.9	520	1 CP84_ARATH	Q42600 arabidopsi
26	82.5	6.9	1068	1 XCF0_MARPO	P12221 marchantia
27	82.5	6.9	515	1 I15R_MOUSE	P11183 mus musculus
28	82.5	6.9	517	1 KTR7_YEAST	P40504 saccharomyc
29	82.5	6.9	875	1 HIR2_YEAST	P32480 saccharomyc
30	81.5	6.8	292	1 TF_RABIT	P24053 oryctolagus
31	81.5	6.8	2054	1 XCF2_PINTH	P41653 pinus thunb
32	80.5	6.7	486	1 VN53_RORTH	P35424 human rotav
33	80.5	6.7	780	1 AFG2_YEAST	P32794 saccharomyc
34	80.5	6.7	878	1 IL3B_MOUSE	P26954 mus musculus

35	80	6.7	918	1 IL6B_HUMAN	P40189 homo sapien
36	80	6.7	993	1 EPB3_MOUSE	P54754 mus musculus
37	79.5	6.6	918	1 IL6B_RAT	P40190 ratius norv
38	79.5	6.6	442	1 THDF_MYCGE	P47254 mycoplasma
39	78.5	6.6	853	1 TGR3_RAT	P26342 ratius norv
40	78.5	6.6	896	1 CYRB_MOUSE	P26955 mus musculus
41	78.5	6.5	1124	1 TIR2_HUMAN	O02763 homo sapien
42	77.5	6.5	274	1 VC06_SPVKA	P32226 swinepox vi
43	77	6.4	377	1 MTC3_CHYNI	P10833 chlorella v
44	77	6.4	460	1 HEMO_RABIT	P20058 oryctolagus
45	77	6.4	537	1 IL2B_RAT	P26896 ratius norv

ALIGNMENTS

RESULT 1
INRL_HUMAN STANDARD: PRT; 557 AA.
AC P17181;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
GN IFNARI OR IFNAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
NC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90124632.
RA Use G., Lutfalla G., Gresser I.;
RT "Genetic transfer of a functional human interferon alpha receptor
into mouse cells: cloning and expression of its cDNA."
RL Cell 60:225-234(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92129376.
RA Lutfalla G., Gardiner K., Proudhon D., Vieh E., Use G.;
RT "The structure of the human interferon alpha/beta receptor gene."
RL J. Biol. Chem. 267:2802-2809(1992).
RN [3]
RP PHOSPHORYLATION BY TYK2.
RX MEDLINE: 95059042.
RA Colaninici O., Yan H., Domanski P., Handa R., Smalley D.,
RA Mollersman J., Witte M., Krishnan K., Krolewski J.;
RT "Direct binding to and tyrosine phosphorylation of the alpha subunit
of the type I interferon receptor by p135tyk2 tyrosine kinase."
RL Mol. Cell. Biol. 14:8133-8142(1994).
CC -I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
-I- I FEWS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
SUBUNITS THEMSELVES.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND
EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.
CC -I- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.
CC -I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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or send an email to license@isb-sib.ch).
DR EMBL: J03171; AAA52730.1; -
DR EMBL: X60459; CAA42992.1; -
DR PIR: A32694; A32694.
DR PIR: S17112; S17112.
DR MTM: 107450; -

KW Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;
 KM Phosphorylation.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 557 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 FT CHAIN 28 557 CHAIN.
 FT DOMAIN 28 436 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 437 457 POTENTIAL.
 FT DOMAIN 458 557 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 79 87 BY SIMILARITY.
 FT DISULFID 199 220 BY SIMILARITY.
 FT MOD_RES 466 466 PHOSPHORYLATION (BY TYR2) (PROBABLE).
 FT MOD_RES 481 481 PHOSPHORYLATION (BY TYR2) (PROBABLE).
 FT MOD_RES 50 50 POTENTIAL.
 FT CARBOHYD 51 51 POTENTIAL.
 FT CARBOHYD 81 81 POTENTIAL.
 FT CARBOHYD 88 88 POTENTIAL.
 FT CARBOHYD 110 110 POTENTIAL.
 FT CARBOHYD 172 172 POTENTIAL.
 FT CARBOHYD 254 254 POTENTIAL.
 FT CARBOHYD 313 313 POTENTIAL.
 FT CARBOHYD 314 314 POTENTIAL.
 FT CARBOHYD 376 376 POTENTIAL.
 FT CARBOHYD 415 415 POTENTIAL.
 FT CARBOHYD 433 433 POTENTIAL.
 FT VARIANT 168 168 L->V.
 FT VARIANT 168 168 /FTID-VAR_002717.
 FT CONFLICT 17 17 G->A (IN REF. 2).
 FT SEQUENCE 557 AA; 63525 MM; 0F6744C8A1ADB37 CMC64;

Query Match 100.0%; Score 1196; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 1,le-98;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MMYVLLGATTLVAVGPMVLSAAGGKNKSPQKVEVDIIDNFIILMNSDESQVNT 60
 Db 1 MMYVLLGATTLVAVGPMVLSAAGGKNKSPQKVEVDIIDNFIILMNSDESQVNT 60
 Oy 61 SFSDYQKGMNMIKLSGCONITSTKCNFSSSLKLVYEEIKLRIRAKENTSSWYEDSF 120
 Db 61 SFSDYQKGMNMIKLSGCONITSTKCNFSSSLKLVYEEIKLRIRAKENTSSWYEDSF 120
 Oy 121 TPFRKAQIGPPVHLAEADKAIVIHISPGTKDSVMALDGLSFTYSLIMKNSGVEERI 180
 Db 121 TPFRKAQIGPPVHLAEADKAIVIHISPGTKDSVMALDGLSFTYSLIMKNSGVEERI 180
 Oy 181 ENIYSRHKIYKLSPEITCYCLKVKAALLTSWKIGVSPVHCITVTENEL 229
 Db 181 ENIYSRHKIYKLSPEITCYCLKVKAALLTSWKIGVSPVHCITVTENEL 229
 RESULT 2
 INRL_BOVIN STANDARD: PRT: 560 AA.
 AC 004790.
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
 GN IFNAR1 OR IFNAR.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LUNG;
 RX MEDLINE: 93076908.
 RA Mouchel-Viehl E., Lutfalla G., Mogensen K.E., Uze G.;
 RT "Specific antiviral activities of the human alpha interferons are
 RT determined at the level of receptor (IFNAR) structure.";
 RL FEBS Lett. 313:255-259(1992).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE: 93076908.
 RA Mouchel-Viehl E., Langer J.A.;
 RT "Cloning and characterization of a bovine alpha interferon receptor.";
 RL Biochim. Biophys. Acta 1173:314-319(1993).
 CC -I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
 CC SUBUNITS THEMSELVES.
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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DR EMBL: X68443; CAA48484.1; -;
 DR EMBL: L06320; AAA02571.1; -;
 DR PIR: S33770; S33770.
 DR PIR: S27387; S27387.
 DR PIR: PF00041; fn3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 560 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 FT CHAIN 25 560 CHAIN.
 FT DOMAIN 25 437 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 438 458 POTENTIAL.
 FT DOMAIN 459 560 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 76 84 BY SIMILARITY.
 FT DISULFID 199 220 BY SIMILARITY.
 FT CARBOHYD 47 47 POTENTIAL.
 FT CARBOHYD 47 47 POTENTIAL.
 FT CARBOHYD 55 55 POTENTIAL.
 FT CARBOHYD 85 85 POTENTIAL.
 FT CARBOHYD 109 109 POTENTIAL.
 FT CARBOHYD 172 172 POTENTIAL.
 FT CARBOHYD 254 254 POTENTIAL.
 FT CARBOHYD 313 313 POTENTIAL.
 FT CARBOHYD 377 377 POTENTIAL.
 FT CARBOHYD 434 434 POTENTIAL.
 FT CONFLICT 422 422 F->V (IN REF. 2).
 FT SEQUENCE 560 AA; 63818 MM; 66D76B72861E1D11 CRC64;

Query Match 65.4%; Score 782.5; DB 1; Length 560;
 Best Local Similarity 67.1%; Pred. No. 5,4e-62;
 Matches 155; Conservative 31; Mismatches 40; Indels 5; Gaps 5;

Oy 2 MMYVLLGATTLVAVGPMVLSAAGGKNKSPQKVEVDIIDNFIILMNSDESQVNT 61
 Db 1 MMYVLLGATTLVAVGPMVLSAAGGKNKSPQKVEVDIIDNFIILMNSDESQVNT 61
 Oy 62 SFSDYQKGMNMIKLSGCONITSTKCNFSSSLKLVYEEIKLRIRAK-ENTSSWYEDS 119
 Db 59 SADYQIGIGTDMKMLKSCGCHITSTKCNFSSVLEENVEKEIKLRIRAKGNTSWYEV 118
 Oy 120 TPFRKAQIGPPVHLAEADKAIVIHIS-PTKDSVMALDGLSFTYSLIMKNSGVEE 178
 Db 119 FVPLKQIGPPVHLAEADKAIVIHIS-PTKDSVMALDGLSFTYSLIMKNSGVEE 178
 Oy 179 RIENIYSRHKIYKLSPEITCYCLKVKAALLTSWKIGVSPVHCITVTENEL 229
 Db 179 RIENIYSRHKIYKLSPEITCYCLKVKAALLTSWKIGVSPVHCITVTENEL 229
 RESULT 3
 INRL_SHEEP STANDARD: PRT: 560 AA.
 AC 028389; Q95206;
 ID 028389; Q95206;

DT 01-NOV-1997 (Rel. 35, Last Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
 DE (INTERFERON ALPHA/BETA RECEPTOR-1).
 GN IFNAR1 OR IFNAR.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-ENDOMETRIUM;
 RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
 RT "Structure of an ovine interferon receptor and its expression in
 RT endometrium";
 RL J. Mol. Endocrinol. 17:207-215(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-ENDOMETRIUM;
 RX MEDLINE; 98006426.
 RA Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;
 RT "Molecular cloning of ovine and bovine type I interferon receptor
 RT subunits from uterus, and endometrial expression of messenger
 RT ribonucleic acid for ovine receptors during the estrous cycle and
 RT pregnancy";
 RL Endocrinology 138:4757-4767(1997).
 CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
 CC SUBUNITS THEMSELVES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
 CC CONCEPTUS AT DAY 15 OF PREGNANCY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; X95939; CAAG5183.1; -;
 DR EMBL; U65978; AAB84231.1; -;
 DR PIR; PF00041; fn3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 560 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 FT CHAIN.
 FT DOMAIN 25 437 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 438 458 POTENTIAL.
 FT DOMAIN 459 560 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 76 84 BY SIMILARITY.
 FT DISULFID 199 220 BY SIMILARITY.
 FT CARBOHYD 47 47 POTENTIAL.
 FT CARBOHYD 55 55 POTENTIAL.
 FT CARBOHYD 85 85 POTENTIAL.
 FT CARBOHYD 108 108 POTENTIAL.
 FT CARBOHYD 109 109 POTENTIAL.
 FT CARBOHYD 172 172 POTENTIAL.
 FT CARBOHYD 222 222 POTENTIAL.
 FT CARBOHYD 285 285 POTENTIAL.
 FT CARBOHYD 313 313 POTENTIAL.
 FT CARBOHYD 359 359 POTENTIAL.
 FT CARBOHYD 377 377 POTENTIAL.
 FT CARBOHYD 434 434 POTENTIAL.
 FT CARBOHYD 434 434 POTENTIAL.
 FT CONFLICT 352 352 S -> G (IN REF. 2).
 FT CONFLICT 522 522 A -> D (IN REF. 2).
 FT SEQUENCE 560 AA: 63918 MW: 7198A1905D4805C CAC64;

Query Match 64.0%; Score 765.5; DB 1; Length 560;
 Best Local Similarity 66.2%; Pred. No. 1.8e-60;
 Matches 153; Conservative 32; Mismatches 41; Indels 5; Gaps 5;
 QY 2 MVLVGLATLVAVGVPMVLSAAGKRLKSPKQEVDDIDDFILRMNSDSGVGVTF 61
 DB 1 MSLSLGATITMLVA-GRWVLPASGEANLKS-ENVEIHIIDDFELKWNSSSEVRVTF 58
 QY 62 SFDFQKGMQWIKLSGCONITSPKCNFSSDKL-NVEEIKRLIRAEK-ENTSSWEVDS 119
 DB 59 SADYQIIGTDNMWKLPPCCOHITSSCKNFSSVELKQVFEKLEIRAREGNTSTWYVFP 118
 QY 120 FTTPRKAQIPPEVHLEAEADKAIVIHIS-PGTRDSVMALDGLSFTYSLIWNSSGVVE 178
 DB 119 FVPLFKAQIGPPDVHLEAEADKAILISLSPGTEDSIMALDRSSFRTSVYIWNSSSLEE 178
 QY 179 RLENITSRHKIYKSPETTCYKKAALLSWKIGVSPVHCITTYENEL 229
 DB 179 RTEVYEDIKYKLSPEITCYLKAKELRLQSRVGCSPYICINTYRHRV 229
 RESULT 4
 INRL_MOUSE STANDARD; PRT; 590 AA.
 ID INRL_MOUSE
 AC P33896;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE 15-FEB-2000 (Rel. 39, Last annotation update)
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
 GN IFNAR1 OR IFNAR OR IFNAR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92262522.
 RA Ue G., Luitalla G., Bandu M.T., Proudhon D., Mogensen K.E.;
 RT "Behavior of a cloned murine interferon alpha/beta receptor expressed
 RT in homospesific or heterospesific background";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).
 CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
 CC SUBUNITS THEMSELVES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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 CC -----
 DR EMBL; M89641; AAA37890.1; -;
 DR PIR; A45283; A45283.
 DR MGD; MG1:107658; IFNAR.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 590 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 FT CHAIN.
 FT DOMAIN 27 429 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 430 449 POTENTIAL.
 FT DOMAIN 450 590 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 78 86 BY SIMILARITY.
 FT DISULFID 199 220 BY SIMILARITY.
 FT CARBOHYD 43 43 POTENTIAL.
 FT CARBOHYD 109 109 POTENTIAL.
 FT CARBOHYD 181 181 POTENTIAL.

FT	CARBOHYD	214	214	POTENTIAL.
FT	CARBOHYD	314	314	POTENTIAL.
FT	CARBOHYD	370	370	POTENTIAL.
FT	CARBOHYD	409	409	POTENTIAL.
FT	CARBOHYD	413	413	POTENTIAL.
SO	SEQUENCE	590 AA;	65776 MW;	7EC6DEF370185D3A CRC64;

Query Match	50.2%;	Score 600.5;	DB 1;	Length 590;
Best Local Similarity	52.0%;	Pred. No. 8.1e-46;		
Matches 119;	Conservative 40;	Mismatches 69;	Indels 1;	Gaps 1;

QY	2	MVLLGATTLVAVGPGVPLVLSAAGGKRLSPQKXVDIIIDNFIILRNRSDESVANTG	61
		1 : : : : : : : : : : : : : : : :	
Db	1	MLAVGAAALVAVGAPVPLVPSAAGGKRLKPPENIDVYIIDNYYLKLKSHGESSVTF	60
QY	62	SFDYOKTGMDMVKILSGCONITSTKCNFSLSLANTYEEIKLIRAEKEN-TSSAYEVDSF	120
		1 : : : : : : : : : : : : : : : : :	
Db	61	SAEYRTKQAKMKVPEQGHHTTTCESFLDNTNYIKTFPVRAEGNGSTSNWVEVPF	120
QY	121	TPFRKAQIGPPEVHLAEADKALVHIISFGTKDSVMALDGLSFYLSLWKNSGVEERI	180
		1 : : : : : : : : : : : : : : : : : : :	
Db	121	IPFTAHKSPPEVRLAEADKALVHVISPGDGGNMMALEKPSFYTIRIQKSSDDKRTI	180
QY	181	ENIYSRHHIYKLSPEPTCYCLVAKALLSWKGVGVSPLHCITTYENEL	229
		: : : : : : : : : : : : : : : : :	
Db	181	NSYTYVEKIPELPEPTCYCLEVKALHPSLKHSNSTVQCCISTVANK	229

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RESULT      5
CRF4_HUMAN
ID          CRF4_HUMAN      STANDARD:      PRT:      325 AA.
AC          008334;
DT          01-FEB-1995 (Rel. 31, Created)
DT          01-FEB-1995 (Rel. 31, Last sequence update)
DT          01-OCT-1996 (Rel. 34, Last annotation update)
DE          CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.
GN          CRF4.
OS          Homo sapiens (Human).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC          Eutheria; Primates; Catarrhini; Hominoidei; Homo.
RN          [1]
RP          SEQUENCE FROM N.A.
RC          TISSUE=FETAL BRAIN;
RX          MEDLINE; 93300510.
RA          Lutfalla G., Gardiner K., Uze G.;
RT          "A new member of the cytokine receptor gene family maps on chromosome
RT          21 at less than 35 kb from IFNAR.";
RL          Genomics 16:366-373(1993).
RN          [2]
RP          SEQUENCE FROM N.A.
RX          MEDLINE; 96054036.
RA          Lutfalla G., McInnis M.G., Antonarakis S.E., Uze G.;
RT          "Structure of the human CRF4 gene: comparison with its IFNAR
RT          neighbor.";
RL          J. Mol. Evol. 41:338-344(1995).
CC          -1- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.
CC          -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC          -1- SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.
CC          -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC          -----
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CC          or send an email to license@isb-sib.ch).
CC          -----
DR          EMBL; Z17227; CAAT8933.1; -
DR          EMBL; U08888; AAA86872.1; -
DR          PIR; A47003; DR
DR          HSSP; P13726; IDAN.

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DR	MM: 123889; -	
KM	Receptor; Transmembrane; Glycoprotein; Signal.	
FT	SIGNAL	1
FT	CHAIN	20
FT	DOMAIN	20
FT	TRANSMEM	221
FT	DOMAIN	250
FT	DISULFID	66
FT	DISULFID	188
FT	CARBOHYD	49
FT	CARBOHYD	68
FT	CARBOHYD	102
FT	CARBOHYD	161
FT	CONFLICT	124
FT	CONFLICT	269
FT	CONFLICT	274
SQ	SEQUENCE	325 AA; 37011 MM; 66706C79F8514B23 C9C64;

Query Match	18.6%;	Score 222.5;	DB 1;	Length 325;
Best Local Similarity	30.3%;	Pred. No. 1.3e-12;		
Matches 66;	Conservative 40;	Mismatches 93;	Indels 19;	Gaps 8;

QY 19 WVL\$AAAGKNLKS-----PQAYEVDIIDDNFLRRNRDESGANTFSDYXKTGMD 71
 : | | | | | : | | | | | : | | | | |
 Db 3 WSLGSWLDGCCLLVSLAGVPPENRNMKSVNFKNLQWESPAPAGNLTFTAOY---LS 58
 : | | | | | : | | | | | : | | | | |
 QY 72 NMIKLSGCONITTRKCNFS\$KLNYAEIKRLRAE-KENTSMWEYD\$TFPFRAQIGP 130
 : | | | | | : | | | | | : | | | | |
 Db 59 YRIODKCMNTLTLEBDRS--LSKYGHILRVAREFPEDHSDWNVT-TCFCYVDITIIIP 115
 : | | | | | : | | | | | : | | | | |
 QY 131 PEVHLA-EDKAIVIHISPGTKDSV-WMALDGL--SFTYSLLIMKNSSGVEEIRIENIYSR 186
 : | | | | | : | | | | | : | | | | |
 Db 116 PGMQVEVLADSLHRMFLPAKIENEYEETMTMKNVMSMTYNHQYWKNGTDEKFQIOPYDFE 175
 : | | | | | : | | | | | : | | | | |
 QY 187 HKIKYSPETTYCJLKVKAKALLSMKIGYSPVHCIXKT 224
 : | | | | | : | | | | | : | | | | |
 Db 176 EVLRNLEFWTTYCVQVRGFELPRNNKAGWSBPVCÖTT 213
 : | | | | | : | | | | | : | | | | |

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RESULT 6
INGRS_HUMAN
ID      INGS_HUMAN      STANDARD;      PRT;      337 AA.
AC      P38484;
DT      01-OCT-1994 (Rel. 30, Created)
DT      01-OCT-1994 (Rel. 30, Last sequence update)
DT      01-NOV-1997 (Rel. 35, Last annotation update)
DE      INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA
DE      RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).
GN      IFNGR2 OR IFNG1T.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=LUNG FIBROBLAST;
RX      MEDLINE; 94170380.
RA      Son J., Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R.,
RA      Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.;
RT      Identification and sequence of an accessory factor required for
RT      activation of the human interferon gamma receptor.";
RL      Cell 76:793-802(1994).
CC      -1- FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR
CC      SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF
CC      THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO
CC      INTERACT WITH GAF, JAK1, AND/OR JAK2.
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- SIMILARITY: CONTAINS 2 FIBROBLASTIN TYPE III-LIKE DOMAINS.
CC      -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC      -----
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DR EMBL: U05875; AAA16955.1; -
DR EMBL: U05877; AAA16956.1; -
DR MIM: 147559; -
DR PFM: PF00041; fn3; 1.
DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 337 INTERFERON-GAMMA RECEPTOR BETA CHAIN.
FT DOMAIN 28 268 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 248 268 POTENTIAL.
FT DOVAIN 269 337 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 56 56 POTENTIAL.
FT CARBOHYD 85 85 POTENTIAL.
FT CARBOHYD 110 110 POTENTIAL.
FT CARBOHYD 137 137 POTENTIAL.
FT CARBOHYD 219 219 POTENTIAL.
FT CARBOHYD 231 231 POTENTIAL.
FT VARIANT 64 64 R -> O.
FT SEQUENCE 337 AA; 37834 MW; 18C61B10AD90E509 CRC64; /FTID-VAR.002718.

Query Match 12.78; Score 151.5; DB 1; Length 337;
Best Local Similarity 24.6%; Pred. No. 2.7e-06;
Matches 61; Conservative 44; Mismatches 94; Indels 49; Gaps 13;

OY 12 VLAVNGPVLVLSAAGG---KNLKSPOKVEVDIDNFIKRW-----NRSDSVGNVTF 62
DB 9 LLLLGVPVAAAAPPDPLSQLPAPQHKIRLYNEQVLSWEPVALSNSTRPVYRVQFK 68
OY 63 FDYQKGMNWKLS-----GCQNTSTKCNFS-----TKLNYEEIKLRRAEK 108
DB 69 YTDKR-----WFTADIMSGVCTQITATECDFTLAASPSAGPMFV-----TLRLREL 119
OY 109 ENT-SSWYEVDSFTPRRAQIQPPEVHLE---AEDKAVIHISPTKDSVMALDGLSFT 164
DB 120 GALHSAMWTMPFQHYRNVTVGPPE-NIEVTPGESLIRFSSPDIDTSAF-----FC.174
OY 165 YSLIWKNSGVKEIEINISNKKY--KLSPTTYCKLVKALLTS---WKIVYSPV 218
DB 175 YVHWWE---KGGIQQVKGPFNSISLNDLKSRYCLOVQOQLMKNKSNIFRVGHSNI 232
OY 219 HCKITVE 226
DB 233 SCYETMAD 240

RESULT 7
INGR_HUMAN STANDARD: PRT: 489 AA.
AC P15260; 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDM119).
GN IFNGRI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89003065.
RA Aguet M., Dembic Z., Meriin G.;
RT "Molecular cloning and expression of the human interferon-gamma
RL Cell 55:273-280(1988).
RN [2]
RP DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.
MEDLINE: 93183911.

RA Stueber D., Friedlein A., Fountoulakis M., Iahn H.-W., Garotta G.;
RT "Alignment of disulfide bonds of the extracellular domain of the
RT Interferon gamma receptor and investigation of their role in
RT biological activity."
RL Biochemistry 32:2423-2430(1993).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.
RX MEDLINE: 95342235.
RA Walter M.R., Windsor W.T., Nagabhushan T.L., Lundell D.J., Lunn C.A.,
RA Zaudouy P.J., Narula S.K.;
RT "Crystal structure of a complex between Interferon-gamma and its
RT soluble high-affinity receptor."
RL Nature 376:230-235(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 COMPLEX WITH ANTIBODY.
RX MEDLINE: 98035727.
RA Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A.,
RA Winkler F.K., Robinson J.A.;
RT "Neutralizing epitopes on the extracellular Interferon gamma receptor
RT (IFNGAMMAR) alpha-chain characterized by homolog scanning mutagenesis
RT and X-ray crystal structure of the A6 fab-IFNGAMMAR1-108 complex."
RL J. Mol. Biol. 273:882-897(1997).
CC -1- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
CC INTERFERON-GAMMA DIMER.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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DR EMBL: J03143; AAA52731.1; -
DR PIR: A31555; A31555.
DR PDB: 1JRH; 25-MAR-98.
DR MIM: 107470; -
DR MIM: 209950; -
DR Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;
KW Immunoglobulin domain; 3D-structure.
FT SIGNAL 1 17
FT CHAIN 18 489
FT DOMAIN 18 245
FT TRANSMEM 246 266
FT DOMAIN 267 489
FT DISULFID 77 85
FT DISULFID 122 167
FT DISULFID 195 200
FT DISULFID 214 235
FT CARBOHYD 34 34
FT CARBOHYD 79 79
FT CARBOHYD 86 86
FT CARBOHYD 179 179
FT CARBOHYD 240 240
FT SEQUENCE 489 AA; 54404 MW; DCF9E574D8F47400 CRC64;

Query Match 9.8%; Score 117.5; DB 1; Length 489;
Best Local Similarity 22.6%; Pred. No. 0.0045;
Matches 52; Conservative 44; Mismatches 99; Indels 35; Gaps 8;

OY 3 VLLGATLVAVNGPVLVLSAAGGKNLKSPOKVEVDIDNFIKRWNSDSVGNV-T 60
DB 1 MALLFLPLVWGVSVRAEMGTADLGPSSVPTPNVITISYNNMPIYVWE--QIMQV 58
OY 61 FSPFYQKGMNWKLSGCQNTSTKCNFSLLNLYEEIKLRRA---EKWTSSVYEV 117


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DB 59 FTVEVKNYGVKNSWIDACINISHYCNISDHVGPNSLWYKARVQKE--SAYAKS 116
OY 118 DSFTPRKAOIGPPEVHLAEKAIYIH-----SPGK-----DSYVM 156
DB 117 EEFVAVCRDKIDPPKIDIKERQIMIDIFHPSVFVNGDEVDYDPEYTCYIRYNYV 176
OY 157 ALDGLSTFTYSLIMKNSGVEERENIYSRHKIYKLSPTTYCLKVAKAL 206
DB 177 RANGSGIYOKILYOK-----EDDCDEIQGLAIPVSSLNSQYCVSAEGLV 221

RESULT 8
INGR_MOUSE STANDARD: PRT: 477 AA.
ID INGR_MOUSE
AC P15261:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1998 (Rel. 38, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR.
GN IFNGR1 OR IFNGR.
OS Mus musculus (Mouse).
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90083245.
RA Munro S., Maniatis T.;
RT "Expression cloning of the murine interferon gamma receptor cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9248-9252(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90046824.
RA Gray P.W., Leong J., Fennie E.H., Farrar M.A., Pingel J.T.,
RT Fernandez-Luna J., Schreiber R.D.;
RT "Cloning and expression of the cDNA for the murine interferon gamma
RT receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8497-8501(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90099370.
RA Hemmi S., Peghinet P., Metzler M., Merlin G., Dembic Z., Aguet M.;
RT "Cloning of murine Interferon gamma receptor cDNA: expression in
RT human cells mediates high-affinity binding but is not sufficient to
RT confer sensitivity to murine interferon gamma.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9901-9905(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90036866.
RA Kumar C.S., Muthukumar G., Frost L.J., Noe M., Ahn Y.H.,
RT Mariano T.M., Pestka S.;
RT "Molecular characterization of the murine Interferon gamma receptor
RT cDNA.";
RL J. Biol. Chem. 264:17939-17946(1989).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90154099.
RA Cofano F., Moore S.K., Tanaka S., Yuhki N., Landolfo S.,
RT Appella E.;
RT "Affinity purification, peptide analysis, and cDNA sequence of the
RT mouse Interferon gamma receptor.";
RL J. Biol. Chem. 265:4064-4071(1990).
RN [6]
RP SEQUENCE OF 1-28 FROM N.A.
RX MEDLINE: 95197006.
RA Raval P., Obici S., Russell S.W., Murphy W.J.;
RT "Characterization of the 5' flanking region and gene encoding the
RT mouse Interferon gamma receptor.";
RL Gene 154:219-223(1995).
CC -1- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
CC INTERFERON-GAMMA DIMER.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

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CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M28995; AAA37895.1; ALT_INIT.
DR EMBL: M26711; AAA37896.1; -.
DR EMBL: M28233; AAA37898.1; -.
DR EMBL: M25764; AAA39177.1; -.
DR EMBL: J05265; AAA39178.1; -.
DR EMBL: U05960; AAA80980.1; -.
DR PIR: A34368; A34368.
DR PIR: A34423; A34423.
DR PIR: A34508; A34508.
DR PIR: A35468; A35468.
DR PIR: A36224; A36224.
DR HSSP: P15260; IYRH.
DR MGD: MGI:107655; IFNGR.
DR Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;
KW Immunoglobulin domain.
FT SIGNAL 1 22
FT CHAIN 23 477
FT DOMAIN 23 253
FT TRANSMEM 254 277
FT DOMAIN 278 477
FT DISULFID 83 91
FT DISULFID 128 174
FT DISULFID 203 208
FT DISULFID 222 243
FT CARBOHYD 61 61
FT CARBOHYD 85 85
FT CARBOHYD 186 186
FT CARBOHYD 204 204
FT CARBOHYD 211 211
FT CONFLICT 95 95
SQ SEQUENCE 477 AA; 52271 MW; AIFC6E9BAAB20A CRC64;

Query Match 8.6%; Score 102.5; DB: 1; Length 477;
Best Local Similarity 22.9%; Pred. No. 0.094;
Matches 54; Conservative 36; Mismatches 87; Indels 57; Gaps 14;

OY 8 ATTIVAVGPMVLSAAGGRNKS--PQVEVDIIDNFIILMNSDESQVNTFSFD 64
DB 7 AGRMILLV--LMSAKVSGALSTEDPEPPVPVPTNVILKSYNL-----NPVQWE 58
OY 65 YQ-----KTGDMNLIKSGCONITSTCNSSSLNLYEELK-----LRIR 105
DB 59 YQNSQPTIFTVOYKVYSGSW--TDSCNTISDHCC-----NIYQIMPDVGSAMARVK 109
OY 106 AE-KENTSSWEVDSEFTFRKAQIGP--EVHLAEADKAIYHISP-----GTRDSYMA 157
DB 110 AKVGKEDDYARSKFEFLMCLKRGVPGLEIRKKKEBLSLVVHPVYVNGEQQMGFG 169
OY 158 LDG--LSFTYSLIMKNSGVEERENIYSRHKIYKLSPTTYC-LKVAKALLTS 209
DB 170 -DGSCTYFTDYTVVEYHNRSG-----ELIHTKHVEKECNETLCELNIISVSTLDS 219

RESULT 9
ID INGR_MOUSE STANDARD: PRT: 575 AA.
AC O6127:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).

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IL10RA OR IL10R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6 X AJ F1; TISSUE-HEMATOPOIETIC;
RX MEDLINE: 94068585.
RA Ho A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;
RT "A receptor for interleukin 10 is related to interferon receptors."
RL Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC
DR EMBL: L12120; AAA16156.1; -
DR WGI: MGI:96538; IL10RA.
DR Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 575 INTERLEUKIN-10 RECEPTOR.
FT DOMAIN 17 241 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 242 262 POTENTIAL.
FT DOMAIN 263 275 POTENTIAL.
FT DISULFID 204 225 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 50 50 POTENTIAL.
FT CARBOHYD 66 66 POTENTIAL.
FT CARBOHYD 113 113 POTENTIAL.
FT CARBOHYD 182 182 POTENTIAL.
FT CARBOHYD 238 238 POTENTIAL.
FT SEQUENCE 575 AA; 64248 MW; 820B9CD576F686B7 CRC64;
SO
Query Match 8.0%; Score 95.5; DB 1; Length 575;
Best Local Similarity 20.5%; Pred. No. 0.5; Mismatches 98; Indels 61; Gaps 10;
Matches 51; Conservative 39; Mismatches 98; Indels 61; Gaps 10;
OY 13 LVAAGPWLAAAGGKNEKSPQVEVDIIDNFIILM-----NRSDSYGNVTFSEDYQRT 68
DB 9 LVTISLSLEFIAYGTETLPSYVFEARFQHIILMKRIPNOSTEYVAL-----KQY 64
OY 69 GMDNRIKLSGCONITSTKCNFSSKLNVYE--IKLRIR-EKENTSSWYEVDS-FTPE 123
DB 65 GNSVNDHICRKAQALSCDITFTLDRSYGARAVAVNSQYSMTTETRT-- 123
OY 124 RKAQIGPPEVHLAEADKAVIHISPTKDSY-MMALDGLSFYSLILWNSSGVERLEN 182
DB 123 -----VDEVIL-----TYDSVTLKADGILYCTIHPPRTTIPAGEYEQ 162
OY 183 IYSRHKIYKLS-----PEY-----TYCLKAAALLTSMKIGVSP 217
DB 163 VKEDLRVYKISIRKFSKLNATKRVKQEFITLVPYIGVAKFCVKVLRLESINNAEMSE 222
OY 218 VHCITTYE 226
DB 223 EOCILITTE 231
RESULT 10
PWP2-CAEEL STANDARD: PRT: 925 AA.
AC P91341;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG.

F55F8.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabdilita; Rhabdilitida;
OC Rhabdilita; Rhabdilitida; Rhabdilitidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX Gating S., Scheet P., Kemp K.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
CC -1- SIMILARITY: BELONGS TO THE PWP2 FAMILY OF WD-REPEAT PROTEINS.
CC
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CC
DR EMBL: U80447; AAB37807.1; -
DR WORKPEP: F55F8.3; CE11192.
DR PRINTS: PR00320; GPROTEINRPT.
DR PROSITE: PS00678; WD_REPEATS; 1.
DR PFWA: PF00400; WD40; 4.
DR Hypothetical protein; Repeat; WD repeat.
FT REPEAT 188 218 WD1.
FT REPEAT 358 388 WD2.
FT REPEAT 400 430 WD3.
FT REPEAT 486 514 WD4.
FT REPEAT 524 554 WD5.
FT REPEAT 599 627 WD6.
FT SEQUENCE 925 AA; 103899 MW; 439F35881B398CD1 CRC64;
SO
Query Match 8.0%; Score 95.5; DB 1; Length 925;
Best Local Similarity 25.7%; Pred. No. 0.91; Mismatches 70; Indels 21; Gaps 4;
Matches 38; Conservative 19; Mismatches 70; Indels 21; Gaps 4;
OY 70 MDNRIKLSGCONIT--STKCNFSSKLNVYEI--KLRIRAKENTSSWYEVDSFTPEFRK 125
DB 1 MDNRIKLSGCONIT--STKCNFSSKLNVYEI--KLRIRAKENTSSWYEVDSFTPEFRK 125
OY 126 AIGPPEVHLAEADKAVIHISPTKDSY-MMALDGLSFYSLILWNSSGVERLEN 182
DB 61 LSISSPGVHLASDGRGVHVVHLLSEKIVTFPSNRKIGSLQSPDATRVAICRENDLQ 120
OY 169 IWKNSGVEERLENTISYRHKIYKLSPEP 196
DB 121 IHEFGKSIENKRVNPFSLSRKLSDS 148
RESULT 11
IL10R_HUMAN STANDARD: PRT: 578 AA.
AC Q13651;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
GN IL10RA OR IL10R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOMA;
RX MEDLINE: 94165477.
RA Liu Y., Wei S.H.-Y., Ho A.S.-Y., de Waal Malefyt R., Moore K.W.;
RT "Expression cloning and characterization of a human IL-10 receptor."
RL J. Immunol. 152:1821-1829(1994).
CC -1- FUNCTION: RECEPTOR FOR IL-10. BINDS IL-10 WITH A HIGH AFFINITY.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: SPLEEN, THYMUS, AND PBMC. FAINT EXPRESSION
 CC IN PANCREAS, SKELETAL MUSCLE, BRAIN, HEART, AND KIDNEY. PLACENTA,
 CC LUNG, AND LIVER SHOWED INTERMEDIATE LEVELS. MONOCYTES, B CELLS,
 CC LARGE GRANULAR LYMPHOCYTES, AND T CELLS EXPRESS HIGH LEVELS OF IL-
 CC 10R.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -----
 CC DR EMBL: U00672; AAA17896.1; -
 CC KW MIM: 146933; -
 CC Receptor: Transmembrane; Glycoprotein; Signal.
 CC FT SIGNAL 1 21
 CC FT CHAIN 22 578 INTERLEUKIN-10 RECEPTOR.
 CC FT DOMAIN 22 235 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 236 256 POTENTIAL.
 CC FT DOMAIN 257 378 CYTOPLASMIC (POTENTIAL).
 CC FT DISULFID 202 223 POTENTIAL.
 CC FT CARBOHYD 50 50 POTENTIAL.
 CC FT CARBOHYD 74 74 POTENTIAL.
 CC FT CARBOHYD 110 110 POTENTIAL.
 CC FT CARBOHYD 154 154 POTENTIAL.
 CC FT CARBOHYD 177 177 POTENTIAL.
 CC FT CARBOHYD 189 189 POTENTIAL.
 CC SQ SEQUENCE 578 AA; 62903 MW; EELB29064338157C CRC64;

Query Match 7.9%; Score 95; DB 1; Length 578;
 Best Local Similarity 19.7%; Pred. No. 0.56; Mismatches 45; Indels 72; Gaps 11;

Matches 51; Conservative 45; Mismatches 45; Indels 72; Gaps 11;
 OY 2 MVLGATTVLVAVGFWLAAAGKLNKSPQKVEVDIDNFIKWNDSDESGVNTF 61
 DB 5 LVVLAA--LISRLG-----SDAHGELPSPSPVMEAFPHILHMTIPNOSTCY 57
 OY 62 SFYQKTGMNWKILSGCONITSTKCNFSSLKINVEE--IKLRIR--EKENTSSW--- 115
 DB 58 EVALLRFGIESMNSISNCOTLS--YDLTAVTLDLYHNGYRVARVADGSRHSNMTVTN 115
 OY 115 --EVDSFTFRKAOIGPPVHLEADKAIYHIS--PGTDSYMMALDGLSTFYSLIWK 171
 DB 116 TRFSVDEVT---LTVG--SVNLEIHNGFLGKIQLPRK-----YCLKVKA 205
 OY 172 NSSGVEERIENTYSRHKIKYKLSPEPT-----YCLKVKA 205
 DB 150 -MAPANDTYESIFSHREYELAIRKVPNGFTTHKKYKHENFSLTSGVEGECVQKPS 208
 OY 206 LITSMKIGVSPVHCIKTT 224
 DB 209 VASRSNKGMSKECISLT 227
 RESULT 12
 TF_BOVIN STANDARD; PRT; 292 AA.
 AC P30931;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).
 GN F3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE-ADRENAL GLAND;
 RX MEDLINE: 92109720.
 RA Takayenko Y., Muta T., Miyata T., Iwanaga S.;
 RL "cDNA and amino acid sequences of bovine tissue factor."
 RT Biochem. Biophys. Res. Commun. 181:1145-1150(1991).
 CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
 CC CIRCULATING FACTOR VII OR VITA. THE (TF-VIIA) COMPLEX ACTIVATES
 CC FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
 CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -----
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 CC -----
 CC DR EMBL: S74147; AAB20755.1; -
 CC KW PIR: J01319; KFB03.
 CC DR HSSP: P24055; IAA21.
 CC DR PRINTS: PR00346; TISSUEFACTOR.
 CC DR PROSITE: PS00621; TISSUE_FACTOR; 1.
 CC DR PFM: PF01108; Tissue_fac; 1.
 CC KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
 CC Palmitate.
 CC FT SIGNAL 1 35
 CC FT CHAIN 36 292 TISSUE FACTOR.
 CC FT DOMAIN 36 248 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 249 271 POTENTIAL.
 CC FT DOMAIN 272 292 CYTOPLASMIC (POTENTIAL).
 CC FT SITE 46 48 WKS MOTIF.
 CC FT CARBOHYD 43 43 POTENTIAL.
 CC FT CARBOHYD 153 153 POTENTIAL.
 CC FT CARBOHYD 181 181 POTENTIAL.
 CC FT DISULFID 81 89 BY SIMILARITY.
 CC FT DISULFID 215 238 BY SIMILARITY.
 CC FT LIPID 274 274 PALMITATE (BY SIMILARITY).
 CC SQ SEQUENCE 292 AA; 32475 MW; 5E471D92BFBC163 CRC64;

Query Match 7.7%; Score 92.5; DB 1; Length 292;
 Best Local Similarity 22.7%; Pred. No. 0.39; Mismatches 40; Conservative 35; Mismatches 40; Indels 70; Gaps 9;

Matches 40; Conservative 35; Mismatches 40; Indels 70; Gaps 9;
 OY 70 MDNWKILSGCONITSTKCNFS--SLKINVEEIKLRIRAKENTSS-----WEVDSFTP 122
 DB 74 LCNW--KNKCFYTTNTECDVDEIVKNREYLAVALSPADTSSVPEPTNSPEFTP 131
 OY 123 FRKAOIGP-----EVHLEADKAIYHISPGKDSYMMALD---GLSTFYSLI 169
 DB 132 YLETNIGOPTIOSFPOVGTKLVNTVODARTLR-----ANSFELSLRDVFGDLNLTLY 186
 OY 170 WR-NSSGVEERIENTYSRHKIKYKLSPEPTYCLKVRAALITSMKIGVSPVHCIKTT 224
 DB 187 WKASSTGKKATTN--TNGFLIDVDKGENYCPHQAVIL--SRVYNOKSESPKICT 239

RESULT 13
 TF_HUMAN STANDARD; PRT; 295 AA.
 AC P13726;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUL-1993 (Rel. 38, Last annotation update)
 DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III)
 GN F3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89247359.
 RA Mackman N., Morrissey J.H., Fowler B., Edgington T.S.;
 RT "Complete sequence of the human tissue factor gene, a highly
 RT regulated cellular receptor that initiates the coagulation protease
 RT cascade.";
 RL Biochemistry 28:1755-1762(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87260946.
 RA Spicer E.K., Horton R., Bloem L., Bach R., Williams K.R., Guha A.,
 RA Krius J., Lin T.C., Nemerson Y., Konigsberg W.H.;
 RT "Isolation of cDNA clones coding for human tissue factor: primary
 RT structure of the protein and cDNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5148-5152(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87244317.
 RA Morrissey J.H., Fakhrai H., Edgington T.S.;
 RT "Molecular cloning of the cDNA for tissue factor, the cellular
 RT receptor for the initiation of the coagulation protease cascade.";
 RL Cell 50:129-135(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88050796.
 RA Scarpati E.M., Wen D., Broze G.J. Jr., Miletich J.P.,
 RA Flaudermeyer R.R., Siegel N.R., Sadler J.E.;
 RT "Human tissue factor: cDNA sequence and chromosome localization of
 RT the gene.";
 RL Biochemistry 26:5234-5238(1987).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88100453.
 RA Fisher K.L., Gorman C.M., Vehar G.A., O'Brien D.P., Lawn R.M.;
 RT "Cloning and expression of human tissue factor cDNA.";
 RL Thromb. Res. 48:89-99(1987).
 RN [6]
 RP DISULFIDE BONDS, AND PALMITOYLATION.
 RX MEDLINE; 89000604.
 RA Bach R., Konigsberg W.H., Nemerson Y.;
 RT "Structure of the extracellular domain of human tissue factor:
 RT location of the factor VIIa binding site.";
 RL Biochemistry 33:10864-10870(1994).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 33-243.
 RX MEDLINE; 94368785.
 RA Muller Y.A., Utsch M.H., Kelley R.F., de Vos A.M.;
 RT "Structure of the extracellular domain of human tissue factor:
 RT location of the factor VIIa binding site.";
 RL Biochemistry 33:10864-10870(1994).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 33-243.
 RX MEDLINE; 96190957.
 RA Muller Y.A., Utsch M.H., de Vos A.M.;
 RT "The crystal structure of the extracellular domain of human tissue
 RT factor refined to 1.7-A resolution.";
 RL J. Mol. Biol. 256:144-159(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 33-251 IN COMPLEX WITH FVIIA.
 RX MEDLINE; 96175641.
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
 CC CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES
 CC FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
 CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- INDUCTION: TF EXPRESSION IS HIGHLY DEPENDENT UPON CELL TYPE. TF

CC CAN ALSO BE INDUCED BY THE INFLAMMATORY MEDIATORS INTERLEUKIN 1
 CC AND TNF, AS WELL AS BY ENDOTOXIN, TO APPEAR ON MONOCYTES AND
 CC VASCULAR ENDOTHELIAL CELLS AS A COMPONENT OF CELLULAR IMMUNE
 CC RESPONSE.
 CC -1- DATABASE: NAME=PROT; NOTE=CD guide CD142 entry;
 CC WWW-http://www.ncbi.nlm.nih.gov/prov/cd/cd142.htm".
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 CC -----
 DR EMBL: J02931; AAA61150.1; -
 DR EMBL: M16553; AAA61151.1; -
 DR EMBL: J02846; AAA61152.1; -
 DR EMBL: M27436; AAA36734.1; -
 DR EMBL: A19048; CAA01438.1; -
 DR PIR: A28320; KFHU3.
 DR PIR: A43645; A43645.
 DR PIR: A47574; A47574.
 DR PDB: 1BOY; 10-UTN-96.
 DR PDB: 2HFT; 29-JAN-96.
 DR PDB: 1DAN; 04-SEP-97.
 DR PDB: 1TFH; 25-FEB-98.
 DR PDB: 1AHM; 19-AUG-98.
 DR PDB: 1TFH; 19-AUG-98.
 DR MIR: 134390; -
 DR PRINTS; PR00346; TISSUEFACTOR.
 DR PROSITE; PS00621; TISSUE_FACTOR; 1.
 DR PFAM; PF01108; Tissue_fac; 1.
 KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
 KW Palmitate; 3D-structure.
 FT SIGNAL 1 32
 FT CHAIN 33 295
 FT DOMAIN 33 251
 FT TRANSMEM 252 274
 FT DOMAIN 275 295
 FT SITE 46 48
 FT SITE 77 79
 FT SITE 190 192
 FT CARBOHYD 156 156
 FT CARBOHYD 169 169
 FT DISULFID 81 89
 FT DISULFID 218 241
 FT LIPID 277 277
 FT CONFLICT 260 260
 FT SEQUENCE 295 AA; 33067 MW; D3486C713ED8EAD0 CRC64;
 SQ
 Query Match 7.7%; Score 92; DB 1; Length 295;
 Best Local Similarity 21.1%; Pred. No. 0.44;
 Matches 52; Conservative 42; Mismatches 100; Indels 52; Gaps 13;
 QY 8 ATTIVAVGVWV--LSAAGGRNLSPOVEVDIIDNFIILNMN-RSDSEVGNVTFSE 63
 DB 17 ARTILL-----GWFAQVAGASGTNTVAAYNLTKSNFTEILEMEKRPVNOVTVQIS- 72
 QY 64 DYORTGDMNWKISGCONITSTKCNFSSLKINVEIKLRIR-----EKENTSS-- 114
 DB 72 ----TKSGDW--KSKCYTDTDECDLD--EIVKDYKQYLAIVFSPAGNVSTSGAG 122
 QY 114 ---WYEDSFPFRKAIGRP-----EVLLEDEDAIVIHISPGKDSYMMALD- 160
 DB 123 EPLTENSPEFTPYLETNLGQPTIOSFPOVGTKVAVTEDETLVR-----RNNTFLSLRD 177
 QY 160 --GLSTYSLILIMNNSGVEERINISRHKIYLSPEYTCLEVKAAAL--LFTSMKIGVY 215
 DB 178 VFGDLDITLYLTKWSSSS-GKTKTKNTNFEILDVDGNGVCFVQAVISRTYVNRKSTD 236
 QY 216 SPVHCI 221

DB 237 SPVECM 242

|||||

RESULT 14

CD45_HUMAN STANDARD: PRT; 1304 AA.

ID CD45_HUMAN

AC P08575

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE LEUCOCYTE COMMON ANTIGEN PRECURSOR (EC 3.1.3.48) (L-CA) (CD45 ANTIGEN) (T200).

GN PTPRC OR CD45.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC (1)

RP SEQUENCE FROM N.A.

RC TISSUE-LYMPHOCYTES;

RX MEDLINE: 88061067.

RA Streuli M., Hall L.R., Saga Y., Schlossman S.F., Salto H.;

RT "Differential usage of three exons generates at least five different mRNAs encoding human leukocyte common antigens.";

RL J. Exp. Med. 166:1548-1566(1987).

RN (2)

RP FUNCTION.

RX MEDLINE: 89017162.

RA Chabonneau H., Tonks N.K., Walsh K.A., Fischer E.H.;

RT "The leukocyte common antigen (CD45): a putative receptor-linked protein tyrosine phosphatase.";

RL Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).

RN (3)

RP MUTAGENESIS.

RX MEDLINE: 90316093.

RA Streuli M., Krueger N.X., Thal T., Tang M., Salto H.;

RT "Distinct functional roles of the two intracellular phosphatase like domains of the receptor-linked protein tyrosine phosphatases LCA and LAR.";

RL EMBO J. 9:2399-2407(1990).

CC -1- FUNCTION: REQUIRED FOR T-CELLS ACTIVATION THROUGH THE ANTIGEN RECEPTOR. THE FIRST PTPASE DOMAIN HAS ENZYMACTIC ACTIVITY, WHILE THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE THE FIRST ONE.

CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN TYROSINE + ORTHOPHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: THERE ARE 8 DIFFERENT VARIANTS OF L-CA, WHICH ARISE BY ALTERNATIVE SPLICING.

CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.

CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -1- DATABASE: NAME-PROW: NOTE-CD guide CD45 entry; WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd45.htm".

CC -----

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CC -----

DR EMBL: Y00638; CA68669.1; -

DR HSSP: P18052; IYPO.

DR MIM: 151460; -

DR PRINTS: PR00700; PRTPHPTASE.

DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.

DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.

DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.

DR PFAM: PF00041; f03; 2.

DR PFAM: PF00102; X-Phosphatase; 2.

KW Glycoprotein; Transmembrane; Phosphorylation; B-cell; T-cell; Repeat; Alternative splicing; Hydrolase; Signal.

FT SIGNAL 1 23

FT CHAIN 24 1304

FT DOMAIN 24 575

FT TRANSMEM 576 597

FT DOMAIN 598 1304

FT DOMAIN 387 479

FT DOMAIN 480 571

FT DOMAIN 670 919

FT DOMAIN 961 1235

FT ACT_SITE 851 851

FT ACT_SITE 1167 1167

FT MUTAGEN 851 851

FT CARBOHYD 78 90

FT CARBOHYD 90 95

FT CARBOHYD 184 184

FT CARBOHYD 190 190

FT CARBOHYD 197 197

FT CARBOHYD 232 232

FT CARBOHYD 260 260

FT CARBOHYD 270 270

FT CARBOHYD 276 276

FT CARBOHYD 335 335

FT CARBOHYD 378 378

FT CARBOHYD 419 419

FT CARBOHYD 468 468

FT CARBOHYD 488 488

FT CARBOHYD 529 529

SO SEQUENCE 1304 AA; 147253 MW; 1F357BC5632618B2 CRC64;

Query Match 7.6%; Score 90.5; DB 1; Length 1304;

Best Local Similarity 20.9%; Pred. No. 3.9;

Matches 36; Conservative 23; Mismatches 60; Indels 53; Gaps 6;

OY 53 DESVGNVTFSSDYOKTGDMNKLSCGQNTSTRCNFSLSKLNYEIKLRIRAKENTS 112

DB 227 DEKYNITVDLYNKK-----ETKLETKLNTNENVEK-----GNNTC 263

OY 113 SMYEDSTPPPRKQIGPEVHLEADKAIYIHISPG----- 151

DB 264 TNNEVNLTCKNNSVSIHNSCTAPDITLIDPPGVKFOQHDCTQVERADPTTICKW 323

OY 151 KDSVMALDGLSFYSL-----LWKNSGVERENTISRRKIYKLSPTTY 198

DB 324 KNIEFTDQNTYIRFCGGMIFDK--EIKENLEPHE-YKQSEILY 371

RESULT 15

6DCS_SOYBN STANDARD: PRT; 315 AA.

ID 6DCS_SOYBN

AC P26690;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-AUG-1992 (Rel. 23, Last annotation update)

DE NAO(P/H) DEPENDENT 6'-DEOXYCHALCONE SYNTHASE (EC 1.-.-.-).

OS Glycine max (Soybean).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Glycyne.

OC [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RP STRAIN-CV HAROSY 63;

RX MEDLINE: 91177016.

RA Welle R., Schroeder G., Schiltz E., Grisebach H., Schroeder J.;

RT "Induced plant responses to pathogen attack. Analysis and heterologous expression of the key enzyme in the biosynthesis of phytoalexins in soybean (Glycine max L. Merr. cv. Harosoy 63).";

RL Eur. J. Biochem. 196:423-430(1991).

CC -1- FUNCTION: CO-ACTS WITH CHALCONE SYNTHASE IN FORMATION OF 4,2',4'-TRIHYDROXYCHALCONE, INVOLVED IN THE BIOSYNTHESIS OF GLYCOLLIN TYPE PHYTOALEXINS.

```
CC -1- PATHWAY: THIS IS THE KEY ENZYME IN THE BIOSYNTHESIS OF
CC PHYTOALEXINS IN SOYBEAN.
CC -1- SUBUNIT: MONOMER.
CC -1- INDUCTION: BY PATHOGEN ATTACK.
CC -1- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE FAMILY.
CC -----
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X55730; CAA39261.1; 1
DR PIR: S14222; S14222.
DR HSSP: P14550; 2ALR.
DR PRINTS: PR00069; ALDKERDTASE.
DR PROSITE: PS00062; ALDOKETO_REDUCTASE_2; 1.
DR PROSITE: PS00063; ALDOKETO_REDUCTASE_3; 1.
DR PROSITE: PS00798; ALDOKETO_REDUCTASE_1; 1.
DR PFM: PF00248; aldo_ket_red; 1.
KW Flavonoid biosynthesis; Oxidoreductase; NADP.
SQ SEQUENCE 315 AA; 35490 MW; C3A6BE07EF330F47 CRC64;

Query Match 7.5%; Score 90; DB 1; Length 315;
Best Local Similarity 21.6%; Pred. No. 0.72;
Matches 49; Conservative 38; Mismatches 76; Indels 64; Gaps 13;

OY 28 KNLKSPQVEVDIIDDNFILRNRSDESYGNVTFSD-----YKGTGDMNLIKSGCON 81
DB 105 KSLKTIQLELYDL---YLHWPSSQP-GKFSPIEVEDLIPDYKGV--WESMECOX 157
OY 82 ITSTSC---NSSSLKN-----VYEIKLRIRAKENTSSWE-----VDSFTF 122
DB 158 LGLTFAIGVSNFSVKRLQNLVSATIRPVVDQVEMNLAMQKKLRPFCKENGIIYTAFFS 217
OY 123 FRK-AQIGPPEVH-----LEADKAIVIHISPTKDSVMALD-GLSFTYSLLIWRN 172
DB 218 LRKGASRGPNEMENDVLAKEIAHGKSI-----AOVSLRWLYEGGVTFV-----PK 264
OY 173 SSGVERIENTY-----SRHKIYKLSPEPTYCLKVKKALLTSW 210
DB 265 SYDKERMNQLHIIFDMALTEODHHRISQISQSRLLISGPTKPOLADLW 311
```

Search completed: June 1, 2000, 04:38:54
Job time: 14317 sec

GenCore version 4.5
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OM protein - protein search, using sw model

```
Run on:      June 1, 2000, 04:38:14 ; Search time 69.16 Seconds
              (without alignments)
              229.577 Million cell updates/sec
```

```

Title:      US-09-240-675-2_COPY_1_229
Perfect score: 1196
Sequence:   1 MMVVLLGATTLVLVAVGPMV.....WKISVSPVHCIKTVENEL 229

```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

```
Minimum DB seq length: 0
Maximum DB seq length: 10000000
```

Post-processing: Minimum Match 0%
Listing first 45 summaries

```
Database :
1:  SP_Archaea:*
2:  SP_Bacteria:*
3:  SP_Fungi:*
4:  SP_Human:*
5:  SP_Invertebrate:*
6:  SP_Mammal:*
7:  SP_mhc:*
8:  SP_Organelle:*
9:  SP_Phage:*
10: SP_Plant:*
11: SP_Rodent:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	430.5	36.0	569	13	Q9YHW0	Q9YHW0	gallus galli
	2	219	18.3	349	11	Q61190	Q61190	mus musculus
	3	203	17.0	332	11	Q63953	Q63953	mus musculus
	4	179	15.0	341	13	Q9YXC8	Q9YXC8	gallus galli
	5	113.5	9.5	484	4	Q14936	Q14936	homo sapien
	6	97.5	8.2	6048	5	Q23020	Q23020	caenorhabdi
	7	97.5	8.2	6831	5	Q23550	Q23550	caenorhabdi
	8	97.5	8.2	7160	5	Q23551	Q23551	caenorhabdi
	9	91.5	7.7	6875	6	Q28733	Q28733	oryctolagus
	10	90.5	7.6	1143	4	Q16614	Q16614	homo sapien
	11	89.5	7.5	508	13	Q9YHV9	Q9YHV9	gallus galli
	12	89.5	7.5	2033	11	Q54711	Q54711	mus musculus
	13	89.5	7.5	2213	6	Q95209	Q95209	oryctolagus
	14	89.5	7.5	2215	11	Q088307	Q088307	mus musculus
	15	89	7.4	239	4	Q15467	Q15467	homo sapien
	16	88.5	7.4	1220	3	Q12465	Q12465	saccharomyc
	17	87.5	7.3	504	4	Q09624	Q09624	homo sapien
	18	87	7.3	874	11	P97378	P97378	mus musculus
	19	87	7.3	1083	5	Q45604	Q45604	caenorhabdi
	20	87	7.3	1120	3	Q08773	Q08773	saccharomyc

21	87	7.3	26926	4	010466	010466	homo sapien
22	86.5	7.2	429	3	006103	006103	saccharomyc
23	84.5	7.1	2214	4	092673	092673	homo sapien
24	83.5	7.0	430	10	023854	023854	brassica ca
25	82.5	6.9	406	1	058459	058459	methanococ
26	82.5	6.9	746	12	090754	090754	foet.-and-mo
27	82	6.9	508	5	020930	020930	caenorhabdl
28	82	6.9	817	13	007784	007784	gallus gallu
29	82	6.9	1093	11	070535	070535	rattus norv
30	81.5	6.8	1040	13	09w675	09w675	brachydania
31	81	6.8	1009	1	058653	058653	methanococ
32	81	6.8	1375	5	054537	054537	drosophila
33	81	6.8	1493	11	p97798	p97798	mus musculu
34	81	6.8	1526	11	094538	094538	drosophila
35	81	6.8	2340	5	060705	060705	mus musculu
36	80.5	6.7	334	11	070367	070367	rattus norv
37	80.5	6.7	962	4	094977	094977	homo sapien
38	80	6.7	513	11	035664	035664	mus musculu
39	79.5	6.6	431	10	023861	023861	brassica ca
40	79.5	6.6	829	2	09xw9	09xw9	caenorhabdl
41	79.5	6.6	1074	2	09x257	09x257	thermotoga
42	79	6.6	247	11	035663	035663	mus musculu
43	79	6.6	248	11	035983	035983	mus musculu
44	79	6.6	442	3	006349	006349	saccharomyc
45	79	6.6	513	11	035238	035238	mus musculu

ALIGNMENTS

	RESULT	1	
DB	O9YHWO	PRELIMINARY:	PRT: 569 AA.
AC	O9YHWO:		
DT	01-MAY-1999 (TREMBLrel. 10, Created)		
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)		
DT	01-MAY-1999 (TREMBLrel. 10, last annotation update)		
DE	INTERFERON ALPHA/BETA RECEPTOR 1.		
CN	IPNAR1.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Archosauria; Aves;		
NC	Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-LIVER:		
RA	REBOUL J, GARDINER K., MONNERON D., UZE G., LUTFALLA G.;		
RT	"Comparative genomic analysis of the interferon/interleukin-10		
RL	receptor gene cluster.";		
RM	Genome Res. 0:0-0(1999). ;		
DR	EMBL; AF082664; AAD13669.1; - .		
KM	Receptor.		
SO	SEQUENCE 569 AA; 64055 MM; F99BC09 CRC32;		
	Query Match	36.0%; Score 430.5; DB 13; Length 569;	
	Best Local Similarity	43.8%; Pred. No. 7.4e-31;	
	Matches 99; Conservative 37; Mismatches 79; Indels 11; Gaps 6;		
Oy	7 GATLTVLVAVGWMVLSAAAGCKNKLSPOKVEVDIIDDNFLMWNRSDSEGVWTFSDGYO 66		
Db	9 GLLAALVLCVLLVVRSCCAGQTNLKSPDIOIYAANTNTLMWTNGDGT-NVTSAQYO 67		
Oy	67 -----KTGDMDNIKLSGCNTITSTKCNFSLSKLNTLYEEILKIRAE-KENTSSWEVDSF 120		
Db	68 CDDDLQTSPEPKELSGCGNCSHTCDPSSALTATYDTIHIIIRARRAKRPMSSIFEM 127		
Oy	121 TPFRRQAIGPPEVHLLEADKAIVIHISPTKDSV--MAADGLSTYSLLIKNSGVEE 178		
Db	128 IPEYIAQIGPPRIALOINGAIKINISPPEANQVQRKM-LTISVFPRYNVINDNSGN-E 185		
Oy	179 RLENITSRKHYKLSPEFTTYCLKYRAALLTSWKIGVSPVPHIKTT 224		
Db	186 KYRSLLPIIDVINDLAPETTYCLKVQATVPLEDKGGLSFSFIHQIKTT 231		

Query Match	18.3%	Score 219;	DB 11;	Length 349;
Best Local Similarity	28.2%	Pred. NO. 4.5e-12;		
Matches 62; Conservative	47;	Mismatches 83;	Indels 28;	Gaps 9

RESULT	3	
Q63953		
ID	Q63953	PRELIMINARY;
		PRT; 332 AA

```

RA  PESTRA 5.0, DEMBIC 2.0;
RT  "Genomic organization and promoter analysis of the gene ifngR2
    encoding the second chain of the mouse interferon gamma receptor.";
RL  Second 1 Immunol 44:599-606(1996).
DR  EMBL; U69589; AAC52938.1; JOINED.
DR  EMBL; U69594; AAC52938.1; JOINED.
DR  EMBL; U69595; AAC52938.1; JOINED.
DR  EMBL; U69596; AAC52938.1; JOINED.
DR  EMBL; U69597; AAC52938.1; JOINED.
DR  EMBL; U69598; AAC52938.1; JOINED.
DR  EMBL; S69336; AAB30165.1; -.
DR  MGD; MGI:107654; IfngR2.
DR  PRAW; PF00041; fn3; 1
SQ  SEQUENCE 332 AA; 37471 MW; 0BF2AE9E CRC32;

```

Query Match	17.0%;	Score 203;	DB 11;	Length 332;
Best Local Similarity	30.1%;	Pred. No. 1.2e-10;		
Matches	69;	Conservative	38;	Mismatches 86;
			Indels	36;
			Gaps	13;

RESULT 4

Query Match	15.0%;	Score 179;	DB 13;	Length 341;
Best Local Similarity	26.0%;	Pred. No. 1.8e-08;		
Matches	53;	Conservative 45;	Mismatches 84;	Indels 22;
				Gaps 9

[illegible]

0Y 148 -PGTKDSVMAALDGL--SFTSLILKNSGVERIENIYSRHK---IYKISPTTYCLK 201
DB 137 PAADREHDKSLKQYSSWIRILLYWK--KGSNKKVIHIDKNSSEILSOLEPTIYCIQ 194
0Y 202 VKAALLTSM-KIGVYSPHYCIKT 224
DB 195 VQ-GVPEWKNKTGERSOELCQIT 217

RESULT 5
ID 014936 PRELIMINARY; PRT; 484 AA.
AC 014936;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89003065.
RA AGUER M., DEMBIC Z., MERLIN G.;
RT "Molecular cloning and expression of the human interferon gamma
receptor.";
RL Cell 55:273-280(1988).
RN [2]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE: 97246734.
RA MERLIN G., VAN DER LEDE B.-J.M., MCKUNE K., KNEZEVIC N.,
RA BANNAARH W., ROMOJIN N., VIGAS-PEQUIGNOT E., KIEFER H., AGUET M.,
RA DEMBIC Z.;
RT "The gene for the ligand binding chain of the human interferon gamma
receptor.";
RL Immunogenetics 45:413-421(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX DEMBIC Z.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U19247; AAC52064.1;
DR EMBL: U19241; AAC52064.1; JOINED.
DR EMBL: U19242; AAC52064.1; JOINED.
DR EMBL: U19243; AAC52064.1; JOINED.
DR EMBL: U19244; AAC52064.1; JOINED.
DR EMBL: U19245; AAC52064.1; JOINED.
DR EMBL: U19246; AAC52064.1; JOINED.
SO SEQUENCE 484 AA; 53818 MW; EBC99D1F CRC32;

Query Match 9.5%; Score 113.5; DB 4; Length 484;
Best Local Similarity 22.9%; Pred. No. 0.022;
Matches 47; Conservative 42; Mismatches 77; Indels 39; Gaps 8;

0Y 3 VILGATLVAVGPNVLSAA-AGKNNKSPQYEVVDIIDNFIILMNRSDSVGNV-T 60
DB 1 MALFELPLVWQVYRAEMGTADLGPSVSPPTVYTIESTYMNPIYWEY-QIMPVVPV 58
0Y 61 FSPDYOKTGMDNWKILSGCONITSTKCNFSLKLVYEELIRIRA--EKENTSSWYEV 117
DB 59 FTVEVKVYGVKNSWIDACINISHYCNISDHVGDPSNSLWVKAKAYGQKE--SAVAKS 116
0Y 118 DSFTPRKAOIGPEVHLAEADKAIVIHISPTKDSVMAALDGLSFTYSLILKNSGVE 177
DB 117 EEFAVCDKGKIGPKLDIRKEKQIMIDI-----FHPSVYV---NGDE 156
0Y 178 ERIENIYSRAKIYKLSPTTYCLKV 202
DB 157 QEVD-----YDEPTTCYIRV 171

RESULT 6
ID 023020

PRELIMINARY; PRT; 6048 AA.
AC 023020; Q27232;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE TWITCHIN.
GN UNC-22 OR 2K617.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Pelodidae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE: 90044042.
RA BENJIN G.M., KIFF J.E., NECKELMANN N., MOERMAN D.G., WATERSON R.H.;
RT "Sequence of an unusually large protein implicated in regulation of
myosin activity in C. elegans.";
RL Nature 342:45-50(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE: 93387664.
RA BENJIN G.M., L'HERNAULT S.W., MORRIS M.E.;
RT "Additional sequence complexity in the muscle gene, unc-22, and its
encoded protein, twitchin, of Caenorhabditis elegans.";
RL Genetics 134:1097-1104(1993).
RN [3]
RP SEQUENCE FROM N.A.
RA HARRIS B.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: X15423; CAA33463.1;
DR EMBL: 273899; CAA38081.1; ALT-INIT.
DR EMBL: 273897; CAA38081.1; JOINED.
DR HSSP: 063450; 1A06.
DR PRAW: PF000641; fn3; 31.
DR PRAW: PF000647; 1g; 13.
DR PRAW: PF00069; PKinase; 1.
DR PRINTS: P00014; FNTYPEIIT.
KM Myosin; Kinase.
SO SEQUENCE 6048 AA; 668449 MW; 1977C602 CRC32;

Query Match 8.2%; Score 97.5; DB 5; Length 6048;
Best Local Similarity 22.8%; Pred. No. 17;
Matches 44; Conservative 22; Mismatches 74; Indels 53; Gaps 10;

0Y 30 LKSPQK---VEV-DIIDNFIILMNRSDSVGNVTFSPDYOK--TGMDNWKILSGCONI 82
DB 1073 LDRPSKPNGLVSDVFDENLNLMSKPPDDGGEPITFYEVKLDIATGRWP---CAKY 1129
0Y 83 TSTRCNFSSILKLVYEELIRIRA-EKENTSSWYEVDSFTPRKAOIGPEVHLAEADKA 141
DB 1130 KDKRAHIDGLAKG-QTYQGRVAKVKNKGSALSLDIDKDKANPDEPKT----- 1180
0Y 142 IVHISFGTDSVMAALDGLSFTYSLILV---KNSGVERIENIYSRAKIYKLSPTTY 198
DB 1180 -----GTPDVVDWADRVV-----LEWEPKSDG-----APITQY 1210
0Y 199 CLKVKAALLTSMK 211
DB 1211 VIEKKGKHGRDQ 1223

RESULT 7
ID 023550 PRELIMINARY; PRT; 6831 AA.
AC 023550;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE UNC-22 PROTEIN.
GN UNC-22.
OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 OC Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA WHITE S.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: 273897; CA98064.1; -
 DR EMBL: 273899; CA98064.1; JOINED.
 DR HSSP: P02751; 1FNA.
 DR PFAM: PF00041; fn3; 31.
 DR PFAM: PF00047; 19; 17.
 DR PFAM: PF00069; Pkinase; 1.
 DR PRINTS: PR00014; FNTYPEIIT.
 SQ SEQUENCE 6831 AA; 752579 MW; 0A66C338 CRC32;

Query Match 8.2%; Score 97.5; DB 5; Length 6831;
 Best Local Similarity 22.8%; Pred. No. 20;
 Matches 44; Conservative 22; Mismatches 74; Indels 53; Gaps 10;

QY 30 LKSPQK---VEV-DIIDNFIKRNRSDESGVNTFSPDYOK--TGMDNMKLSGCONI 82
 DB 1856 LDRPSKNGPLEVSDVFEDNLSMKRPDDGGEPLEYEVEKLDATGMRVP---CAKV 1912
 QY 83 TSTCNFSSSLKLVYEIEIKLRIR-A-EKENTSSWTEVDSFTPFKRAQIGPEVHLEADKA 141
 DB 1913 KDTKAHIDGLKKG--QTYOFKRAVKNKGASDALTSTDKTKAKNPYDEPKT----- 1963
 QY 142 IVIHISPTKDSVMALDGLSFTYSLLIW--KNSSGVEERIENTYSRHKIYKLSPEPTY 198
 DB 1963 -----GTPDYVDMDADRVS-----LEWEPPKSDG-----APITQY 1993
 QY 199 CLKVKAALLTSWK 211
 DB 1994 VIEKKGKGRDQW 2006

RESULT 8
 Q23551 PRELIMINARY; PRT; 7160 AA.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE ZK617.1B PROTEIN.
 GN ZK617.1B.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 OC Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HARRIS B.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERS M.,
 RA BOWFIELD J., BURTON J., CONNELL M., COPESEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOMKNEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SUTLSON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLDMAN P.;
 RT "2.2 kb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RP SEQUENCE FROM N.A.
 RA WHITE S.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL: 273899; CA98082.1; -
 DR EMBL: 273897; CA98082.1; JOINED.
 DR EMBL: 273897; CA98065.1; -
 DR EMBL: 273899; CA98065.1; JOINED.
 DR HSSP: P02751; 1FNA.
 DR PFAM: PF00041; fn3; 31.
 DR PFAM: PF00047; 19; 17.
 DR PFAM: PF00069; Pkinase; 1.
 DR PRINTS: PR00014; FNTYPEIIT.
 SQ SEQUENCE 7160 AA; 789211 MW; EDD567FE CRC32;

Query Match 8.2%; Score 97.5; DB 5; Length 7160;
 Best Local Similarity 22.8%; Pred. No. 21;
 Matches 44; Conservative 22; Mismatches 74; Indels 53; Gaps 10;

QY 30 LKSPQK---VEV-DIIDNFIKRNRSDESGVNTFSPDYOK--TGMDNMKLSGCONI 82
 DB 2185 LDRPSKNGPLEVSDVFEDNLSMKRPDDGGEPLEYEVEKLDATGMRVP---CAKV 2241
 QY 83 TSTCNFSSSLKLVYEIEIKLRIR-A-EKENTSSWTEVDSFTPFKRAQIGPEVHLEADKA 141
 DB 2242 KDTKAHIDGLKKG--QTYOFKRAVKNKGASDALTSTDKTKAKNPYDEPKT----- 2292
 QY 142 IVIHISPTKDSVMALDGLSFTYSLLIW--KNSSGVEERIENTYSRHKIYKLSPEPTY 198
 DB 2292 -----GTPDYVDMDADRVS-----LEWEPPKSDG-----APITQY 2322
 QY 199 CLKVKAALLTSWK 211
 DB 2323 VIEKKGKGRDQW 2335

RESULT 9
 Q28733 PRELIMINARY; PRT; 6875 AA.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1998 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE TITIN (FRAGMENT).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CE12;
 RA LABEIR S.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-6805 FROM N.A.
 RC STRAIN-CE12;
 RX MEDLINE: 92258380.
 RA LABEIR S., GAUTEL M., LAKEY A., TRINICK J.;
 RT "Towards a molecular understanding of titin.";
 RL EMBO J. 11:1711-1716(1992).
 RN [3]
 RP SEQUENCE OF 4305-5320 FROM N.A.
 RC TISSUE-PCOAS MUSCLE;
 RX MEDLINE: 90238553.
 RA LABEIR S., BARLOW D.P., GAUTEL M., GIBSON T., HOLT J., HSIEH C.T.,
 RA FRANCIS U., LEONARD K., WARDLE J., WHITTING A., TRINICK J.;
 RT "A regular pattern of two types of 100-residue motif in the sequence
 RT of titin.";
 RL Nature 345:273-276(1990).
 DR EMBL: X64696; CA445937.1; -
 DR EMBL: X17329; CA435207.1; -
 DR HSSP: P56276; 1TLK.
 DR PFAM: PF00041; fn3; 50.
 DR PFAM: PF00047; 19; 3.
 KW Myosin: Muscle protein.
 FT NON_TER 1 6875 6875

SEQUENCE 6875 AA; 759127 MW; E5D3B61F CRC32;

Query Match
Best Local Similarity 21.7%; Score 91.5; DB 6; Length 6875;
Matches 54; Conservative 24; Mismatches 76; Indels 95; Gaps 10;

QY 8 ATTLVAVGPVWLSAAAGCNKLPQKVEVDIIDNFLRNKSDSVGNVTFSPDYOK 67
DB 221 ATVNVLDRPGP-----VRNLKIP-----DVSSDRCTRIRMDPEDD----- 256
QY 68 TGMDMWIKISGC--QINISTKCNFSSKIKNY-----EIKILIRAK 108
DB 256 -----GGEIONYLEKCESRMRWSTYSATVLPPTVTRILIEGNEYIFRVAEN 306
QY 109 E-----NTSWYEDSFTEPRKAQIGPEVHLEADKAIV-----HISP 148
DB 307 KIGTGPPESKVIAKTYKDRGRDPPEVTVSKEMTVWSPPEYDGKSTGYLEK 366
QY 149 GTKDSVMALDGLSTFTYSLILKNSGVEERIENTYSRRKIYKLSPEPTYCLKRAALT 208
DB 367 KEKHSVRM-----VFNKSAIPER-----RLKVONLIPGHEYFRVKA----- 405
QY 209 SMKIGVYSP 217
DB 405 ENELGVGP 413

RESULT 10
Q16614 PRELIMINARY: PRT; 1143 AA.

AC Q16614
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE T200 LEUKOCYTE COMMON ANTIGEN (CD45, LC-A) PRECURSOR (EC 3.1.3.48)
DE (CD45, LC-A).
GN PTPRC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87275816.
RA RALPH S.J., THOMAS M.L., MORTON C.C., TROMBRIDGE I.S.;
RT "Structural variants of human T200 glycoprotein (leukocyte-common antigen)".
RL EMBO J. 6:1251-1257(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA;
RX MEDLINE; 89009812.
RA HALL L.R., STREUBI M., SCHLOSSMAN S.F., SAITO H.;
RT "Complete exon-intron organization of the human leukocyte common antigen (CD45) gene".
RL J. Immunol. 141:2781-2787(1988).
DR EMBL; M23492; AAD15273.1; JOINED.
DR EMBL; M23461; AAD15273.1; JOINED.
DR EMBL; M23462; AAD15273.1; JOINED.
DR EMBL; M23466; AAD15273.1; JOINED.
DR EMBL; M23467; AAD15273.1; JOINED.
DR EMBL; M23468; AAD15273.1; JOINED.
DR EMBL; M23469; AAD15273.1; JOINED.
DR EMBL; M23470; AAD15273.1; JOINED.
DR EMBL; M23471; AAD15273.1; JOINED.
DR EMBL; M23472; AAD15273.1; JOINED.
DR EMBL; M23473; AAD15273.1; JOINED.
DR EMBL; M23474; AAD15273.1; JOINED.
DR EMBL; M23475; AAD15273.1; JOINED.
DR EMBL; M23476; AAD15273.1; JOINED.
DR EMBL; M23477; AAD15273.1; JOINED.
DR EMBL; M23478; AAD15273.1; JOINED.
DR EMBL; M23479; AAD15273.1; JOINED.

DR EMBL; M23480; AAD15273.1; JOINED.
DR EMBL; M23481; AAD15273.1; JOINED.
DR EMBL; M23482; AAD15273.1; JOINED.
DR EMBL; M23483; AAD15273.1; JOINED.
DR EMBL; M23484; AAD15273.1; JOINED.
DR EMBL; M23485; AAD15273.1; JOINED.
DR EMBL; M23486; AAD15273.1; JOINED.
DR EMBL; M23487; AAD15273.1; JOINED.
DR EMBL; M23488; AAD15273.1; JOINED.
DR EMBL; M23489; AAD15273.1; JOINED.
DR EMBL; M23490; AAD15273.1; JOINED.
DR EMBL; M23491; AAD15273.1; JOINED.
DR EMBL; Y00062; CA86269.1; JOINED.
DR HSSP; P18052; IYFO.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PFAM; PF00041; fn3; 2.
DR PFAM; PF00102; X-PHOSPHATASE; 2.
DR PRINTS; PRO0700; PRTPHPTASE.
KW Signal; Alternative splicing; Hydrolyase.
FT SIGNAL 1 23
FT CHAIN 24 1143
FT SIGNAL 24 1143
SO SEQUENCE 1143 AA; 130897 MW; 97A3A561 CRC32;

Query Match
Best Local Similarity 7.6%; Score 90.5; DB 4; Length 1143;
Matches 36; Conservative 23; Mismatches 60; Indels 53; Gaps 6;

QY 53 DESVGNVTFSPDYOKTGMWIKISGCQINISTKCNFSSKIKNYEELKIRAKETS 112
DB 66 DEKANTIVDYLYNK-----ETKLETAFLNNEVEEC-----GNNTC 102

QY 113 SWEYDSETPPRKAQIGPEVHLEADKAIVHISPT----- 151
DB 103 TNEVHNTECKNMSVSHSCAPKXTLLDVPQYERQLHDCQVEAKDTTICKW 162

QY 151 KDSVMALDGLSTFTYSL---LINKSSGVEERIENTYSRRKIYKLSPEPTY 198
DB 163 KNIETFTCDTQNTYRFGCGNMIFDNK---EIKLENLEPEHE-YKCDSEILY 210

RESULT 11
Q9YHV9 PRELIMINARY: PRT; 508 AA.

AC Q9YHV9
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE INTERFERON ALPHA/BETA RECEPTOR 2.
DE INTERFERON ALPHA/BETA RECEPTOR 2.
GN IFNAR2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RA REBOUL J., GARDINER K., MONNERON D., UZE G., LUTFALLA G.;
RT "Receptor gene cluster of the interferon/interleukin-10 receptor gene cluster".
RL Genome Res. 0:0-0(1999).
DR EMBL; AF082665; AAD13670.1; JOINED.
DR HSSP; P13726; IYFH.
KW Receptor.
SO SEQUENCE 508 AA; 57049 MW; 2DC4E498 CRC32;

Query Match
Best Local Similarity 7.5%; Score 89.5; DB 13; Length 508;
Matches 61; Conservative 35; Mismatches 96; Indels 71; Gaps 15;

QY 2 MVLVIGAT---TLVAVGPVWLSAAAGCNKLPQKVEVDIIDNFLRNKSDSVGNVTFSPDYOK 52
DB 1 MVLVIGATPLRYQLVFSI---LCAACYSSLSERKIPREPDNLQMTSNFQHIISRAHS 57

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OY 53 DESVC---NWPSFQYQKTGMNWKLSGCGQITSTKCNFSLKLNVEE-----IKLNR 105
Db 58 DPTVFTYRLVLS-----SHSNMKAIOACSTIVOPFCNCLDDFOVVSDETSAPVQSPVG 111
OY 106 AERKENTSSWEYDSTFTPRKAOIGPPEVHLEAEADKAIYHIS-PGT---KDSVMALDGL 161
Db 112 TEVFNSLLH-----FSPISFTFLGPENLNSCVHCINTITLPTTHLRKNKL----- 162
OY 162 SFTYSLLIWKNSGVEERIEENIYSNRK-----LYKLSPEPTYCLKV----- 203
Db 162 ---LSLFDIYNKVNVEITLRTVGECHKRSPEKYTEEPESIVIEELYPNMRNCVSVMTAS 218
OY 203 --KALLTSMKIGVSPVHCIT 223
Db 219 LNKHSIPSAWK-----CIT 233

RESULT 12
ID 054711 PRELIMINARY; PRT: 2033 AA.
AC 054711;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE SORTLIN-RELATED RECEPTOR, LDLR CLASS A REPEATS-CONTAINING PRECURSOR
DE (GP250) (FRAGMENT).
CN SORL1.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RA HEKMAN-BORGMEYER I., HAMPE W., SCHINKE B., METHNER A., NYKAER A.,
RA SUDSENS U., FENGER U., HERBARTH B., SCHALLER H.C.;
RL Mech. Dev. 0:0-0(1997).
DR EMBL: AF031816; AAC16739.1; -
DR HSSP: P01130; IATJ
DR MGD: MGI:1202296; Sor11.
DR PROSITE; PS01209; LDLR_1; 10.
DR PFAM; PF00041; In3; 4.
DR PFAM; PF00057; Idl_recept_a; 11.
DR PFAM; PF00058; Idl_recept_b; 5.
KW Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 2033 AA; 227305 MW; DC8108CD CRC32;

Query Match 7.5%; Score 89.5; DB 11; Length 2033;
Best Local Similarity 19.2%; Pred. No. 22;
Matches 33; Conservative 33; Mismatches 77; Indels 29; Gaps 7;

OY 44 NEILRMNSDESU-----GNV-TFSFDYQKTGMNWKLSGCGQITSTKCNFS 90
Db 1474 NLOLNLSEEEGVIIIGHNAPVHTGLIREYIVERSGSGKMMASQASNSTEIK---- 1530
OY 91 SLKLNVVEIKRIARAEKENTSSWEYDSTFTPRKAOIGPPEVHLEAEADKAIY----- 144
Db 1530 NLLNLAALTVAR-AAVTSRGIGMNSDSTIKTKIKRVIOAPRIHIDSDENSLSFTLWMD 1588
OY 144 --IHISPGKDSVMALDGLSFTYSLLIWKNSGVEERIEENIYSNRKIYKLS 193
Db 1589 GDIKYN-GVYVNLFWSPDAHKQEKKTLSRGSALSHKYSNL-TAHTSYEIS 1638

RESULT 13
ID 095209 PRELIMINARY; PRT: 2213 AA.
AC 095209;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

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OS   Lr11.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN   (1)
RP   SEQUENCE FROM N.A.
RC   TISSUE-LIVER.
RX   MEDLINE: 96394640.
RA   YAMAZAKI H., BUJO H., KUSUNOKI J., SEIMIYA K., KANAKI T., MORISAKI N.,
RA   SCHNEIDER W.J., SATO Y.:
RT   "Elements of neural adhesion molecules and a yeast vacuolar protein
RT   sorting receptor are present in a novel mammalian low density
RT   11poprotein receptor family member."
RL   J. Biol. Chem. 271:24761-24768(1996).
DR   EMBL: D86350; BAA13075.1; -.
DR   HSSP; P01130; 1A5J.
DR   PROSITE; PS01209; LDLRA_1; 10.
DR   PFAM; PF00057; ldl_recept_a; 11.
DR   PFAM; PF00058; ldl_recept_b; 4.
DR   PFAM; PF00041; fn3; 5.
DR   PRINTS; PR00261; LDLRECEPTOR.
DR   PRINTS; PR00014; ENTPEP111.
KW   Glycoprotein.
SQ   SEQUENCE 2213 AA: 247764 MW: 835F3995 CRC32:

Query Match          7.5%; Score 89.5; DB 6; Length 2213;
Best Local Similarity 17.1%; Pred. No. 24;
Matches 32; Conservative 36; Mismatches 76; Indels 43; Gaps 7.

OY   32 SPQAYVDIIDDN--FLIRNRSDSEYGNV-TSEFDYQKGTGMNWKLSGCONITSTKC 87
DB   1652 APOINQLSLHGEEGVIVGHMSPPTHGLIREYIYEYSRSGSKVWTSERAASNFEIK- 1711
OY   88 NFFSLKLVNVEIKRIRAEKENTSMWEYVDSEFTPEFRKAOIGPPEVHLEAEDEKAVIHHS 147
DB   1711 ---NLVNTLTLYVR-AAVTSGRTGNWSDSKSITTVKGAIPPHIHIDNVE----- 1760
OY   148 PGTGDSVMALDGLSFTYSL-----LIWKNSSGVBER--IENIYSRRKIYK 191
DB   1760 -----NSLSFTLTVDGNIKRVNGYVYVLFWAFPTFHKQEKKTMMNQGSSVSHKVN 1808
OY   192 LSPETTY 198
DB   1809 LTAOTAY 1815

RESULT 14
O88307 PRELIMINARY; PRT; 2215 AA.
AC   O88307;
DT   01-NOV-1998 (TREMBLrel. 08, Created)
DT   01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE   Lr11.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
RN   (1)
RP   SEQUENCE FROM N.A.
RC   TISSUE-LIVER.
RA   KANAKI T., BUJO H., HIRAYAMA S., TANAKA K., YAMAZAKI H., SEIMIYA K.,
RA   MORISAKI N., SCHNEIDER W.J., SATO Y.:
RT   "Developmental regulation of Lr11 expression in murine brain."
RL   DNA Cell Biol. 0:0-0(1998).
DR   EMBL; AB015790; BAA31219.1; -.
DR   HSSP; P01130; 1A5J.
DR   PROSITE; PS01209; LDLRA_1; 10.
DR   PFAM; PF00057; ldl_recept_a; 11.
DR   PFAM; PF00058; ldl_recept_b; 5.
DR   PFAM; PF00041; fn3; 4.
DR   PRINTS; PR00261; LDLRECEPTOR.
DR   PRINTS; PR00014; ENTPEP111.

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2000, 05:53:09 ; Search time 903.62 Seconds
(without alignments)
-1445.806 Million cell updates/sec

Title: US-09-240-675-1
Perfect score: 1343
Sequence: 1 CTCGACGATCTCGCGCGC.....ATACCTCTAATGAGGTACC 1343

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 882769 seqs, -486395729 residues

Total number of hits satisfying chosen parameters: 1765538

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_dal:*
2: gb_dal:*
3: gb_com:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_pl1:*
10: gb_pl2:*
11: gb_pl3:*
12: gb_pl3:*
13: gb_pl3:*
14: gb_sy:*
15: gb_un:*
16: gb_vl:*
17: em_fun:*
18: em_hum1:*
19: em_hum2:*
20: em_hum2:*
21: em_hum2:*
22: em_hum2:*
23: em_hum2:*
24: em_hum2:*
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26: em_hum2:*
27: em_hum2:*
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29: em_hum2:*
30: em_hum2:*
31: em_hum2:*
32: gb_hlg1:*
33: gb_hlg2:*
34: gb_hlg2:*
35: gb_hlg2:*
36: em_bal:*
37: em_bal:*
38: em_hum3:*
39: em_hum4:*
40: gb_pr4:*
41: gb_hlg3:*
42: gb_hlg4:*
43: gb_hlg5:*
44: gb_hlg6:*

45: gb_hlg7:*
46: em_hlg1:*
47: em_hlg2:*
48: em_hlg3:*
49: em_hum5:*
50: gb_pl3:*
51: gb_pl3:*
52: gb_pl3:*
53: gb_hlg8:*
54: gb_hlg9:*
55: gb_hlg10:*
56: gb_hlg11:*
57: gb_hlg12:*
58: gb_hlg13:*
59: gb_hlg14:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1343	100.0	1343	5 A26593	A26593 Human Inter
2	1343	100.0	1343	5 A32389	A32389 Interferon
3	1343	100.0	1343	5 A76127	A76127 Sequence 1
4	1334	99.3	1755	5 A26595	A26595 Human Inter
5	1334	99.3	1755	5 A32391	A32391 Interferon
6	1334	99.3	1755	5 A76129	A76129 Sequence 3
7	1330.8	99.1	2755	5 H0MIFNRA	H0MIFNRA Human Inter
8	1330.8	99.1	2755	5 G28571	G28571 Human Inter
9	1330.8	99.1	2784	5 ARO30347	ARO30347 Sequence 1
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11	824.2	61.4	3230	3 BOVINRRA	BOVINRRA Bos taurus IF
12	824.2	61.4	3284	3 BOVINRRA	BOVINRRA Bos taurus
13	821	61.1	2914	3 OMOIFNARE	OMOIFNARE Ovis aries
14	819.4	61.0	2559	3 OMOIFNARE	OMOIFNARE Ovis aries
15	540.2	40.2	3894	12 MUSIFNAR	MUSIFNAR Mus musculus
16	251.8	18.7	22937	9 AP000297	AP000297 Homo sapi
17	251.8	18.7	32906	9 HSFNAR	HSFNAR Homo sapi
18	251.8	18.7	100000	9 AP000044	AP000044 Homo sapi
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28	49.8	3.7	41667	7 SPBC365	SPBC365 S. pombe c
29	49	3.6	168	5 I50850	I50850 Sequence 8
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32	45	3.4	135599	7 CPU30821	CPU30821 Cytophora
33	44.8	3.4	175815	45 AC009621	AC009621 Homo sapi
34	44.8	3.3	145578	44 AC016875	AC016875 Homo sapi
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ALIGNMENTS

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RESULT 1
A26593      1343 bp      DNA      PAT      02-OCT-1995
LOCUS       Human interferon alpha receptor gene.
DEFINITION  A26593
ACCESSION   A26593
VERSION     A26593.1 GI:1247458
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1343)
REFERENCE
AUTHORS     WATER-SOLUBLE POLYPEPTIDES HAVING HIGH AFFINITY FOR INTERFERONS
TITLE       alpha AND beta
JOURNAL     Patent: WO 9218626-A 17 29-OCT-1992;
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BASE COUNT  449 a      254 c      264 g      376 t
ORIGIN
Query Match      100.0%; Score 1343; DB 5; Length 1343;
Best Local Similarity 100.0%; Pred. No. 2.8e-296;
Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
A32389      1343 bp      DNA      PAT      08-JUL-1996
LOCUS       Interferon receptor gene.
DEFINITION  A32389
ACCESSION   A32389
VERSION     A32389.1 GI:1567382
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominiidae; Homo.

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Query Match 100.0%; Score 1343; DB 5; Length 1343;
 Best Local Similarity 100.0%; Pred. No. 2.8e-296;
 Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 VERSION A76127.1 GI:6088263
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 ORGANISM unidentified.
 REFERENCES
 1 (bases 1 to 1343)
 AUTHORS Benoit,P. and Meyer,F.
 TITLE MONOCLONAL ANTIBODIES AGAINST THE INTERFERON RECEPTOR, WITH
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 Patent: WO 9320187-A 14-OCT-1993;
 EUROPE BIOTECHNOLOGIE (FR); BENOIT PATRICK (FR)
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BASE COUNT		449 a	254 c	264 g	376 t		
ORIGIN							
Query Match		100.0%	Score 1343:	DB 5:	Length 1343:		
Best Local Similarity		100.0%	Pred. No. 2.8e-296:				
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BASE COUNT		449 a	254 c	264 g	376 t		
ORIGIN							
Query Match		100.0%	Score 1343:	DB 5:	Length 1343:		
Best Local Similarity		100.0%	Pred. No. 2.8e-296:				
Matches 1343:		Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:		
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Db	901	TCTTCTCTCAAAAGCTTTTCCAAAAGAAATTTACCTTCCGCGGACAGCATCTGATG	960				
Qy	961	GAATAACACATCTTTTGGTCTGAAGAATAAAGTTGATACGTGAATATACAGCTTCC	1020				
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Qy	1021	TACTTCTCGAGCTTTTAAATAGATAGCCCTAGTATTCATTCATATCTATCCGGG	1080				
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Qy	1201	CAGTTCCTAATTGAAACCACTGACTGTATATGTGTGAAACCGACACACACATGG	1260				
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 Query Match 99.3%; Score 1334; DB 5; Length 1755;
 Best Local Similarity 100.0%; Pred. No. 3.1e-294;
 Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 121 CTCTCAAAAGTGAAGTGCACATCATAGATGACACTTATCTGTGAGTGAACAG 180
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 QY 181 GCGATGAGTCTGTGCGGAGTGTGACTTTTCATTCGATTAACAAAACTGGATGATA 240
 DB 181 GCGATGAGTCTGTGCGGAGTGTGACTTTTCATTCGATTAACAAAACTGGATGATA 240
 QY 241 ATTGGATTAATTTGTCTGGGTGTCAGAAATATTACTAGTACCAATGCACTTTCTTAC 300
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 QY 361 CTTCAGTATGAGGTTGACTCATTTTACACATTTCCGAAAGTCAGATGGTCTCCAG 420
 DB 361 CTTCAGTATGAGGTTGACTCATTTTACACATTTCCGAAAGTCAGATGGTCTCCAG 420
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 DB 421 AAGTACATTAGAACCTGAAGTAAGCAATAGTATGATACATCTCTCTGGAACAAAG 480
 QY 481 ATAGGTTATGAGGCTTGTGATGTTAAGTTTACATATAGCTTACTTATCTGGAAGA 540
 DB 481 ATAGGTTATGAGGCTTGTGATGTTAAGTTTACATATAGCTTACTTATCTGGAAGA 540
 QY 541 ACTCTTCAGTGTAGAGAAAGATTGAATAATTTATTCAGACATATAATTTATAAC 600
 DB 541 ACTCTTCAGTGTAGAGAAAGATTGAATAATTTATTCAGACATATAATTTATAAC 600
 QY 601 TCTCACCAGAGACTTATTGTCTTAAAGTTAAAGCAAGCTACTTACGTCATGGAAGA 660
 DB 601 TCTCACCAGAGACTTATTGTCTTAAAGTTAAAGCAAGCTACTTACGTCATGGAAGA 660
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 DB 721 CAGAAAAATATAGAGTCAAGTGTCCAAAAATCAGAACTATGTTCTTAAATGGGATTATAC 780
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 DB 901 TCTTCTCAAAAGCTTTTCCAAAAAGAAATTTACCTCTCCGCGGTACAGCATCTGATG 960
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DB 961 GAAATTAACACATCTTTTGTGCTGAAGAGATTAAGTTGATCTGAAATACAAAGCTTTC 1020
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 DB 1021 TACTCTCCAGTCTTTTAACATAGATCCCTTAGTATGATTCATTCATATATCGTG 1080
 QY 1081 CTCGAAAGAGTCTGGAACAGCGCTGTGATCCAGATTAATCCATGATTTATGAATA 1140
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 DB 1141 TTTTGGGAAAAACCTTCAATGCTGAGAAAAATATATCGAAGAAAAATCGATGTA 1200
 QY 1201 CAGTTCTAATTTGAACACAGTCTGATTTGTGTAAGGACAGACACACATG 1260
 DB 1201 CAGTTCTAATTTGAACACAGTCTGATTTGTGTAAGGACAGACACACATG 1260
 QY 1261 ATGAAAGCTGAATTAAGAGAGTGTGATGAGCGCTGATGAGAAAAACAAACAG 1320
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 QY 1321 GAAATACCTCTAA 1334
 DB 1321 GAAATACCTCTAA 1334

RESULT 5
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 LOCUS A32391 1755 bp DNA PAT 08-JUL-1996
 DEFINITION Interferon alpha and beta receptor gene.
 ACCESSION A32391
 VERSION A32391.1 GI:1567384
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 1755)
 JOURNAL Patent: FR 2657881-A 20 09-AUG-1991;
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 HCIRKIVENLPPENILEVSVQNVLVLMKYDYAMTFOVLAFLKPNPNHLK
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 VPKLPLUYICVAAARAHMDEKLNKSYSDAECETKRGNTSKIMLYICIALALAL
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BASE COUNT 593 a 324 c 334 g 504 t
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 Query Match 99.3%; Score 1334; DB 5; Length 1755;
 Best Local Similarity 100.0%; Pred. No. 3.1e-294;
 Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 CTGAGGAGATCTGGGGCGCTCCAGATGATGTCCTCTGGGCGGAGACCTTAG 60


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Oy 181 GCGATGATCTGTGCGGAATGTACTTTTTCATTGATTATCAAAAAAAGTGGATGATA 240
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Db 181 GCGAGATCTGTGCGGAATGTACTTTTTCATTGATTATCAAAAAAAGTGGATGATA 240
Oy 241 ATGGATATAAATGCTGGGTGTCAGAAATATCTAGTACCAAAAGCAACTTCTTGAC 300
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Db 241 ATGGATATAAATGCTGGGTGTCAGAAATATCTAGTACCAAAAGCAACTTCTTGAC 300
Oy 301 TCAAGCTGAATGTTATGAGAAATTAATGCGTATAGAGCAGAAAAAGAAACACTT 360
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Oy 301 TCAAGCTGAATGTTATGAGAAATTAATGCGTATAGAGCAGAAAAAGAAACACTT 360
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Oy 361 CTTCATGATGATGAGTGTACTGATTTACACATTTTCGCAAAAGCTGATGCTCCAG 420
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Oy 421 AAGTCAATTGAAGCTAGATAGGCAATGTAGTACATCTCTCTGGAACAAAG 480
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Oy 841 ACCATTGTATTAATGAGAAACAAATACCTGATGTGAATAATGTCAAAATCACCAGTGTG 900
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Db 1141 TTTTGGGAAACACTCAATGCTGAGAGAAAAATATCGAGAAAAAAGTGTGTA 1200
Oy 1201 CAGTCTTAATTTGAACACACTGATGATTTGTGTAAGCCAGACACACACATG 1260
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Db 1201 CAGTCTTAATTTGAACACACTGATGATTTGTGTAAGCCAGACACACACATG 1260
Oy 1261 ATGAAAGCTGAATTAAGCAAGTGTGTTTGTAGTACGCTGTATGTGAGAAAAACAAACGAG 1320
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Db 1261 ATGAAAGCTGAATTAAGCAAGTGTGTTTGTAGTACGCTGTATGTGAGAAAAACAAACGAG 1320
Oy 1321 GAAATACCTTAAA 1334
Db 1321 GAAATACCTTAAA 1334

RESULT 7
HUMIFNRA 2755 bp mRNA PRI 08-NOV-1994
LOCUS Human Interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds.
DEFINITION J03171.1 GI:184645
ACCESSION J03171.1
VERSION J03171.1
KEYWORDS Interferon-alpha receptor.
SOURCE Human cell line DAUDI, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE Use G., Lutfalla G. and Gresser I.
AUTHORS Genetic transfer of a functional human Interferon alpha receptor
TITLE Into mouse cells: cloning and expression of its cDNA
JOURNAL Cell 60 (2), 225-234 (1990)
MEDLINE 90124632
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
        by G. Use, 29-NOV-1989, for release after publication.
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             LSTYSILIRKNSGVERENIENSRKRIKLSPEITTYCLKVRALILTSKIGYSFY
             HCTITVENLPPPENLEVSQNONVYLKWDVYANNTFOVWHALRKPNQHLTK
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BASE COUNT 867 a 553 c 578 g 757 t
ORIGIN

Query Match 99.1%; Score 1330.8; DB 9; Length 2755;
Best Local Similarity 99.9%; Pred. No. 1,7e-293;
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Oy 61 TGTCTGTCGCGGTGGCCCATGGGTGTGTCGCGAGCGGCGGAGAAAAATCTAAAT 120
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Db 113 TGCCTGCGCCGTGGCCCATGGGCTGTGTCGCCGACGCCGAGGTGAAAAATCTAAAT 172
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QY 181 GCGATGAGTGTGCGGGAAATGTGACTTTTTCATCGATTTATCAAAAAAGGGGTGATA 240
Db 233 GCGATGAGTGTGCGGGAAATGTGACTTTTTCATCGATTTATCAAAAAAGGGGTGATA 292
QY 241 ATTGATGAAAATGTCTGGGTGTGCAAAATATTACTAGTACCAATGCAACTTTCTTCAC 300
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QY 361 CTTCATGATGAGTGTGACTCATTTACACCATTTCCAAAGCTCAGATTGCTCTCAG 420
Db 413 CTTCATGATGAGTGTGACTCATTTACACCATTTCCAAAGCTCAGATTGCTCTCAG 472
QY 421 AAGTACATTTAGAACTGAAAGATTAAGCAATAGTATACATCTCTCTGGAACAAAG 480
Db 473 AAGTACATTTAGAACTGAAAGATTAAGCAATAGTATACATCTCTCTGGAACAAAG 532
QY 481 ATAGTGTATGTCGGCTTGGATGCTTAAGCTTTACTATAGTCTTCTATCTGGAAGA 540
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Db 653 TCTCACCAGAGACTACTTATTTGTCTAAAGTAAAGCAGACACTTACTGATGATAA 712
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QY 781 ATGCAAAACATGACCTTTCAAGTTCAGTGTCCAGCCCTTTTAAAGAAATCTGGA 840
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QY 1321 GAAATACCTCTAAA 1334
Db 1373 GAAATACCTCTAAA 1386

RESULT 8
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LOCUS human STS SHGC-35315, sequence tagged site.
DEFINITION G28571
ACCESSION G28571 GI:1408386
VERSION G28571.1
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2755)
AUTHORS Myers,R.M.
JOURNAL Unpublished (1996)
COMMENT
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 415/7259687
Fax: 415/7259689
Email: myers@shgc.stanford.edu

Primer A: TGACAGAAATGAACCTGTCA
Primer B: TTTAAATAGTTAAGAGCTTCCCG
STS size: 175
PCR Profile:
Initial Incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/uL
Total Vol: 10 uL
Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from J03171
-- Washington University/Merck EST sequence.
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primer_bind 1750..1924
primer_bind 1750..1771
BASE COUNT 867 a 553 c 578 g 757 t
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Query Match 99.1%; Score 1330.8; DB 13; Length 2755;
 Best Local Similarity 99.9%; Pred. No. 1.7e-293;
 Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 DB 173 CTCCTCAAAAAGTAGAGTCGATCATAGATGACAACTTATCCGAGGTGAACAGGA 232
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 QY 181 GCGATGAGTCCTCGGGAATGTAATTTTCATTCGATTATCAAAAACCTGGATGATA 240
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 DB 233 GCGATGAGTCCTCGGGAATGTAATTTTCATTCGATTATCAAAAACCTGGATGATA 292
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 DB 893 ACCATTGTATATAATGGAACAAATACAGTGTGAATATGCAAAATACCAAGTGG 952
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 QY 901 TCTTTCTCAAAAAGTTTCCAAAAAGAAATTTACCTTCCGCGGTACAAGCATCTGATG 960
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QY 1021 TACTTCCTCAGTCTTTTAACATTAAGTCCCTAGTATCATTCATATCATATGCGTG 1080
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 DB 1193 TTTTGGGAAAACACTCAATGCTGAGAGAAAATATGAGAGAAAAAATGATGTTA 1252
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RESULT 9
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 LOCUS AR030347 Sequence 1 from patent US 5861258.
 DEFINITION AR030347
 ACCESSION AR030347
 VERSION AR030347.1 GI:5943561
 KEYWORDS
 SOURCE
 Unknown.
 ORGANISM
 Unknown.
 UNCLASSIFIED.
 REFERENCE
 1 (bases 1 to 2784)
 Mogenssen, K. Erik, Use, G., Lutfalla, G. and Gresser, I.
 TITLE
 Use of the alpha interferon receptor and cells which express the
 receptor, for identification of alpha interferon agonists
 JOURNAL
 Patent: US 5861258-A 1 19-JAN-1999;
 FEATURES
 Location/Qualifiers
 1..2784
 source
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 BASE COUNT 896 a 553 c 578 g 757 t
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Query Match 99.1%; Score 1330.8; DB 5; Length 2784;
 Best Local Similarity 99.9%; Pred. No. 1.7e-293;
 Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 DB 173 CTCCTCAAAAAGTAGAGTCGATCATAGATGACAACTTATCCGAGGTGAACAGGA 232
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 QY 181 GCGATGAGTCCTCGGGAATGTAATTTTCATTCGATTATCAAAAACCTGGATGATA 240
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 DB 233 GCGATGAGTCCTCGGGAATGTAATTTTCATTCGATTATCAAAAACCTGGATGATA 292
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 QY 241 ATTGATATAAATGTCCTGGGTGTCAGAAATATAGTACCAAAATGCAAACTTTCTCAG 300
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 293 ATTGATATAAATGTCCTGGGTGTCAGAAATATAGTACCAAAATGCAAACTTTCTCAG 352
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 QY 301 TCAAGCTGAATGTTATGAAGAAATTAATTCGATTAAGACAGAAAAAGAACACTT 360


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Db 353 TCAAGCTGATGTTATGAAAGAAATTAATGGCTATAGAGAGAGAAAAAGAAACACTT 412
QY 361 CTTCATGATGATAGAGTTGACTCATTTACACCAATTTGCAAGAGCTGAGTTGGTCTCCAG 420
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LOCUS 193602 2784 bp DNA
DEFINITION Sequence 1 from patent US 5731169.
ACCESSION 193602
VERSION 193602.1 GI:3938072
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unpublished.
AUTHORS (bases 1 to 2784)
Mogenssen, K. Erik, Use, G., Lutfalla, G. and Gresser, I.
TITLE cDNA fragment coding the alpha interferon receptor gene and process
for the preparation of a corresponding protein
JOURNAL Patent: US 5731169-A 1 24-MAR-1998;
FEATURES
Source Location/Qualifiers
1..2784
BASE COUNT 896 a 553 c 578 g 757 t
ORIGIN
Query Match 99.1%; Score 1330.8; DB 5; Length 2784;
Best Local Similarity 99.9%; Pred. No. 1/e-293;
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTGCAAGGAGATCGCGGCGCTCCAGATGATGCTGCTCTGGGCGGAGACCTTAG 60
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QY	781	ATCGAAACATGACCTTTCTCAAGTCAGTGTGCTCCAGCGCTTTTAAAAAGAAATCCTGGAA	840
Db	833	ATCGAAACATGACCTTTCTCAAGTCAGTGTGCTCCAGCGCTTTTAAAAAGAAATCCTGGAA	892
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Db	893	ACCATTTGTATAAATGGAACAATACCTGACTGTGAAATATGTCAAAACCTACCCAGTGTG	952
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RESULT	11		
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LOCUS			
DEFINITION	BTFFNR 3230 bp mRNA	MAM	20-JAN-1993
VERSION	B.taurus BTFFNR mRNA for Interferon receptor type I.		
KEYWORDS	X68443.1 GI:431		
SOURCE	Cytokine receptor; Interferon receptor.		
ORGANISM	Bos taurus.		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;		
AUTHORS	Artidodocila; Ruminantia; Pecora; Bovidae; Bovinae; Bos.		
TITLE	1 (bases 1 to 3230)		
JOURNAL	Submitted (14-SEP-1992) G. Lutfalla, CNRS Lab of Viral		
REFERENCE	Oncology-IRSC, 7 Rue Guy Moquet BP 8, 94801 Villejuif Cedex, FRANCE		
AUTHORS	2 (bases 1 to 3230)		
TITLE	Mouchel-Viehl, E., Mogensen, K.E. and Uze, G.		
JOURNAL	Specific antiviral activities of the human alpha interferons are		
MEDLINE	determined at the level of receptor (IFNR) structure		
FEATURES	FEB 8 Lett. 313 (3), 255-255 (1992)		
FEATURES	93076908		
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Db 1363 TGAAGAGCTGAATGAAGAGCTTTTATAGAGGCTGTATGAGAAAAACAACAG 1422
Oy 1322 AATACCTCTMAA 1334
Db 1423 AATACCTCTMAA 1435

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RESULT 12
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LOCUS BOVIFNRA 3284 bp mRNA MAN 11-AUG-1993
DEFINITION Bos taurus alpha-Interferon receptor (IFNAR) mRNA, complete cds.
ACCESSION 106320
VERSION 106320.1 GI:163187
KEYWORDS alpha-Interferon receptor.
SOURCE Bos taurus Lung cDNA to mRNA.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Bovidae; Bos.
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
1 (bases 1 to 3284)
REFERENCE 1 (bases 1 to 3284)
AUTHORS Lim,J.K. and Langer,J.A.

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TITLE Cloning and characterization of a bovine alpha Interferon receptor
JOURNAL Blochm. Biophys. Acta 1173 (3), 314-319 (1993)
MEDLINE 93305725
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Query Match 61.4%; Score 824.2; DB 3; Length 3284;
Best Local Similarity 79.3%; Pred. No. 5.9e-178;
Matches 1057; Conservative 0; Mismatches 258; Indels 18; Gaps 6;

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RESULT 15
 MUSIFNAR 3894 bp mRNA ROD 27-APR-1993
 LOCUS MUSIFNAR 3894 bp mRNA ROD 27-APR-1993
 DEFINITION Mus musculus interferon alpha/beta receptor (IFNAR) mRNA, complete cds.

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ACCESSION M89641
VERSION M89641.1 GI:194111
KEYWORDS B2 repeat; Interferon receptor; Interferon-alpha/beta receptor.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukariyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Uze, G., Lutfalla, G., Bandu, M., T., Proudhon, D. and Mogensen, K.E.
TITLE Behavior of a cloned murine interferon alpha/beta receptor expressed in homospicific or heterospicific background
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778 (1992)
MEDLINE 92262522
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        /rpt_family="B2"
    polyA_site
        3894
        /gene="IFNAR"
    BASE COUNT 1005 a 973 c 974 g 942 t
    ORIGIN

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Query Match 40.2%; Score 540.2; DB 12; Length 3894;
 Best Local Similarity 65.6%; Pred. No. 3.5e-113;
 Matches 864; Conservative 0; Mismatches 423; Indels 30; Gaps 4;

Job time: 17841 sec

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OY 322 AATTTAAATGGGTATTAAGAGCAAAAAA---CACTTCTCATGCTATGAGTTG 378
Db 387 AAACACAGTTTGTGTCAAGAGAGAGGAAAGCAACGACATCTTCGTGAATGAGTTG 446
OY 379 ACTCAATTTACCACTTTGCAAGGTCAGATGTGCTCCAGAGTACATTTAGAAGCTG 438
Db 447 ATCCGTTTATTCATTTCTACACAGCTCAGATAGACCCCCCAGAACTAGTTGAAGCTG 506
OY 439 AAGATTAAGCAATAGTATACACATCTCTCGAACAAGATAGTATATGAGGCTT 498
Db 507 AAGATTAAGCAATAGTATACACATCTCTCGAACAAGATAGTATATGAGGCTG 566
OY 499 TGGATGCTTAAGCTTTACATATAGCTTATCTGGAAGAACTCTTGAGGTAGAAG 558
Db 567 TGGAGAAACCTTCCTCACTTACACCATGCAATCTGGCAGAGCTTCCAGTGACAAA 626
OY 559 AAAGATTAAGCAATAGTATACACATCTCTCGAACAAGATAGTATATGAGGCTT 618
Db 627 AAACATTTACTCTACGTATTTATGTAAGAAAGTACAGACTCTTGCCAGAGCTACTT 686
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Db 687 ACTGTTAAGATTAAGCAATACATCCGCTCACTTAAGAAACAGCAATTTACAGACTG 746
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Db 747 TGCAGTGTAAAGCAGCAGTGAATGAATGAATGAATGCTGTGCCAGAAATCTCAAGTGG 806
OY 739 GTGCCAAATACGAACATATGTTCTTAATGGGATTA---TACATATGCAAACTAGACT 795
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OY 796 TTCAAGTTCAGTGTCTCAAGGCTTTTAAAGGAATCCTGGAAACCATTTGTATTAAT 855
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OY 856 GGAACCAATACCTGCTGTAAGAAATGTAAGAACTACCCAGTGTGCTTCTCTCAAAAG 915
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Db 1266 AGCCGCTGACTGTGATCTGTGTCAGGCGAGAGTGTCTTCAAG---GCCCTGTGAATA 1322
OY 1276 AAGCAGTGTTTTACTGAGCTGTATGTGAGAAAAAACAACAGGAAATACCTCTTA 1332
Db 1323 AGACGAGCAACTCAGTGAAGAGCTGTGAGAAAAACAGTCCAGAGATTTTCCA 1379

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Run on: June 1, 2000, 05:54:19 ; Search time 64.86 Seconds
      (without alignments)
      5180.511 Million cell updates/sec
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Title: US-09-240-675-1

Sequence: 1 CTGCAGGATCTGCGGCGC.....ATACCTCTAATGAGGTACC 1343

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum	DB	seq	length:	0
Maximum	DB	seq	length:	10000000

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : N_Geneseq_36:★

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1343	100.0	1343	1	Q14239	Encodes soluble form of
2	1343	100.0	1343	1	O30532	Sequence encoding
3	1343	100.0	1343	1	O49655	Human interferon γ
4	1338.2	99.6	1343	1	O86467	IFN- γ extracellular domain
5	1334	99.3	1755	1	Q14240	Encodes complete form of
6	1334	99.3	1755	1	Q30533	Sequence encoding
7	1334	99.3	1755	1	O49624	Human interferon γ
8	1332.4	99.2	1755	1	O86458	Human IFN receptor
9	1330.8	99.1	2784	1	Q11701	Human alpha-interferon
10	126	9.4	360	1	T73529	Transmembrane form of
11	49	3.6	168	1	T73529	Interferon alpha-1
12	40.6	3.0	6119	1	Q11377	Genes encoding T.
13	40.2	3.0	1953	1	T43223	Anticardiac pest toxin
14	40.2	3.0	2425	1	O05679	bPGS1208 gene, N60
15	38.6	2.9	1953	1	O38654	at isolate 43f coding
16	38.6	2.9	1977	1	N91495	Bacillus thuringiensis
17	38.6	2.9	2190	1	Q27945	Sequence of CytII
18	38	2.8	7900	1	X13068	Enterococcus faecalis
19	37.8	2.8	1607	1	V75167	Staphylococcus aureus
20	37.8	2.8	110000	1	V21209_-09	Continuation (10 c
21	37.4	2.8	4228	1	Q28027	Borrelia burgdorferi
22	37	2.8	1511	1	O28302	AMEPV tk DNA. New
23	37	2.8	1511	1	O66798	AMEPV thymidine kinase
24	37	2.8	1511	1	V14508	AMEPV entomopoxvirus
25	36.8	2.7	615	1	X30838	Streptococcus pneumoniae
26	36.8	2.7	20199	1	V52139	Streptococcus pneumoniae
27	36.2	2.7	1951	1	O94449	Bacterial transmembrane
28	36.2	2.7	1951	1	T49507	Transferrin receptor
29	36.2	2.7	1951	1	V21443	H. influenzae strain
30	36.2	2.7	4663	1	X20273	Borrelia burgdorferi
31	35.6	2.7	2636	1	O10871	Human brain specific
32	35.6	2.7	110000	1	V21209_-02	Continuation (3 of
33	35.4	2.6	1291	1	O14659	Part of B1260 gene
34	35.4	2.6	1972	1	Q14089	B. thuringiensis

C 35	35.4	2.6	354.3	1	Q14669	Dipeptan active to
C 36	35.4	2.6	354.3	1	Q81178	B.t. toxin PS71M3
C 37	35.4	2.6	394.0	1	N93054	Delta-endotoxin cr
C 38	35.4	2.6	457.1	1	N93059	Delta-endotoxin cr
C 39	35.4	2.6	493.4	1	N81490	Insecticidal (Dip
C 40	35.4	2.6	539.1	1	V71729	Upstream sequence
C 41	35.4	2.6	540.7	1	V71738	Upstream sequence
C 42	35.2	2.6	1146.4	1	V48328	Interleukin 18 con
C 43	35.2	2.6	2899.4	1	V15826	Genomic DNA for
C 44	34.8	2.6	127.1	1	Q46869	Growth factor gene
C 45	34.8	2.6	1122.5	1	N91695	Sequence of fowipo

ALIGNMENTS

Query	1	CTCGAGGAGATCTGGCGGCGCTCCAGATGATGTCGTCTCTCTGGGCGCGACGACCTTAG	60
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Best Local Similarity		100.0%; Pred. No. 0;	
Matches 1343; Conservative		0; Mismatches	0; Indels
		0; Gaps	
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Db	121	CTCTCTCAAAAAGTAGAGAGTGGACATCATAGATGACCACTTATCTCTAGGTGGAACAGA	180
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Db	241	ATTGGATAAAAATTTCTGTGGGTGTTCAGAAATTTACTAGTACCAAAATGCAATTTTCTTCAC	3000


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QY 301 TCAAGCTGAATGTTTATGAAGAAATTAATGGCGTATAGAGCAGAAAAAGAAACACTT 360
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QY 361 CTTCATGATGATGAGGTGACTCATTTACACCAATTCGCAAAAGCTCAGATTGCTCCAG 420
DB 361 CTTCATGATGATGAGGTGACTCATTTACACCAATTCGCAAAAGCTCAGATTGCTCCAG 420
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QY 1081 CTGCAAAACAGTGTGGAACACGCTGTGATCCAGAGTTTCCAGATTCATTAAGAAATTA 1140
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DB 1261 ATGAAAAAGCTGATTAAGAGAGTGTGTTAGTGACGCTGATGAGAAAAACAAACAG 1320
QY 1321 GAAATACCTCTAATGAGTACC 1343
DB 1321 GAAATACCTCTAATGAGTACC 1343

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RESULT 2
ID 030532
Q030532 standard; DNA: 1343 BP.
AC Q030532.
DT 31-MAR-1993 (first entry)
DE Sequence encoding a soluble form of the interferon (IFN) receptor
KM with a high affinity for IFN-alpha and -beta.
OS Interferon receptor; alpha-interferon; beta-interferon; ss.
FH Synthetic.
FT Key Location/Qualifiers
FT cds 27..1337
FT /tag= a
MO0218626-A.
PN 29-OCT-1992.
PD 17-APR-1991; F00318.
PR 17-APR-1991; MO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI EId P, Gresser I, Lutfalla G, Meyer F, Mogensen KE.
PI Tovey M, Uze G.
DR WPI: 92-382110/46.
DR P-PSDB: R28495.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
PT and beta - useful as immunosuppressants, for treating auto-immune
PT diseases and transplant rejection
PS Claim 10; Fig 1; 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
CC IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template. For example,
CC bacteriophage lambda ZAP, containing the entire coding sequence of
CC the IFN-alpha and -beta receptor (Q030533), was incubated with Q1495
CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
CC IFFN is the transmembrane and cytoplasmic domains. Both forms bind
CC IFN in the same way as antibodies so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 1343 BP; 449 A; 254 C; 264 G; 376 T;

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Query Match 100.0%; Score 1343; DB 1; Length 1343;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 121 CTCCTCAAAAATAGAGGTCGACATCATAGATGAACAATTTACTGAGGTGGAACAGGA 180
DB 121 CTCCTCAAAAATAGAGGTCGACATCATAGATGAACAATTTACTGAGGTGGAACAGGA 180
QY 181 GCGATGAGTCTGCGGAGATGACTTTCTTCAATGATTATCAAAAACTGGGATGATA 240
DB 181 GCGATGAGTCTGCGGAGATGACTTTCTTCAATGATTATCAAAAACTGGGATGATA 240
QY 241 ATTGGATAAATTTGCTGGGTGTCAGAAATTTACTAGTACCAATGCAACTTTTTCAC 300
DB 241 ATTGGATAAATTTGCTGGGTGTCAGAAATTTACTAGTACCAATGCAACTTTTTCAC 300
QY 301 TGAAGCTGAATTTATGAGAGAAATTAATGCGTATAGAGCAGAAAAAGAAACACTT 360
DB 301 TGAAGCTGAATTTATGAGAGAAATTAATGCGTATAGAGCAGAAAAAGAAACACTT 360
QY 361 CTTCATGATGATGAGGTGACTCATTTACACCAATTCGCAAAAGCTCAGATTGCTCCAG 420
DB 361 CTTCATGATGATGAGGTGACTCATTTACACCAATTCGCAAAAGCTCAGATTGCTCCAG 420
QY 421 AAGTACATTAGAGCTGAAGATAGGCAATAGTATACACATCTCTCTGGAAACAAAAG 480
DB 421 AAGTACATTAGAGCTGAAGATAGGCAATAGTATACACATCTCTCTGGAAACAAAAG 480

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Db 421 AAGTACATTAGAGAGCTGAAGATTAAGGCAATGCTGATACATCTCTCGAACAACAAAG 480
 Qy 481 ATAGTGTATGTGGCTTTGGATGGTTTAAAGCTTTACATATAGCTTACTTATCTGAAAA 540
 Db 481 ATAGTGTATGTGGCTTTGGATGGTTTAAAGCTTTACATATAGCTTACTTATCTGAAAA 540
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 Db 601 TCTCACCAGAGACTTATGCTTAAAGTAAAGACGACTACTTTCGTCATGAAAA 660
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 Db 721 CAGAAAAATATAGAGTCACTGTCACAAATCAGACATAGTTCTTAAATGGATTATACAT 780
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 Db 781 ATGCAAAATGACCTTTCAAGTTCAAGTGGCTCCAGCCCTTTTAAAGGAATCCTGGAA 840
 Qy 841 ACCATTGTATTAATGAAGAAATACCGTACGATGTAAGAAATGTCAAAACTACCCAGTGTG 900
 Db 841 ACCATTGTATTAATGAAGAAATACCGTACGATGTAAGAAATGTCAAAACTACCCAGTGTG 900
 Qy 901 TCTTTCCTCAAAAGCTTTTCCAAAAAGAAATTTACCTTCTCCGCTACAGCATCTGATG 960
 Db 901 TCTTTCCTCAAAAGCTTTTCCAAAAAGAAATTTACCTTCTCCGCTACAGCATCTGATG 960
 Qy 961 GAAATTAACACATCTTTGGTGTGAAGATTAAGTGTGATCTGAAATACAAAGCTTCC 1020
 Db 961 GAAATTAACACATCTTTGGTGTGAAGATTAAGTGTGATCTGAAATACAAAGCTTCC 1020
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 Db 1021 TACTTCCTCAAGCTTTTAAACATTAGATCCCTTAGTATCATCATATCTATTCGGTG 1080
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 Db 1081 CTCCAAAAACAGTCTGAAAAACAGCCTGTGATCAGGATATCCAGTATTTTGAATTA 1140
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 Db 1141 TTTTGGGAAACACTTCAATGCTGAGAGAAAAATTTCCAGAAAAAAATCTGATGTTA 1200
 Qy 1201 CAGTTCCTAATTTGAACACAGTACTGTATTTGTGTGAAGCCAGAGACACACATGG 1260
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 Qy 1261 ATGAAAGCTGAATAAAAGCAGTGTGTTAGTGACGCTGTATGTGAAGAAACAAACAG 1320
 Db 1261 ATGAAAGCTGAATAAAAGCAGTGTGTTAGTGACGCTGTATGTGAAGAAACAAACAG 1320
 Qy 1321 GAAATACCTCTAATGAGGTACC 1343
 Db 1321 GAAATACCTCTAATGAGGTACC 1343

RESULT 3

ID 049625 standard; DNA: 1343 BP.
 AC 049625:

DT 20-APR-1994 (first entry)
 DE Human interferon receptor extracellular domain coding sequence.
 KW IFN-R; extracellular domain; monoclonal antibody; viral infection;
 cell proliferation; allograft rejection; systemic lupus erythematosus;
 psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;
 immunodeficiency; measles virus; Interferon-alpha-beta; ss.

OS Homo sapiens. Location/Qualifiers
 FH Key 27..1337
 FT cds
 FT /tag- "a"
 FT /note- "encodes extra cellular domain of IFN-R"
 PN EP-563487-A.
 PD 06-OCT-1993.
 PE 31-MAR-1992; 400902.
 PR 31-MAR-1992; EP-400902.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG.
 DR WPI: 93-312951/40.
 DP P-PSDB: R42635 (part).
 PT Monoclonal antibody to human interferon type-I receptor - having
 PT neutralising activity against human type I interferon, used for
 PT therapy and diagnosis
 PS Disclosure: Fig 2: 21pp: English.
 CC Monoclonal antibodies produced against soluble forms of the human
 CC interferon alpha-beta receptor based on the full-length human IFN-R
 CC sequence are claimed. (See 049624 for sequence coding for
 CC full-length IFN-R). The antibodies are useful for treatment and
 CC prophylaxis of disorders involving cell proliferation and/or viral
 CC infection.
 SO Sequence 1343 BP; 449 A; 254 C; 264 G; 376 T;
 Query Match 100.0%; Score 1343; DB 1; Length 1343;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTCGAGGATCTGGCGGCTCCAGATGATGTCGTCCTCTGGCGGCGAGACCTAG 60
 Db 1 CTCGAGGATCTGGCGGCTCCAGATGATGTCGTCCTCTGGCGGCGAGACCTAG 60
 Qy 61 TGCCTGTCGCGTGGGCCCATGSGGTTCGCGAGCCGCGAGGAAAAATCTAAAT 120
 Db 61 TGCCTGTCGCGTGGGCCCATGSGGTTCGCGAGCCGCGAGGAAAAATCTAAAT 120
 Qy 121 CTCCTCAAAAAGTGAAGTGCACATCATAGATGACAACTTATCTGAGTGAACAGA 180
 Db 121 CTCCTCAAAAAGTGAAGTGCACATCATAGATGACAACTTATCTGAGTGAACAGA 180
 Qy 181 GCGATGACTGTCGGGAATGACTTTTTCATTCGATATCAAAAACTGGATGATA 240
 Db 181 GCGATGACTGTCGGGAATGACTTTTTCATTCGATATCAAAAACTGGATGATA 240
 Qy 241 ATTGGATTAATTTGTCGGGTGTCAGAAATATTACTAGACCAATGCAACTTCTCTAC 300
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 Qy 361 CTTATGATAGAGTTGACTCATTTACACCATTTCCGAAAGTCAAGTTGGTCTCCAG 420
 Db 361 CTTATGATAGAGTTGACTCATTTACACCATTTCCGAAAGTCAAGTTGGTCTCCAG 420
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 Qy 481 ATAGTGTATGTGGCTTTGGATGGTTTAAAGCTTTACATATAGCTTACTTATCTGAAAA 540
 Db 481 ATAGTGTATGTGGCTTTGGATGGTTTAAAGCTTTACATATAGCTTACTTATCTGAAAA 540
 Qy 541 ACTCTTCAGGTTAGAGAGAGATTTGAAAAATATTATTTCCAGACATAAAATTTTAAAC 600
 Db 541 ACTCTTCAGGTTAGAGAGAGATTTGAAAAATATTATTTCCAGACATAAAATTTTAAAC 600
 Qy 601 TCTCACCAGAGACTTATGCTTAAAGTAAAGACGACTACTTTCGTCATGAAAA 660
 Db 601 TCTCACCAGAGACTTATGCTTAAAGTAAAGACGACTACTTTCGTCATGAAAA 660

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OY 661 TTGGTCTATAGTCCAGTACATGTGTAAGACACAGTTGAAATGAACTACCTCCAC 720
DB 661 TTGGTCTATAGTCCAGTACATGTGTAAGACACAGTTGAAATGAACTACCTCCAC 720
OY 721 CAGAAATATAGAGTGTGCTCCAAATGAACTATGTTCTTAATGGATATATACAT 780
DB 721 CAGAAATATAGAGTGTGCTCCAAATGAACTATGTTCTTAATGGATATATACAT 780
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OY 841 ACCATTGTATTAATGGAACCAATACCTAGTGTGAATATGCAAAATACCAAGTGTG 900
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DB 1321 GAAATACCTTAATGAGTACC 1343

RESULT 4
O86457
ID O86457 standard: DNA: 1343 BP.
AC O86457;
DT 16-OCT-1995 (first entry)
DE IFN-R extracellular domain.
KW IFN-R: interferon receptor; interferon-alpha; interferon-beta;
KM monoclonal antibody; immunomodulator; AIDS; ss.
OS Homo sapiens.
FH key Location/Qualifiers
FT cds 27..1337
FT /tag- a
PD 23-MAR-1995.
PF 16-SEP-1994. E03114.
PR 17-SEP-1993. EP-402279.
PI (EURI-) LAB EURO BIOTECHNOLOGIE SA.
PA Benlizi EJ, Tovey MG;
DR MPI: 95-131187/17.
P-PSDB: R71723
PT Compn. of monoclonal antibodies against interferon receptor -
PS useful as immuno-modulator, eg. for treating AIDS
disclosure: Fig. 2a-2b; 105bp; English.
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CC DNA encoding the extracellular domain of the human IFN class I
CC receptor is given in O86457. Monoclonal antibodies were raised
CC against the recombinant soluble form of the encoded protein (R1723)
CC expressed in either E. coli or COS cell hosts.
SQ Sequence 1343 BP; 449 A; 257 C; 261 G; 376 T;

Query Match 99.6%; Score 1338.2; DB 1; Length 1343;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1340; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CTGCAAGGATCTGCGGCGCTCCAGATGATGTCCTCTGGGCGGAGACCTAG 60
DB 1 CTGCAAGGATCTGCGGCGCTCCAGATGATGTCCTCTGGGCGGAGACCTAG 60
OY 61 TCGTCGTCGCGGCGGCGGCGGCTCCAGATGATGTCCTCTGGGCGGAGACCTAG 120
DB 61 TCGTCGTCGCGGCGGCGGCGGCTCCAGATGATGTCCTCTGGGCGGAGACCTAG 120
OY 121 CTCTCAAAATGAGTGTGAGATGATGATGATGATGATGATGATGATGATGATG 180
DB 121 CTCTCAAAATGAGTGTGAGATGATGATGATGATGATGATGATGATGATGATG 180
OY 181 GCGATGAGTGTGCGGGAATGATGATGATGATGATGATGATGATGATGATGATG 240
DB 181 GCGATGAGTGTGCGGGAATGATGATGATGATGATGATGATGATGATGATGATG 240
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OY 301 TCAAGCTGAATTTTATGAGAAATTAATTAATTAATTAATTAATTAATTAAT 360
DB 301 TCAAGCTGAATTTTATGAGAAATTAATTAATTAATTAATTAATTAATTAAT 360
OY 361 CTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB 361 CTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
OY 421 AAGTACATTTAGAGCTGAGTAAAGCAATTAATTAATTAATTAATTAATTAAT 480
DB 421 AAGTACATTTAGAGCTGAGTAAAGCAATTAATTAATTAATTAATTAATTAAT 480
OY 481 ATAGTGTATGAGGCTTGAATGATGATGATGATGATGATGATGATGATGATG 540
DB 481 ATAGTGTATGAGGCTTGAATGATGATGATGATGATGATGATGATGATGATG 540
OY 541 ACTCTCAGGTGATGAGAAAGATTAATTAATTAATTAATTAATTAATTAATTA 600
DB 541 ACTCTCAGGTGATGAGAAAGATTAATTAATTAATTAATTAATTAATTAATTA 600
OY 601 ACTCTCAGGTGATGAGAAAGATTAATTAATTAATTAATTAATTAATTAATTA 660
DB 601 ACTCTCAGGTGATGAGAAAGATTAATTAATTAATTAATTAATTAATTAATTA 660
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OY 841 ACCATTGTATTAATGGAACCAATACCTAGTGTGAATATGCAAAATACCAAGTGT 900
DB 841 ACCATTGTATTAATGGAACCAATACCTAGTGTGAATATGCAAAATACCAAGTGT 900
OY 901 TCTTCTCAAAAGCTTTTCCAAAGAAATTAACCTTCTCCGCTCAAGATCTGTATG 960
DB 901 TCTTCTCAAAAGCTTTTCCAAAGAAATTAACCTTCTCCGCTCAAGATCTGTATG 960
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QY 1081 CTCCAAAACAGTCTGGAACACGCGTGTATCCAGGATTAATCCAGATTATCAAAATTA 1140
DB 1081 CTCCAAAACAGTCTGGAACACGCGTGTATCCAGGATTAATCCAGATTATCAAAATTA 1140
QY 1141 TTTTGGGAAAACACTTCAAAATGCTGAGAAAAATATCGAGAAAAAAGTATGTTA 1200
DB 1141 TTTTGGGAAAACACTTCAAAATGCTGAGAAAAATATCGAGAAAAAAGTATGTTA 1200
QY 1201 CAGTTCTTAATTTGAACCACTGACTGATATTTGTGAAAGCCAGACACACCATGG 1260
DB 1201 CAGTTCTTAATTTGAACCACTGACTGATATTTGTGAAAGCCAGACACACCATGG 1260
QY 1261 ATGAAGCTGATAAAGCACTGTTTATGAGAGCGCTGTATGAGAAAAAACCAG 1320
DB 1261 ATGAAGCTGATAAAGCACTGTTTATGAGAGCGCTGTATGAGAAAAAACCAG 1320
QY 1321 GAAATACCTCTTAATGAGTACC 1343
DB 1321 GAAATACCTCTTAATGAGTACC 1343
RESULT 5
ID Q14240
Q14240 Q14240 standard; DNA: 1755 BP.
AC Q14240:
DE 16-JAN-1992 (first entry)
DE Encodes complete Interferon- α /pna/beta receptor.
KW IFN; autoimmune disease; graft rejection; histocompatibility; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 27..1760 /*tag- a
FT FR2657881-A.
PD 09-AUG-1991.
PR 05-FEB-1990; 001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE.
PI Toyey HG, Uze G;
DR WPI: 91-31978/44.
DR P-PSDB: R14488.
PT New water-soluble polypeptide(s) with affinity for IFN- α and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Dislosure: Page 47; 32pp; French.
CC The protein encoded by this sequence corresponds to the complete
CC Interferon- α and/or beta receptor. The invention covers
CC derivatives of the receptor obtained by deleting the transmembrane
CC and cytoplasmic domains of the native receptor or by substitution.
CC See also Q14239.
SQ Sequence 1755 BP; 593 A; 324 C; 334 G; 504 T;

Query Match 99.3%; Score 1334; DB 1; Length 1755;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGATCTGCGGGCTCCAGATGATGCTGCTCTCTGCGCGGAGACCTTAG 60
DB 1 CTGCAAGGATCTGCGGGCTCCAGATGATGCTGCTCTCTGCGCGGAGACCTTAG 60
QY 61 TGCTGTGCGCCGTGGCCCATGGGTGTCTCCGACGCCAGTGGAAAAATCTAAAT 120
DB 61 TGCTGTGCGCCGTGGCCCATGGGTGTCTCCGACGCCAGTGGAAAAATCTAAAT 120

DB 61 TGCTGTGCGCCGTGGCCCATGGGTGTCTCCGACGCCAGTGGAAAAATCTAAAT 120
QY 121 CTCTCAAAAAGTAGAGTGCATCATAGATGACAATCTATCTGAGTGAACAGA 180
DB 121 CTCTCAAAAAGTAGAGTGCATCATAGATGACAATCTATCTGAGTGAACAGA 180
QY 181 GCGATGAGTCTGTGGGAATGCACTTTTCATTGCAATATCAAAAAAAGTGGATGATA 240
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QY 241 ATTGGATTAATTTGCTGGGTGCTGAGAAATATCTAGTACCAATGCACTTTCTTCAC 300
DB 241 ATTGGATTAATTTGCTGGGTGCTGAGAAATATCTAGTACCAATGCACTTTCTTCAC 300
QY 301 TCAAGCTAGTATTATGAGAAATTAATTCGATATAGAGCAAAAAAGAAACACTT 360
DB 301 TCAAGCTAGTATTATGAGAAATTAATTCGATATAGAGCAAAAAAGAAACACTT 360
QY 361 CTTCATGGTATGAGGTGACTCAATTAACACATTTCCGAAAGCTCAGATTGCTCCAG 420
DB 361 CTTCATGGTATGAGGTGACTCAATTAACACATTTCCGAAAGCTCAGATTGCTCCAG 420
QY 421 AAGTACATTTGAAGCTGAAATAGGCAATAGATACATCTCTCTGGAACAAAAG 480
DB 421 AAGTACATTTGAAGCTGAAATAGGCAATAGATACATCTCTCTGGAACAAAAG 480
QY 481 ATAGTATATGAGGCTTTGATGTTTAACTTATACATATAGCTTATCTGAAAA 540
DB 481 ATAGTATATGAGGCTTTGATGTTTAACTTATACATATAGCTTATCTGAAAA 540
QY 541 ACTCTCAGTGTAGAAAGAAAGATGAAATATTTATCCAGACATTAATTTATAAC 600
DB 541 ACTCTCAGTGTAGAAAGAAAGATGAAATATTTATTTCCAGACATTAATTTATAAC 600
QY 601 TCTACCAAGACACTACTTATGCTAAAGCTTAAGAGCACTCTTACGTCATGAGAAA 660
DB 601 TCTACCAAGACACTACTTATGCTAAAGCTTAAGAGCACTCTTACGTCATGAGAAA 660
QY 661 TTGGTGTATAGTCCAGTACATGTTAAGACACAGTGAAGAAATGAACTACCTCCAC 720
DB 661 TTGGTGTATAGTCCAGTACATGTTAAGACACAGTGAAGAAATGAACTACCTCCAC 720
QY 721 CAGAAATATAGAGTCAAGTCCCAAAATCAGAACTATGTTCTTAATGGATTAACAT 780
DB 721 CAGAAATATAGAGTCAAGTCCCAAAATCAGAACTATGTTCTTAATGGATTAACAT 780
QY 781 ATGCAAAATACCTTTCAATGTCAGTGCCTCCAGCCTTTTAAAAAGAAATCTCGAA 840
DB 781 ATGCAAAATACCTTTCAATGTCAGTGCCTCCAGCCTTTTAAAAAGAAATCTCGAA 840
QY 841 ACCATTGTATTAATGAGAAACAAATACCTGACTGAAATATGTCAAAACCTCCAGTGTG 900
DB 841 ACCATTGTATTAATGAGAAACAAATACCTGACTGAAATATGTCAAAACCTCCAGTGTG 900
QY 901 TCTTCTCAAAAAGCTTTTCCAAAAGAAATTAACCTTCTCCGGTACACATCTGATG 960
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DB 1081 CTCCAAAACAGTCTGGAACACGCGTGTATCCAGGATTAATCCAGATTATCAAAATTA 1140
QY 1141 TTTTGGGAAAACACTTCAAAATGCTGAGAAAAATATCGAGAAAAAAGTATGTTA 1200
DB 1141 TTTTGGGAAAACACTTCAAAATGCTGAGAAAAATATCGAGAAAAAAGTATGTTA 1200

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OY 1201 CAGTTCCTAATTGAACACGACTGTATATTGTGTGAAGCCAGACACACCATG 1260
DB 1201 CAGTTCCTAATTGAACACGACTGTATATTGTGTGAAGCCAGACACACCATG 1260
OY 1261 ATGAAAAGCTGAATAAAGCAGTGTATTAGTACGCTGTATGTGAGAAAACAAACCG 1320
DB 1261 ATGAAAAGCTGAATAAAGCAGTGTATTAGTACGCTGTATGTGAGAAAACAAACCG 1320
OY 1321 GAATACCTCTAAA 1334
DB 1321 GAATACCTCTAAA 1334

RESULT 6
O30533
ID 030533 standard; DNA; 1755 BP.
AC 030533;
DR 31-MAR-1993 (first entry)
DE Sequence encoding a soluble form of the interferon (IFN) receptor
DE with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-interferon; beta-interferon; ss.
OS Synthetic.
FH key Location/Qualifiers
FT cds 27..1700
FT key /*tag= a
PN MO9218626-A.
PD 29-OCT-1992.
PF 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eld P. Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PI Tovey M, Ize G.
DR WPI: 92-382110/46.
DR P-PDB: R28496.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
PT and beta - useful as immunosuppressants, for treating auto-immune
PT diseases and transplant rejection
PS Claim 10: Fig 2: 58pp: English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
CC IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template. For example,
CC bacteriophage lambda ZAP, containing the entire coding sequence of
CC the IFN-alpha and -beta receptor (O30533), was incubated with oligos
CC O30534 and O30535. R28496 represents the complete receptor. R28495
CC lacks the transmembrane and cytoplasmic domains. Both forms bind
CC IFN in the same way as antibodies, so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 1755 BP; 593 A; 325 C; 333 G; 504 T;

Query Match 99.3%; Score 1334; DB 1; Length 1755;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 ATTGATATAATTGTCTGGGTGTGAGAAATATTACTAGACCAATGCACTTTCTTCAC 300
OY 301 TCAAGCTGAATGTTTATGAGAAATTAATTCGCTATAGAGCAGAAAAGAAACACTT 360
DB 301 TCAAGCTGAATGTTTATGAGAAATTAATTCGCTATAGAGCAGAAAAGAAACACTT 360
OY 361 CTGATGATAGAGTTGACCTATTACCATTTCCAAAGCTCAGATGTCCTCCAG 420
DB 361 CTGATGATAGAGTTGACCTATTACCATTTCCAAAGCTCAGATGTCCTCCAG 420
OY 421 AAGTACATTTAGAAAGCTGAAGTAAGCAATAGTATACACATCTCTCTGGAACAAAG 480
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OY 661 TTGGTGTATATAGTCCAGTACATTTGATTAAGACACAGTTGAAATAGACTACCTCCAC 720
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OY 841 ACCATTTGATTAATGAAACAAATACCTGACTGTGAAATGTCAAAACTCCACAGTGTG 900
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OY 1081 CTCGAAAACAGTCTGGAACACAGCCTGTGATCCAGATTAATCCACTGTTATATAATTA 1140
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OY 1141 TTTTGGGAAAAACACTTCAATGCTGAGAGAAAAATATGAGAAAAAACTGATGTTA 1200
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OY 1261 ATGAAAAGCTGAATAAAGCAGTGTATTAGTACGCTGTATGTGAGAAAACAAACCG 1320
DB 1261 ATGAAAAGCTGAATAAAGCAGTGTATTAGTACGCTGTATGTGAGAAAACAAACCG 1320
OY 1321 GAATACCTCTAAA 1334
DB 1321 GAATACCTCTAAA 1334

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KM monoclonal antibody; immunomodulator; AIDS; ss.
 OS Homo sapiens. Location/Qualifiers
 FH Key 27.1700
 FT cds /*tag= a
 PN MO9507716-A.
 PD 23-MAR-1995.
 PF 16-SEP-1994. E03114.
 PR 17-SEP-1993; EP-402279.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Beniziri EJ, Tovey MG;
 DR WPI: 95-131187/17.
 DP P-PSDB: R75356.
 PT Compens. of monoclonal antibodies against interferon receptor
 PS useful as immunomodulator, eg. for treating AIDS
 PS Disclosure: Fig.3A-28; 105pp; English.
 CC DNA encoding the extracellular domain of the human IFN class I
 CC receptor is given in Q86457; the full IFN receptor gene
 CC is given in Q86458. Immunomodulator monoclonal antibodies were
 CC raised against the recombinant soluble form of the extracellular
 CC domain (R71723) expressed in E. coli or COS cell hosts.
 SO Sequence 1755 BP: 592 A: 324 C: 334 G: 505 T:

Query Match 99.2%; Score 1332.4; DB 1; Length 1755;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 661 TTGGTGTCTATAGTCCAGTACATTTGATAAAGACACAGTTGAAAAATGAATCTACTCAC 720
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QY 721 CAGAAAAATATAGAACTAGTGTCCAAAAATCAGAACTATGTTCTTAATGGATTATACAT 780
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Db 721 CAGAAAAATATAGAACTAGTGTCCAAAAATCAGAACTATGTTCTTAATGGATTATACAT 780

QY 781 ATGCAAAATATGACCTTTCAAGTTCAGTGGCTCCAGCCTTTTAAAAAGAAATCTGGAA 840
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Db 781 ATGCAAAATATGACCTTTCAAGTTCAGTGGCTCCAGCCTTTTAAAAAGAAATCTGGAA 840

QY 841 ACCATTTGATTAATATGAAACAAATATCAGTGTGAAATATGCAAAATCTACCAAGTGTG 900
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Db 841 ACCATTTGATTAATATGAAACAAATATCAGTGTGAAATATGCAAAATCTACCAAGTGTG 900

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Db 901 TCTTTCTCAAAAAGCTTTTCCAAAAAGAAATTTACCTTCTCCGCTACACATCTGATG 960

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Db 1021 TACTTCTCCAGTCTTTTACATTTAGATCCCTTAGTATTCATTCATATATCGGTG 1080

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Db 1081 CTCGCAAAACAGTGTGAAACACGCGCTGTGATCCAGAGATTATTCACGATTTATGAATTA 1140

QY 1141 TTTTGGAAAAACATTCATTAATGCTGAGAGAAAAATATGAGAAAAAACTGATGTTA 1200
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Db 1141 TTTTGGAAAAACATTCATTAATGCTGAGAGAAAAATATGAGAAAAAACTGATGTTA 1200

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Db 1201 CAGTTCCTAATTTGAAACACAGTGTATATGTTGTGAAAGCCAGACACACACATG 1260

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Db 1261 ATGAAAAAGCTGAATTAAGACAGTGTTTTAGTACGCTGTATGTAGAAAAAACACAG 1320

QY 1321 GAAATACCTCTAAA 1334
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Db 1321 GAAATACCTCTAAA 1334

RESULT 9
 011701.
 ID 011701 standard; DNA: 2784 BP.
 AC 011701.
 DT 18-JUL-1991 (first entry)
 DE Human alpha-interferon receptor protein encoding sequence.
 KW Human alpha IFN; IFN agonists; antiviral; anti tumour agent;
 OS Homo sapiens.
 PH Key Location/Qualifiers
 FT cds 79.1752
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 FT /product= human alpha IFN
 FT signal_peptide 79.159
 FT /*tag= b
 FT /product= signal peptide
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 FT /*tag= c
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 QY 1321 GAAATACCTCTTAA 1334
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 DB 1373 GAAATACCTCTTAA 1386

RESULT 10

T73519
 ID T73519 standard; cDNA: 360 BP.
 AC T73519;
 DT 23-SEP-1997 (first entry)
 DE Transmembranal interferon alpha-receptor cDNA fragment.
 KW Interferon alpha-receptor; IFNAR; ss.
 OS Homo sapiens.
 FH Key
 FT exon
 FT Location/Qualifiers
 FT 112..113
 FT /note= "exon IX-exon X junction"
 FT 258..259
 FT /tag= b
 FT /note= "exon X-exon XI junction"
 FT 10..30
 FT /tag= c
 FT /note= "primer 1270-1290"
 FT 71..82
 FT /tag= d
 FT /note= "primer 1331..1342"
 FT 238..255
 FT /tag= e
 FT /note= "primer 1498..1515"
 FT 262..282
 FT /tag= f
 FT /note= "primer 1522..1542"
 FT 341..360
 FT /tag= g
 FT /note= "primer 1601..1619"

PN AU9475977-A.
 PD 11-MAY-1995.
 PE 20-OCT-1994; 075977.
 PR 24-OCT-1993; IL-107378.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (ABRA/) ABRAMOVICH C.
 PI Abramovich C, Ratovitski E, Revel M;
 WPI: 95-200634/27.
 PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Disclosure: Fig 6: 46pp; English.
 CC A cDNA sequence (T73519) corresponds to nucleotides 1360-1620 of
 CC a cDNA clone for human interferon alpha receptor (IFNAR, see also
 CC W21804), covering the region that codes for the transmembrane
 CC region of IFNAR. Differential splicing of IFNAR gene transcripts
 CC (see also T73520 and T73521) produces novel soluble, non-membrane
 CC bound forms of IFNAR (see also W21805 and W21806) that can be used
 CC to inhibit, modulate or modify the activities of interferons alpha
 CC and beta in cells, tissues and organisms, or for diagnostic
 CC purposes.
 SO Sequence 360 BP: 117 A: 64 C: 62 G: 117 T;

Query Match 9.4%; Score 126; DB 1; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.9e-24;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1209 AATTGAAACACTGACTGATATGTGTGAAAGCCAGACACACATGATGAAAG 1268
 |||||||
 DB 1 AATTGAAACACTGACTGATATGTGTGAAAGCCAGACACACATGATGAAAG 60
 |||||||
 QY 1269 CTGGAATTAAGCAGTGTCTTTAGTACGCTGTGTGAGAAAACAAACAGAAATACC 1328
 |||||||
 DB 61 CTGGAATTAAGCAGTGTCTTTAGTACGCTGTGTGAGAAAACAAACAGAAATACC 120

QY 1329 TCTTAA 1334
 |||||||
 DB 121 TCTTAA 126

RESULT 11

T73521
 ID T73521 standard; cDNA: 168 BP.
 AC T73521;
 DT 23-SEP-1997 (first entry)
 DE Interferon alpha-receptor splice-deleted form 2 cDNA.
 KW Interferon alpha-receptor; IFNAR; ss.
 OS Homo sapiens.
 FH Key
 FT exon
 FT AU9475977-A.
 PD 11-MAY-1995.
 PE 20-OCT-1994; 075977.
 PR 24-OCT-1993; IL-107378.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (ABRA/) ABRAMOVICH C.
 PI Abramovich C, Ratovitski E, Revel M;
 WPI: 95-200634/27.
 PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Example 3: Fig 6: 46pp; English.
 CC A cDNA sequence (T73521) corresponds to a portion of splice-deleted
 CC IFN alpha-receptor (IFNAR) form 2 gene transcript, covering a
 CC region which, in comparison with transmembranal IFNAR cDNA (see
 CC also T73519), has 2 in-phase deletions of nucleotides 1318-1341 in
 CC exon IX and of nucleotides 1360-1518, i.e. the end of exon IX and
 CC all of exon X. IFNAR spliced-deleted form 2 (W21806) is predicted
 CC to have a shortened extracellular domain, no transmembrane domain
 CC and a truncated intracellular domain. The cDNA clone was detected
 CC after PCR amplification of human U266 myeloma RNA. Recombinant,
 CC soluble non-membrane bound IFNAR spliced-deleted form 1 can be
 CC expressed in host cells and used to inhibit, modulate or modify the
 CC activities of interferons alpha and beta, or for diagnostic
 CC purposes.
 SO Sequence 168 BP: 58 A: 31 C: 32 G: 47 T;

Query Match 3.6%; Score 49; DB 1; Length 168;
 Best Local Similarity 100.0%; Pred. No. 0.0004;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1218 CCACGTGACTGATATGTGTGAAAGCCAGACACACACATGATGAA 1266
 |||||||
 DB 1 CCACGTGACTGATATGTGTGAAAGCCAGACACACACATGATGAA 49
 |||||||

RESULT 12

Q11377
 ID Q11377 standard; DNA: 6119 BP.
 AC Q11377;
 DT 02-JUL-1991 (first entry)
 DE Genes encoding T. hyo 39 kD family 1 antigens 1-4.
 KW Swine dysentery; vaccine; ss.
 OS Treponema hyodysenteriae serotype B204.
 FH Key
 FT cds
 FT Location/Qualifiers
 FT 750..1910
 FT /tag= a
 FT /label= gene 1
 FT /note= "39 kD antigen 1"
 FT 2067..3227
 FT /tag= b
 FT /label= gene 2
 FT /note= "39 kD antigen 2"
 FT 3381..4550
 FT /tag= c
 FT /label= gene 3
 FT /note= "39 kD antigen 3"
 FT 4707..5859
 FT /tag= d

Query Match 9.4%; Score 126; DB 1; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.9e-24;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FT /label= gene 4
 FT /note= *39 kD antigen 4*
 PN M09104036-A.
 PD 04-APR-1991.
 PF 11-SEP-1990: U05129.
 PR 13-SEP-1989: US-406535.
 PA (MLTE-) ML Technology Ventures.
 PI Gade J, Dragon E, McCann M;
 DR WPI: 91-117317/16.
 DR P-PSDB: R11484, R11485, R11486, R11487.
 PT Treponema hyodysenteriae antigens - having molecular wt. of 39 kD
 PT and their DNA codes, and use for preparing vaccine.
 PS Claim 18; Page 49; 84pp: English.
 CC The DNA includes family 1 contg. genes 1-4 encoding 39 kD antigens
 CC of T. hyo. The sequence was obtd. from clones isolated from a T.
 CC hyo genomic library in lambda gtl1. The antigens can be expressed
 CC and used to prepare vaccines to protect against swine dysentery.
 CC See also 011378-011409.
 SQ Sequence 6119 BP; 2111 A; 683 C; 990 G; 2323 T;

Query Match 3.0%; Score 40.6; DB 1; Length 6119;
 Best Local Similarity 50.3%; Pred. No. 0.33;
 Matches 100; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

OY 537 AAAAAGCTCTGAGTGTAGAGAAAGATGAAATATTATTCAGACATTAATAT 596
 DB 5217 ACATATTATACAGATAGATAGCTTTTAATGAATATATTAATAATGACAA 5276
 OY 597 AAACGTCTACAGACACTATTATGCTAAAGTTAAAGCAGACTACTACGTCATG 656
 DB 5277 TTAGATATATAAAATGCTCGATGTTGTAATAATATGAGAGAACTTTTTCAG 5336
 OY 657 AAAATGCTGTCTATAGTCCAGTACATGTATTAAGACACAGCTGAAATGACACT 716
 DB 5337 TCATTGGTTTGAACAAGATTCATTTTTGAATACACTGTTGGAATGTAACAT 5396
 OY 717 CCACGAGAAATATAGAG 735
 DB 5397 AATCCTTTTATTAAGTAG 5415

RESULT 13
 ID T43223 standard; DNA; 1953 BP.
 AC T43223:
 DT 28-JAN-1997 (first entry)
 DE Antiscarab pest toxin 43F coding sequence.
 KW Toxin 50C(b); scarab pest; toxin; insect; scarabaeidae; pest control;
 KW larval stage insect; grain; tuberous crop; white grub; chafer grub;
 KW cyclocephala; popillia; 43F gene; ds.
 OS Bacillus thuringiensis strain tolworthi.
 PN US5554534-A.
 PD 10-SEP-1996.
 PF 30-SEP-1994; 315468.
 PR 16-DEC-1991; US-808316.
 PR 30-JAN-1992; US-828430.
 PR 01-FEB-1993; US-014941.
 PR 30-SEP-1994; US-315468.
 PA (MICO) MTCOGEN CORP.
 PI Foncecrada L, Michaels TE, Narva KE;
 DR P-PSDB: M06419.
 DR WPI: 96-424659/42.
 PT New nucleic acid encoding B. thuringiensis toxin active against
 PT scarab(s) - also related toxin and transformed microbes, effective
 PT against adult pests and their larvae
 PS Example 3; Column 37-42; 24pp: English.
 CC T43221-T43223 represent the coding sequences for toxins that are active
 CC against scarab pests. This sequence was isolated from the Bacillus
 CC thuringiensis strain tolworthi. Insects in the family Scarabaeidae
 CC constitute a serious pest control problem, especially when destructive
 CC larval stage insects infest high value turf found in golf courses,
 CC playing fields and lawns. The larvae of many species also attack grains,

CC tuberous crops, and ornamentals. The larvae are known as white grubs, or
 CC chafer grubs, and can be found in decaying organic matter, or in the soil
 CC where they consume plant roots. In Europe and the U.S. populations of
 CC these larvae and adults have developed resistance to chemical
 CC insecticides such as the organochlorines and DDT. The toxins encoded by
 CC these sequences, and intact cells that are capable of expressing the
 CC proteins, can be used to control many pests of the family scarabaeidae,
 CC such as species of Cyclocephala, and Popillia. The toxins are active
 CC against larvae (present in soil) and against adults.
 SQ Sequence 1953 BP; 679 A; 323 C; 344 G; 607 T;

Query Match 3.0%; Score 40.2; DB 1; Length 1953;
 Best Local Similarity 45.2%; Pred. No. 0.25;
 Matches 147; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

OY 314 TTATGAGAAATTAATGGCTATTAAGCGCAAAAGAAAGAAAGCTTCTGATGTA 373
 DB 1089 TTATGTAGAAAGCTAGACCTAGTATAGCTTAAGATACAAATCACTCCCATTTATGG 1148
 OY 374 GGTGACTCATTTACACCATTTCCGAAAGCTCAGATTGGTCTCCAGAGTACATTAGA 433
 DB 1149 AGATTAATCTATTGACCTATACAAAGCTAAGCTTTGATGACAAAAGTTATCGAAC 1208
 OY 434 AGCTGAGATAGGCAATAGTATGATACACATCTCTCCGAAACAAAGTATAGTTATG 493
 DB 1209 TATAGCTAATACAGACATAGCGGCTTTCCGATGCGCAAGATATATTTGGTTAGCA 1268
 OY 494 GCGTTGATGTTTAAAGCTTTACATATAGCTTACTTCTGAAAAAAGCTTTCAGGCT 553
 DB 1269 AGTTGATTTTGTCAATATGATGATCAAAAAATGAACATAGTACAAATATGATTC 1328
 OY 554 AGAAGAAAGATTGAAATATTATTCAGACATATAATTTAACTCTCCAGAGAC 613
 DB 1329 AAAAAGATACATGCTCTTTTAGTGCGACAGATTCATGACCATATACACAGAAAC 1388
 OY 614 TACTTATTTGCTAAAGTTAAAGCA 638
 DB 1389 AACAGATGACCACTTGAAAAAGCA 1413

RESULT 14
 ID 005679 standard; DNA; 2425 BP.
 AC 005679:
 DT 03-JAN-1991 (first entry)
 DE btPGS1208 gene.
 KW Toxin; crystal; insecticide; ss.
 OS Bacillus thuringiensis strain PGS1208.
 FH Key Location/Qualifiers
 FT cds 342..2297
 FT /*tag= a
 FT /product=74 kD btPGS1208 protoxin
 FT mat_peptide 513..2294
 FT /*tag= b
 FT /product=67 kD btPGS1208 toxin
 PN EP-382990-A.
 PD 22-AUG-1990.
 PR 15-FEB-1989; 400428.
 PR 15-FEB-1989; EP-400428.
 PA (PLAN-) PLANT GENETIC SYST.
 PI Peferoen M, Lambert B, Joos H;
 DR WPI: 90-25362/34.
 DR P-PSDB: R06460.
 PT New Bacillus thuringiensis strains - producing toxin active
 PT against Coleoptera
 PS Claim 3; Fig 1; 30pp: English.
 CC The btPGS1208 strain was isolated from grain dust and was deposited
 CC at the DSM (19/1/1989) under Acc. No. 5131. The protoxin crystals
 CC produced on expression of the gene can be digested with trypsin to
 CC produce the mature protein. Plants contg. the gene are resistant
 CC to Coleoptera pests while the crystals are useful as insecticides.
 CC The gene can also be truncated and used to produce chimeric genes

CC together with the btp6S1245 gene (005680).
SQ Sequence 2425 BP; 872 A; 366 C; 429 G; 758 T;

Query Match 3.0%; Score 40.2; DB 1; Length 2425;
Best Local Similarity 45.2%; Pred. No. 0.28;
Matches 147; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 314 TTATGAAGAAATTAATGGCTATAGACAGAAAAAAGAAACCTTCTCATGATGA 373
DB 1430 TTATGTAAGAACTAGACCTAGTAGATGATGATGATGATGATGATGATGATG 1489
QY 374 GGTGACCTATTTACACCTATTTGCAAGCTCAGATGGCTCTCCAGAGTACATTTAGA 433
DB 1490 AGATTAATCTATTTGCAACCTTACAAAAGCTAGCTTTGATGAGCAAAAAGTTATGAC 1549
QY 434 AGCTGAAGATGAAGCAATAGTATGATGATGATGATGATGATGATGATGATG 493
DB 1550 TATAGCTAATACAGACATACGCGCTTTCCGATGGCAAGATATATTTGGTTAGAA 1609
QY 494 GCGTTGGATGCTTTAGCTTTACATTTAGCTTTACATTTAGCTTTAGCTTTAGCT 553
DB 1610 AGTTGATTTTATGCTAATGATGATGATGATGATGATGATGATGATGATG 1669
QY 554 AGAAGAAAGATTAATTAATTTATTCAGACATTAATTAATTAATTAATTAATTA 613
DB 1670 AAAAAGATTAACATGCGCTATTTAGTGCACAGATTTCTATGACCATTTACACAGAAC 1729
QY 614 TACTTATTTGCTAAAGTTAAAGCA 638
DB 1730 AACAGATGAACCACTTGAAGCA 1754

RESULT 15

ID Q38654 standard; DNA; 1953 BP.
AC Q38654;
DT 15-JUL-1993 (first entry)
DE Bt isolate 43F coding sequence.
KW Lepidopteran-active; toxin; T1; R1; plant; cell; Bt; ss.
OS Bacillus thuringiensis.
PN W09304587-A.
PD 18-MAR-1993.
PR 11-SEP-1992; 007697.
PR 12-SEP-1991; US-758020.
PR 09-SEP-1992; US-941650.
PA (MCO) MYCOGEN CORP.
PI Bradish GA, Oyeda KA;
DR WPI; 93-100566/12.
P-PSDB: R33769.
PT Controlling lepidopteran pests - using compsn. of Bacillus
PT thuringiensis strains or plants or microorganisms transformed
PT with their toxin genes
PS Claim 13; Page 25-27; 38pp; English.
CC The sequences given in Q38653-55 encode lepidopteran-active toxins.
CC These sequences were used within a T1 or R1 plasmid, to transform
CC plant cells. Whole plants can then be regenerated from the
CC transformed cells. The toxin may also be produced by cloning
CC Bacillus thuringiensis (Bt). It may then be applied directly to
CC the plant locus.
SQ Sequence 1953 BP; 679 A; 320 C; 347 G; 607 T;

Query Match 2.9%; Score 38.6; DB 1; Length 1953;
Best Local Similarity 44.9%; Pred. No. 0.68;
Matches 146; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

QY 314 TTATGAAGAAATTAATGGCTATAGACAGAAAAAAGAAACCTTCTCATGATGA 373
DB 1089 TTATGTAAGAACTAGACCTATAGTAGATGATGATGATGATGATGATGATG 1148
QY 374 GGTGACCTATTTACACCTTACAAAAGCTAGCTTTGATGAGCAAAAAGTTATGAC 433

DB 1149 AGATAATCTATTTGAAGCTATACAAAAGCTAAGCTTTGATGAGCAAAAAGTTATGAC 1208
QY 434 AGCTGAAGATTAAGCAATAGATGATGATGATGATGATGATGATGATGATG 493
DB 1209 TATAGCTAATACAGACATAGCGGCTTTCCGATGGCAAGATATATTTGGTTAGCAA 1268
QY 494 GCGTTGGATGCTTTAGCTTTACATTTAGCTTTACATTTAGCTTTAGCTTTAGCT 553
DB 1269 AGTTGATTTTATGCTAATGATGATGATGATGATGATGATGATGATGATG 1328
QY 554 AGAAGAAAGATTAATTAATTTATTCAGACATTAATTAATTAATTAATTAATTA 613
DB 1329 AAAAAGATTAACATGCGCTATTTAGTGCACAGATTTCTATGACCATTTACACAGAAC 1388
QY 614 TACTTATTTGCTAAAGTTAAAGCA 638
DB 1389 AACAGATGAACCACTTGAAGCA 1413

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2000, 05:53:48 : Search time 49.94 seconds
(without alignments)
3495.593 Million cell updates/sec

Title: US-09-240-675-1
Perfect score: 1343
Sequence: 1 CTGCAGGATCTCGCGCGC.....ATACCTTAATGAGGTACC 1343

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 230463 seqs, 64992525 residues

Total number of hits satisfying chosen parameters: 460926

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1343	100.0	1343	4	US-08-307-588-1
2	1334	99.3	1755	4	US-08-307-588-3
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4	1330.8	99.1	2784	3	US-08-466-974-1
5	1330.8	99.1	2784	3	US-08-471-453-1
6	126	9.4	360	1	US-08-328-256-1
7	49	3.6	168	1	US-08-328-256-8
8	40.2	3.0	1953	1	US-08-315-468-5
9	39.4	2.9	1659	4	US-08-943-087-47
10	38.6	2.9	2430	6	PCT-US92-00040-1
11	37	2.8	1511	1	US-07-991-867B-8
12	37	2.8	1511	2	US-08-107-755A-8
13	37	2.8	1511	4	US-08-544-332-8
14	36.2	2.7	1951	2	US-08-487-890A-112
15	36.2	2.7	1951	4	US-08-478-435-112
16	36.2	2.7	1951	4	US-08-337-483-112
17	36.2	2.7	1951	4	US-08-478-373-112
18	36.2	2.7	1951	5	US-08-474-671-112
19	36.2	2.7	1951	5	US-08-483-577A-112
20	35.6	2.7	1575	4	US-08-853-659A-10
21	35.6	2.7	2636	4	US-08-820-170A-21
22	35.6	2.7	15512	4	US-08-853-659A-5
23	35.6	2.7	15512	4	US-08-853-659A-8
24	35.6	2.7	15512	4	US-08-853-659A-63
25	35.6	2.7	15512	4	US-08-853-659A-66
26	35.6	2.7	24701	4	US-08-853-659A-2
27	35.6	2.7	24701	4	US-08-853-659A-3

28	35.6	2.7	24701	4	US-08-853-659A-60	Sequence 60, Appl
29	35.6	2.7	24701	4	US-08-853-659A-61	Sequence 61, Appl
30	35.4	2.6	1291	1	US-07-952-755-2	Sequence 2, Appl1
31	35.4	2.6	1291	5	US-08-443-679-2	Sequence 2, Appl1
32	35.4	2.6	1482	5	US-08-996-441B-69	Sequence 69, Appl
33	35.4	2.6	1956	5	US-08-996-441B-51	Sequence 51, Appl
34	35.4	2.6	1956	5	US-08-996-441B-55	Sequence 55, Appl
35	35.4	2.6	1956	5	US-08-996-441B-57	Sequence 57, Appl
36	35.4	2.6	1959	5	US-08-996-441B-1	Sequence 1, Appl1
37	35.4	2.6	1959	5	US-08-996-441B-3	Sequence 3, Appl1
38	35.4	2.6	1959	5	US-08-996-441B-5	Sequence 5, Appl1
39	35.4	2.6	1959	5	US-08-996-441B-7	Sequence 7, Appl1
40	35.4	2.6	1959	5	US-08-996-441B-9	Sequence 9, Appl1
41	35.4	2.6	1959	5	US-08-996-441B-11	Sequence 11, Appl
42	35.4	2.6	1959	5	US-08-996-441B-13	Sequence 13, Appl
43	35.4	2.6	1959	5	US-08-996-441B-15	Sequence 15, Appl
44	35.4	2.6	1959	5	US-08-996-441B-17	Sequence 17, Appl
45	35.4	2.6	1959	5	US-08-996-441B-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-307-588-1
Sequence 1, Application US/08307588
Patent No. 5919453
GENERAL INFORMATION:
APPLICANT: BENOTT, Patrick
APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
TITLE OF INVENTION: INTERFERON
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/GUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1343 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS

LOCATION: 27..1334
US-08-307-588-1

Query Match 100.0%; Score 1343; DB 4; Length 1343;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 GCGATGCTGTGCGGGAATGACTTTTCATTCGATTCATCAAAAAACCTGGATGATA 240
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QY 301 TCAAGCTGAATGTTTATGAAGAAATTAATGCGTATAGAGCAGAAAAACACATT 360
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QY 841 ACCATTTGTATTAATGAAAAAATACCTGATGTAATGTCAAAACTACCAAGTGTG 900
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DB 901 TCTTCTCAAAAGCTTTTCAAAAAGAAATTAACCTTCGCGGTACAAAGCATGTGAG 960
QY 961 GAAATACACATCTTTTGTGCTGAAGAGATTAAGTTTGAATGAAATCAAGCTTTC 1020
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DB 1021 TACTTCTCAGTCTTTAATAGTATAGTATGATTCATTCATATATATGCTG 1080
QY 1081 CTCCAAAACAGTGTGAAACACGCTGTGATCCAGAGATTATCCATGATTATGAATTA 1140
    |||
DB 1081 CTCCAAAACAGTGTGAAACACGCTGTGATCCAGAGATTATCCATGATTATGAATTA 1140
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DB 1141 TTTTGGGAAAAACCTTAAATGCGAGAGAAAAATTAAGAAAAAACTGATGTA 1200
QY 1201 CAGTTCCTAATTGAAACACAGTGTATATGTTGTGAAGCCAGAGCAGACCATAG 1260
    |||
DB 1201 CAGTTCCTAATTGAAACACAGTGTATATGTTGTGAAGCCAGAGCAGACCATAG 1260
QY 1261 ATGAAAAGCTGAATTAAGCAATGTTTATGAGCGCTGTATGTGAGAAAAACCAAC 1320
    |||
DB 1261 ATGAAAAGCTGAATTAAGCAATGTTTATGAGCGCTGTATGTGAGAAAAACCAAC 1320
QY 1321 GAAATACCTCTAATGAGGTACC 1343
    |||
DB 1321 GAAATACCTCTAATGAGGTACC 1343

RESULT 2
US-08-307-588-3
; Sequence 3, Application US/08307588
; Patent No. 5919453
;
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVIE, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/GUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1755 base pairs
TYPE: nucleic acid
```

STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 27..1697
 US-08-307-588-3

Query Match 99.3%; Score 1334; DB 4; Length 1755;
 Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;
 Matches 1334; Conservative 0; Mismatches 0;

QY 1 CTGACGAGATCTGCGGGGCTCCAGATGATGCTGCTCTGCGGCGCAGCAGCTAG 60
 Db 1 CTGACGAGATCTGCGGGGCTCCAGATGATGCTGCTCTGCGGCGCAGCAGCTAG 60
 QY 61 TGTCTGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 Db 61 TGTCTGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 QY 121 CTCTCAAAAAGTAGAGGTGACATCATATGACAACTTATCTGAGGTGGAACGGA 180
 Db 121 CTCTCAAAAAGTAGAGGTGACATCATATGACAACTTATCTGAGGTGGAACGGA 180
 QY 181 GCGATGAGTCTGCGGAGATGACCTTTTCAATGATATCAAAAAGTGGGATGATA 240
 Db 181 GCGATGAGTCTGCGGAGATGACCTTTTCAATGATATCAAAAAGTGGGATGATA 240
 QY 241 ATTGATAAATTTGCTGGGTGTCAGAAATATCTAGTACCAAACTGCACTTTCTTAC 300
 Db 241 ATTGATAAATTTGCTGGGTGTCAGAAATATCTAGTACCAAACTGCACTTTCTTAC 300
 QY 301 TCAAGCGATGTTTGAAGAAATTAATGCGTATTAAGCAGAAAAGAAACCTT 360
 Db 301 TCAAGCGATGTTTGAAGAAATTAATGCGTATTAAGCAGAAAAGAAACCTT 360
 QY 361 CTTCATGATGAGGTGATCTATTTACACATTTGCGAAAGCTCAGATGCTCTCAG 420
 Db 361 CTTCATGATGAGGTGATCTATTTACACATTTGCGAAAGCTCAGATGCTCTCAG 420
 QY 421 AAGTACATTTGAAGCTGAAGATTAAGCAATAGTATACATCTCTCTGGAACAAAG 480
 Db 421 AAGTACATTTGAAGCTGAAGATTAAGCAATAGTATACATCTCTCTGGAACAAAG 480
 QY 481 ATAGTGTATGCGCTTGTGATGCTTAAAGCTTAACTATAGTTTCTATCTGAAAA 540
 Db 481 ATAGTGTATGCGCTTGTGATGCTTAAAGCTTAACTATAGTTTCTATCTGAAAA 540
 QY 541 ACTCTCAGGTGTAAGAAAGATTAATTTATTCAGACATTAATTTATTAAC 600
 Db 541 ACTCTCAGGTGTAAGAAAGATTAATTTATTCAGACATTAATTTATTAAC 600
 QY 601 TCTCACCAGAGACTACTTATTTCTAAAGCTTAAAGCAGACACTTACTCAAGAAAA 660
 Db 601 TCTCACCAGAGACTACTTATTTCTAAAGCTTAAAGCAGACACTTACTCAAGAAAA 660
 QY 661 TTGCTGCTATGCTCAGTATGATTAAGCAAGTGAAGAAAGAACTACTCTCAC 720
 Db 661 TTGCTGCTATGCTCAGTATGATTAAGCAAGTGAAGAAAGAACTACTCTCAC 720
 QY 721 CAGAAAATATGAAGTCACTGCTCAAAATCAGAACTATGTTCTTAAATGGATATCAT 780
 Db 721 CAGAAAATATGAAGTCACTGCTCAAAATCAGAACTATGTTCTTAAATGGATATCAT 780
 QY 781 ATGCAAAATGACCTTTCAAGTCAAGGCTCCAGGCTTTTAAAGAAATCTGGA 840
 Db 781 ATGCAAAATGACCTTTCAAGTCAAGGCTCCAGGCTTTTAAAGAAATCTGGA 840
 QY 841 ACCATTTGATTAATGAACAAATACTGCTGAAATGCTAAAGAACTACCAAGTGTG 900
 Db 841 ACCATTTGATTAATGAACAAATACTGCTGAAATGCTAAAGAACTACCAAGTGTG 900

QY 901 TCTTCTCAAAACGTTTTCAAAAGAAATTTACTCTCGCGGTACAGATCTGATG 960
 Db 901 TCTTCTCAAAACGTTTTCAAAAGAAATTTACTCTCGCGGTACAGATCTGATG 960
 QY 961 GAAATTAACATCTTTTGTGCTGAAGATTAAGTTTATCTGAAATACAAAGCTTTC 1020
 Db 961 GAAATTAACATCTTTTGTGCTGAAGATTAAGTTTATCTGAAATACAAAGCTTTC 1020
 QY 1021 TACTTCTCAGCTTTTAACTATGATCCCTTAGTATGATCATCTATCTATGCGTG 1080
 Db 1021 TACTTCTCAGCTTTTAACTATGATCCCTTAGTATGATCATCTATCTATGCGTG 1080
 QY 1081 CTCCAAAACAGTCTGGAACACAGCCTGTATGATCAGAGATTATCAGTATTAAGAAATTA 1140
 Db 1081 CTCCAAAACAGTCTGGAACACAGCCTGTATGATCAGAGATTATCAGTATTAAGAAATTA 1140
 QY 1141 TTTTGGGAAAACACTTTAAATGCTGAGAGAAAAATTTGAGAAAAAACTGATGTTA 1200
 Db 1141 TTTTGGGAAAACACTTTAAATGCTGAGAGAAAAATTTGAGAAAAAACTGATGTTA 1200
 QY 1201 CAGTCTCAATTTGAACACAGTCTGATATTTGTTGTAAGCAGACACACCATGG 1260
 Db 1201 CAGTCTCAATTTGAACACAGTCTGATATTTGTTGTAAGCAGACACACCATGG 1260
 QY 1261 ATGAAAAGCTGAATAAAGCAGTGTTTTATGACGCTGTATGTGAGAAAAACAAACGAG 1320
 Db 1261 ATGAAAAGCTGAATAAAGCAGTGTTTTATGACGCTGTATGTGAGAAAAACAAACGAG 1320
 QY 1321 GAAATACCTCTAAA 1334
 Db 1321 GAAATACCTCTAAA 1334

RESULT 3

US-08-471-454-1
 Sequence 1, Application US/08471454
 Patent No. 5731169

GENERAL INFORMATION:

APPLICANT: MOGENSEN, Knud E.
 APPLICANT: UZE, Gilles
 APPLICANT: LOTFALLA, Georges
 APPLICANT: GRESSER, Ion
 TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
 TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
 TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHUYE P. C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,454
 FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

Prior Application Data:
 APPLICATION NUMBER: US 07/900,642

FILING DATE: 15-JUN-1992
 APPLICATION NUMBER: FR 89/13770

FILING DATE: 20-OCT-1989
 ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 960-7

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000

REFERENCE/DOCKET NUMBER: 960-7
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 TELEX: 200797 NIXN UR
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2784 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-466-974-1

Query Match 99.1% Score 1330.8 DB 3 Length 2784
 Best Local Similarity 99.9% Pred. No. 0:
 Matches 1332: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCGAGGAGATCGCGGGCTCCAGATGATGTCCTCTCTGCGCGCGAGACCTTAG 60
 DB 53 CTGGTGGATCTCGCGGGCTCCAGATGATGTCCTCTCTGCGCGCGAGACCTTAG 112
 QY 61 TGCCTGTCG 120
 DB 113 TGCCTGTCG 172
 QY 121 CTCCTCAAAAGTAGAGAGTGCATCATAGATGACAACTTATCCGTGAGTGAACAGA 180
 DB 173 CTCCTCAAAAGTAGAGAGTGCATCATAGATGACAACTTATCCGTGAGTGAACAGA 232
 QY 181 GCGATGAGTCTGCGGGAATGACTTTTTCATTCGATTACAAAACTGGATGATA 240
 DB 233 GCGATGAGTCTGCGGGAATGACTTTTTCATTCGATTACAAAACTGGATGATA 292
 QY 241 ATTGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 DB 293 ATTGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 352
 QY 301 TCAAGCTGAATGTTATGAAGAAATTAATGCGTATGAAGACAGAAAAAGAAACACT 360
 DB 353 TCAAGCTGAATGTTATGAAGAAATTAATGCGTATGAAGACAGAAAAAGAAACACT 412
 QY 361 CTTCATGATGAGTGTACTCATATTACACATTCGCAAGCTCAGATGGTCTCCAG 420
 DB 413 CTTCATGATGAGTGTACTCATATTACACATTCGCAAGCTCAGATGGTCTCCAG 472
 QY 421 AAGTACATTTAGAACTGAAGATAGCAATAGTATACACATCTCTCTGAGACAAAG 480
 DB 473 AAGTACATTTAGAACTGAAGATAGCAATAGTATACACATCTCTCTGAGACAAAG 532
 QY 481 ATAGTGTATGCTGGCTTGGATGTTAAGTTACATATAGTACTTATCTGAAAA 540
 DB 533 ATAGTGTATGCTGGCTTGGATGTTAAGTTACATATAGTACTTATCTGAAAA 592
 QY 541 ACTCTCAGTGTAGAGAAAGAGATTGAATAATTATTCAGACATTAATTTTAAAC 600
 DB 593 ACTCTCAGTGTAGAGAAAGAGATTGAATAATTATTCAGACATTAATTTTAAAC 652
 QY 601 TCTACACGAGACTACTTATTTCTTAAAGTTAAAGCAGCACTTACGTCATGAAAA 660
 DB 653 TCTACACGAGACTACTTATTTCTTAAAGTTAAAGCAGCACTTACGTCATGAAAA 712
 QY 661 TTGGTGTATAGTCCATACATTTGATTAAGACAGACAGTGAAGAAATGACTCTCAC 720
 DB 713 TTGGTGTATAGTCCATACATTTGATTAAGACAGACAGTGAAGAAATGACTCTCAC 772
 QY 721 CAGAAATATAGAACTAGTCTCAAAATCAGAACTATGTTCTTAAATGGATATACAT 780
 DB 773 CAGAAATATAGAACTAGTCTCAAAATCAGAACTATGTTCTTAAATGGATATACAT 832
 QY 781 ATGCAACATGACCTTTCAAGTTCAGTGTCTCAGCGCTTTTAAAGAAATCTCGAA 840

DB 833 ATGCAACATGACCTTCAAGTTCAGTGTCTCAGCGCTTTTAAAGAAATCTCGAA 892
 QY 841 ACCATTGTATTAATGGAACCAATACCTGACTGTGAAAAATGTCACCAACAGTGTG 900
 DB 893 ACCATTGTATTAATGGAACCAATACCTGACTGTGAAAAATGTCACCAACAGTGTG 952
 QY 901 TCTTCTCAAAAGCTTTTCCAAAAAGAAATTTACCTTCTCCGGTACCAAGCATGTATG 960
 DB 953 TCTTCTCAAAAGCTTTTCCAAAAAGAAATTTACCTTCTCCGGTACCAAGCATGTATG 1012
 QY 961 GAAATTAACATCTTTTGGCTGAGAGATTAAGTTGATGATGATGATGATGATGATG 1020
 DB 1013 GAAATTAACATCTTTTGGCTGAGAGATTAAGTTGATGATGATGATGATGATGATG 1072
 QY 1021 TACTTCTCAGTCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 DB 1073 TACTTCTCAGTCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1132
 QY 1081 CTCCAAAACAGTCTGGAACAGCGCTGTATGATGATGATGATGATGATGATGATG 1140
 DB 1133 CTCCAAAACAGTCTGGAACAGCGCTGTATGATGATGATGATGATGATGATGATG 1192
 QY 1141 TTTTGGGAAAAACACTTCAAAATGCTGAGAGAAATTTATGAGAAAAAATGATGTTA 1200
 DB 1193 TTTTGGGAAAAACACTTCAAAATGCTGAGAGAAATTTATGAGAAAAAATGATGTTA 1252
 QY 1201 CAGTCTCAATTTGAAACCACTGATGATGATGATGATGATGATGATGATGATGATG 1260
 DB 1253 CAGTCTCAATTTGAAACCACTGATGATGATGATGATGATGATGATGATGATGATG 1312
 QY 1261 ATGAAAGCTGAATTAAGACAGTGTGTTTACTGACGCTGTATGAGAAAAAATGATG 1320
 DB 1313 ATGAAAGCTGAATTAAGACAGTGTGTTTACTGACGCTGTATGAGAAAAAATGATG 1372
 QY 1321 GAAATACCTCTAAA 1334
 DB 1373 GAAATACCTCTAAA 1386

RESULT 5

US-08-471-453-1
 Sequence 1, Application US/08471453
 Patent No. 5886153
 GENERAL INFORMATION:
 APPLICANT: MOGENSEN, Knud E.
 APPLICANT: UZE, Gilles
 APPLICANT: LUTFALLA, Georges
 TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
 TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERBYE P. C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,453
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/900,642
 FILING DATE: 15-JUN-1992
 APPLICATION NUMBER: FR 89/13770
 FILING DATE: 20-OCT-1989

```

? ACTOR/REY/AGENT INFORMATION:
?
? NAME: BYRNE, THOMAS E.
?
? REGISTRATION NUMBER: 32,205
?
? REFERENCE/DOCKET NUMBER: 960-7-7-
?
? TELECOMMUNICATION INFORMATION:
?
? TELEPHONE: (703) 816-4000
?
? TELEFAX: (703) 816-4100
?
? TELEX: 200797 NIKN UR
?
? INFORMATION FOR SEQ ID NO: 1:
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 2764 base pairs
?
? TYPE: nucleic acid
?
? STRANDEDNESS: single
?
? TOPOLOGY: linear
?
? MOLECULE TYPE: DNA (genomic)
US-08-471-453-1

```

Query Match	99.1%	Score 1330.8	DB 3	Length 2784
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1332	Conservative	0	Mismatches 2	Indels 0
			Gaps	0

QY	1	CTGCAGGGATCTGCGCGGGCTCCCGAGTATATGTCCTCTCGGGCGGACGACCTTGG	60
Db	53	CTGGGGGATCTGCGGGCGGCTCCGAGATATGTCGTCTCTGGCGGACGACCTTGG	112
QY	61	TGCTGTCGCGGTGGGCCCATGGGTGTGTGCCAGCCGACGAGTGGAAAAATCTAAAT	120
Db	113	TGCTGTCGCGGTGGGCCCATGGGTGTGTGCCAGCCGACGAGTGGAAAAATCTAAAT	172
QY	121	CTCCCAAAAAAGTAAAGTCCGACATCATATGATGACAACTTTATCCTGAGGTGGAAACGA	180
Db	173	CTCCCAAAAAAGTAAAGTCCGACATCATATGATGACAACTTTATCCTGAGGTGGAAACGA	232
QY	181	CGGATGAGTCTCTCGGGAATGACATTTTCATTCGATATATCAAAAAATGGGATGATA	240
Db	223	CGGATGAGTCTCTCGGGAATGACATTTTCATTCGATATATCAAAAAATGGGATGATA	292
QY	241	ATTGGATAAAAATGTCTGGGTGCAGAAATATTACTAGTACCAATGCCAATTTTCTTCAC	300
Db	293	ATTGGATAAAAATGTCTGGGTGCAGAAATATTACTAGTACCAATGCCAATTTTCTTCAC	352
QY	301	TCAAGCTGAATGTTTATGAAAGAAATTAATTCGCTATTAAGACAGAAAAAGAAACACTT	360
Db	353	TCAAGCTGAATGTTTATGAAAGAAATTAATTCGCTATTAAGACAGAAAAAGAAACACTT	412
QY	361	CTTCATGGTATGAGGTGTGACTCATTTACACCAATTTCCGAAACCTGACATGTGGCTCCAG	420
Db	413	CTTCATGGTATGAGGTGTGACTCATTTACACCAATTTCCGAAACCTGACATGTGGCTCCAG	472
QY	421	AAGTACATTATGAAAGCTGAAGATTAAGGCATATGATGATACACTTCCTCGGAACAATAAG	480
Db	473	AAGTACATTATGAAAGCTGAAGATTAAGGCATATGATGATACACTTCCTCGGAACAATAAG	532
QY	481	ATAGTGTATGTGGCCTTTGGATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAAA	540
Db	533	ATAGTGTATGTGGCCTTTGGATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAAA	592
QY	541	ACTCTTCAGGCTGTAAAGAAAGGATTGAAAAATTTTATTCGAGACTAATAAATTTATAAAC	600
Db	593	ACTCTTCAGGCTGTAAAGAAAGGATTGAAAAATTTTATTCGAGACTAATAAATTTATAAAC	652
QY	601	TCTCACAGAGACTCTTATTGTCTAAAAAGTTAAAGCACACACTACTACTGCTATGGAAAA	660
Db	653	TCTCACAGAGACTCTTATTGTCTAAAAAGTTAAAGCACACACTACTACTGCTATGGAAAA	712
QY	661	TTGCTGTATAGTCCAGTACATTGTATTAAGACACACACTTGAAAAATGAACTACCTCCAC	720
Db	713	TTGCTGTATAGTCCAGTACATTGTATTAAGACACACACTTGAAAAATGAACTACCTCCAC	772
QY	721	CAGAAAAATATAGAACTCAAGTCTCCAAATCAGAACTATGTCTTTAATGGATTATACAT	780
Db	773	CAGAAAAATATAGAACTCAAGTCTCCAAATCAGAACTATGTCTTTAATGGATTATACAT	832

RESULT 6
US-08-328-256-1
Sequence 1, Application US/08328256
Patent No. 564379
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328, 256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.

REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-328-256-1

Query Match 9.4%; Score 126; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.7e-26;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1209 AATTGAAACCACTGACTGTATATTTGTGAAAGCCAGACACCATGATGAAAG 1268
DB 1 AATTGAAACCACTGACTGTATATTTGTGAAAGCCAGACACCATGATGAAAG 60
OY 1269 CTGAATTAAGCAGTGTGTTTGTGACCGCTGTATGTGAGAAAAACAACCGAATATCC 1328
DB 61 CTGAATTAAGCAGTGTGTTTGTGACCGCTGTATGTGAGAAAAACAACCGAATATCC 120
OY 1329 TCTAAA 1334
DB 121 TCTAAA 126

RESULT 7
US-08-328-256-8
Sequence 8, Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVIYSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..168
US-08-328-256-8

Query Match 3.6%; Score 49; DB 1; Length 168;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1218 CCACTGACTGTATATTTGTGAAAGCCAGACACCATGATGAAA 1266
DB 1 CCACTGACTGTATATTTGTGAAAGCCAGACACCATGATGAAA 49

RESULT 8
US-08-315-468-5
Sequence 5, Application US/08315468
Patent No. 5554534
GENERAL INFORMATION:
APPLICANT: Michaels, Tracy Ellis
APPLICANT: Foncerra, Luis
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Process for Controlling Scarab Pests
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,468
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/014,941
FILING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/808,316
FILING DATE: 16-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA73.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1953 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: tolworthi

FILING DATE: 31-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-29 P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2430 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..2099
PCT-US92-00040-1

Query Match 2.9% Score 38.6; DB 6; Length 2430;
Best Local Similarity 44.9%; Pred. No. 0.17;
Matches 146; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

QY 314 TATGAGAAATTAATTCGCTAAGACAGAAAAACACTCTTCATGATGA 373
DB 1232 TATGAGAACTAGACAGATCTAGTAAACAAATTAATTCCTCCATTTATGG 1291
QY 374 GGTGACATTTACACATTTGGCAAGCTCAGATTGGCCCGCAAGATATTAGA 433
DB 1292 AGTAAATCTAGCAACCTGTAACAAAGTTAAGCTTGAGCAAAAAGTTATGAGC 1351
QY 434 AGCTGAAGATTAAGCAATAGTATACATCTCTCGAACAAGATAGTATGTC 493
DB 1352 TATAGCTAATACAGACAGTACCGCTCGCAATGGCAATATATTTGGCTTACGA 1411
QY 494 GCGTTGATGTTTAAAGCTTACATATAGCTTATCTGAAAAAATCTTCAGGTG 553
DB 1412 AGTTGATTTAGCAATATGATGATCAAAAAATGAACCTAGTACAAACATATGATTC 1471
QY 554 AGAAGAAAGATGAAAAATTTATTCACACATATAATTTAACTCTCACCAGAGC 613
DB 1472 AAAAAGAAACATGGCCATAGGTGACAGATTTCTATTGACCAATTTACCACAGAAC 1531
QY 614 TACTTATGCTTAAAGTTAAAGCA 638
DB 1532 AACGATGACCACTTGAAGCA 1556

RESULT 11
US-07-991-867B-8/C
Sequence 8, Application US/07991867B
Patent No. 5476781
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B

FILING DATE: 12-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UP14.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Amsacta moorei entomopoxvirus
FEATURE:
NAME/KEY: CDS
LOCATION: complement (18..218)
FEATURE:
NAME/KEY: CDS
LOCATION: complement (234..782)
FEATURE:
NAME/KEY: CDS
LOCATION: 852..1511
US-07-991-867B-8

Query Match 2.8% Score 37; DB 1; Length 1511;
Best Local Similarity 46.1%; Pred. No. 0.38;
Matches 124; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 962 AATAACACATCTTTTGGCTGAAGAGATAAGTTGATGATGAAATCAAGCTTCT 1021
DB 995 AATATATATATGCAATCTCTTAATTAATCTTATTTTAAATATATATTAATAC 936
QY 1022 ACTTCTCAGCTTTTAACATAGATCCCTTGTGATTCATTCATATATATGCTGC 1081
DB 935 ATATCTCTGTTTATATATATTTTAAATATATATTTTAAATATTTTAAAT 876
QY 1082 TCCAAACAGCTGGAACACCGCTGTATCCAGATATCCAGATTTATGAATAT 1141
DB 875 TATATGAAATTTAGTAATTCATTTGATATTTTATTTTTCATGATTAATTT 816
QY 1142 TTTTGGAAAACTCAATGCTGAGAGAAAAATATATGAGAAAAAACTGATGTAC 1201
DB 815 TTTTGAATAAT 756
QY 1202 AGTTCCTAATTTGAAACCACTGATGCTAT 1230
DB 755 ATGTTTCTGGCAAAAACAGAAATTTGAT 727

RESULT 12
US-08-107-755A-8/C
Sequence 8, Application US/08107755A
Patent No. 5721352
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System

NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Salivanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,755A
FILING DATE: 19-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,658
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Salivanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF114.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Amesctia moorei entemopoxvirus
FEATURE:
NAME/KEY: CDS
LOCATION: complement (18..218)
NAME/KEY: CDS
LOCATION: complement (234..782)
FEATURE:
NAME/KEY: CDS
LOCATION: 852..1511
US-08-107-755A-8

Query Match 2.8%; Score 37; DB 2; Length 1511;
Best Local Similarity 46.1%; Pred. No. 0.38; Mismatches 145; Indels 0; Gaps 0;
Matches 124; Conservative 0;
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DB 995 ATATATATATGCAATCTCTTAATACTATTTTATATATATATATATATATAC 956
DB 1022 ACTTCTCCAGCTTTTAACATGATCCCTTACTGATTCATTCATATATCGGTGC 1081
DB 935 ATATCTCTGTTATATATTTTATTAATATATATATTAATAATATTAATAAT 876
DB 1082 TCCAAACAGCTGGAACAGCGCTGATCCAGATTAATCCAGTATTAATTAAT 1141
DB 875 TATATCAGATTTAGTAATCCATTTGATTAATTTATTTTTCATTGATTAATTT 816
DB 1142 TTTTGGAAACACTCAATCTGAGAGAAATTAATGAGAAAAAACTGATGTAC 1201
DB 815 TTTTGGAAAAATATATCAATATATAAAAAAATGTCATTAATTAATTTGGTCC 756
DB 1202 AGTTCCATTTGAAACCACTGACTAT 1230

DB 755 ATGTTTCTGCAACACAGATTTGAT 727

RESULT 13

US-08-544-332-8/C

Sequence 8, Application US/08544332

Patent No. 5935777

GENERAL INFORMATION:

APPLICANT: Moyer, Richard W.

APPLICANT: Hall, Richard L.

APPLICANT: Grudl, Michael E.

TITLE OF INVENTION: No. 5935777e1 Entomopoxvirus Expression System

NUMBER OF SEQUENCES: 77

CORRESPONDENCE ADDRESS:

ADDRESSEE: Gerard H. Bencen

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/544,332

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/991,867

FILING DATE: 07-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/107,755

FILING DATE: 19-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO 92/14818

FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/827,685

FILING DATE: 30-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/657,584

FILING DATE: 19-FEB-1991

ATTORNEY/AGENT INFORMATION:

NAME: Bencen, Gerard H.

REGISTRATION NUMBER: 35,746

REFERENCE/DOCKET NUMBER: UF114.C4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100

TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1511 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Amesctia moorei entemopoxvirus

FEATURE:

NAME/KEY: CDS

LOCATION: complement (18..218)

FEATURE:

NAME/KEY: CDS

LOCATION: complement (234..782)

FEATURE:

NAME/KEY: CDS

LOCATION: 852..1511

US-08-544-332-8

Query Match 2.8%; Score 37; DB 4; Length 1511;

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:      TOPOLOGY:  linear
:      FEATURE:
:      NAME/KEY:  CDS
:      LOCATION:  1...1890
:      US-08-487-890A-112

Query Match      2.7%:  Score 36.2;  DB 2;  Length 1951;
Best Local Similarity 49.7%:  Pred. No. 0.72;
Matches 92;  Conservative 0;  Mismatches 93;  Indels 0;  Gaps 0;

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Db  1526  TTACGGATRAAAAAGCTACAGCGCAATRAAAAAGACGCCGATRAATCAAAATACCGTATTTA 1585

Oy  589  AAAATTATTAACCTCTCACCCAGAGACTTATTGTCTTAAAGTTAAAGCAGACCTACTTA 648
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  1586  GAATTAAGCGACACTTTAAAAATAATGATAATGCGCTTCAAAGGTACACCAACCCGAGAAA 1645

Oy  649  CGTCATGGAAAAATGGTGCTATAGTCCAGTACATTGTATAAAGCCACAGCTGGAANAATG 708
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  1646  ATTTTGTAATGATGTGTACACATAGTCAAACTGCAAAATACCCAAATTAATATTAAACTG 1705

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2000, 05:52:42 ; Search time 610.76 Seconds
(without alignments)
8912.632 Million cell updates/sec

Title: US-09-240-675-1

Perfect score: 1343

Sequence: 1 CTCGACGAGACTCGCGCGC.....ATACCTTAATGAGGTACC 1343

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4857316 seqs, 202611650 residues

Total number of hits satisfying chosen parameters: 9714632

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

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109: gb_gss16:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result

Query

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
C 1	495.4	36.9	538	80	AM366810	AM366810 CM1-HT015
C 2	491.4	35.2	505	30	AA258405	AA258405 zrf62b09.s
C 3	446.4	33.2	456	79	AM292243	AM292243 UI-H-B12
C 4	414.8	30.9	571	46	A1458581	A1458581 t3j97d01.x
C 5	395	29.4	403	79	AM292242	AM292242 UI-H-B12
C 6	365.8	27.2	383	31	AA308713	AA308713 EST179523
C 7	341.2	25.4	380	30	AA258750	AA258750 zrf62b09.x
C 8	277.4	20.7	504	33	AA447894	AA447894 zxl1a06.r
C 9	271	20.2	444	61	AA163325	AA163325 t239a08.x
C 10	205.6	15.3	269	21	T96831	T96831 ye51d09.r1
C 11	185	13.8	452	81	AM435471	AM435471 UI-R-B10P
C 12	174.4	13.0	563	29	AA168022	AA168022 MS66C03.r
C 13	145.8	10.9	528	85	AA0684103	AA0684103 HS.2162.B
C 14	128.8	9.6	310	43	A1178178	A1178178 EST221843
C 15	58.6	4.4	1101	82	CNS00396	CNS00396
C 16	56.6	4.2	475	24	H70424	H70424 ye03b10.r1
C 17	53.4	4.0	387	21	T96832	T96832 ye51d09.s1
C 18	53.2	4.0	1101	82	CNS00396	CNS00396
C 19	50.4	3.8	1204	83	CNS016E2	CNS016E2
C 20	48.6	3.6	697	83	CNS018M5	CNS018M5
C 21	46.2	3.4	1101	82	CNS003B6	CNS003B6
C 22	45.4	3.4	1101	82	CNS000D1	CNS000D1
C 23	45.4	3.4	1101	82	CNS00EVL	CNS00EVL
C 24	44.6	3.3	928	82	CNS00C2B	CNS00C2B
C 25	44.6	3.3	1101	83	CNS0174K	CNS0174K
C 26	44.2	3.3	1001	82	CNS01400	CNS01400
C 27	44	3.3	928	82	CNS00DKY	CNS00DKY
C 28	43.8	3.3	928	85	AA550690	AA550690 1927m3 gm
C 29	43.8	3.3	987	83	CNS014PQ	CNS014PQ
C 30	43.6	3.2	1101	83	CNS017X	CNS017X
C 31	43.4	3.2	781	82	CNS009DO	CNS009DO
C 32	43.2	3.2	1101	82	CNS00RYG	CNS00RYG
C 33	42.8	3.2	579	92	A0965871	A0965871 LER1F79F
C 34	42.8	3.2	597	92	A0965870	A0965870 LER1F79F
C 35	42.8	3.2	597	92	A0965870	A0965870 LER1F79F
C 36	42.8	3.2	1201	83	CNS0167M	CNS0167M
C 37	42.6	3.2	1101	83	CNS0182P	CNS0182P
C 38	42.6	3.2	1225	83	CNS0161D	CNS0161D
C 39	42.2	3.1	1101	82	CNS00KAE	CNS00KAE
C 40	42	3.1	1086	82	CNS00YXK	CNS00YXK
C 41	41.8	3.1	1101	82	CNS00LJT	CNS00LJT
C 42	41.6	3.1	524	82	CNS00079	CNS00079
C 43	41.6	3.1	1097	82	CNS012J5	CNS012J5
C 44	41.6	3.1	1101	82	CNS010OX	CNS010OX
C 45	41.6	3.1	1101	83	CNS017ZQ	CNS017ZQ

ALIGNMENTS

RESULT 1
AM366810/c 538 bp mRNA EST 04-FEB-2000
LOCUS CM1-HT0152-041099-021-f06 HT0152 Homo sapiens cDNA, mRNA sequence.
DEFINITION AM366810
ACCESSION AM366810
VERSION AM366810.1 GI:6871460
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
TITLE HCGP http://www.ludwig.org.br/ORESTES
JOURNAL The FAPESP/LICR Human Cancer Genome Project
COMMENT On Mar 10, 1998 this sequence version replaced gi:2948481.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM1&cl=CM1-HT0152-041099-021-f06&cl=1999-10-04&cl=1)
Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence stop: 538.
Location/Qualifiers
1..538
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="HT0152"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 157 a 87 c 107 g 187 t
ORIGIN

Query Match 36.9%; Score 495.4; DB 80; Length 538;
Best Local Similarity 95.2%; Pred. No. 2.7e-11;
Matches 511; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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OY 681 CATTGATTAAGACCAAGTGAATGAACACCTCCACGAAATATAGAGTCACT 740
DB 538 CATTGATTAAGACCAAGTGAATGAACACCTCCACGAAATATAGAGTCACT 479
OY 741 GTCCAAATCAGACTATGTTCTTAATGGATTATACATGCAACATGACCTTCAA 800
DB 478 GTCCAAATCAGACTATGTTCTTAATGGATTATACATGCAACATGACCTTCAA 419
OY 801 GTTCAGTGGCTCCAGCCCTTTTAAAGAGATCCTGGAAACATTTGATTAAGGAA 860
DB 418 GTTCAGTGGCTCCAGCCCTTTTAAAGAGATCCTGGAAACATTTGATTAAGGAA 359
OY 861 CAAATACCGACTGGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 920
DB 358 CAAATACCGACTGGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 299
OY 921 CAAAAGGAATTTACCTCTCCGCTACAGCATGATGAAATACACATCTTTTGG 980
DB 298 CAAAAGGAATTTACCTCTCCGCTACAGCATGATGAAATACACATCTTTTGG 239
OY 981 TCTGAAGAGATTAAGTTGATACCTGAATACAGCTTTCTCTCCATCTTTTAC 1040
DB 238 TCTGAAGAGATTAAGTTGATACCTGAATACAGCTTTCTCTCCATCTTTTAC 179
OY 1041 ATTAGATCCCTAGTATGATCATATCATATCATATGATGATGATGATGATGATG 1100
DB 178 ATTAGATCCCTAGTATGATCATATCATATCATATGATGATGATGATGATGATG 119
OY 1101 ACGCCTGTGATCCAGATTTATCCACTGATTATGAAATATTTTGGGAAACCTTCA 1160
DB 118 ACGCCTGTGATCCAGATTTATCCACTGATTATGAAATATTTTGGGAAACCTTCA 59
OY 1161 AATGCTGAGAGAAATTTATGAGAAATGATGATGATGATGATGATGATGATGAT 1217
DB 58 AATGCTGAGAGAAATTTATGAGAAATGATGATGATGATGATGATGATGATGATG 2
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RESULT 2
AA258405/c 505 bp mRNA EST 17-MAR-1997
LOCUS AA258405
DEFINITION zrf62b09.s1 Soares_NHMHU_S1 Homo sapiens cDNA clone IMAGE:667961 3'
similar to gb:J03171 INTERFERON-ALPHA RECEPTOR PRECURSOR (HUMAN);

mRNA sequence.
 AA258405.1 GI:1893676
 VERSION
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 505)
 Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Treaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)
 On Sep 12, 1995 this sequence version replaced gi:1393828.
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -41m3 fwd. ET from Amersham
 High quality sequence stop: 418.
 Location/Qualifiers
 1..505
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:667961"
 /clone_11b="Soares.NHMPU.S1"
 /tissue_type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab_host="DH10B"
 /note="Organ: mixed (see below). Vector: pT73D-Pac
 (Pharmacia) with a modified polylinker. Site 1: Not I;
 Site 2: Eco RI. Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte 2NBH, pregnant uterus
 NBHPU, and fetal heart NBH19W) were mixed, and ss circles
 were made in vitro. Following BAP purification, this DNA
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479."
 BASE COUNT 151 a 79 c 106 g 169 t
 ORIGIN
 Query Match 36.6%; Score 491.4; DB 30; Length 505;
 Best Local Similarity 99.6%; Pred. No. 2, 6e-110;
 Matches 503; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Db 265 TCCTCAAAACGTTTCCAAAAAGCAATTTACCTTCGCCGCGTACAGCATCTGATGGAAA 206
 Qy 965 TAACACATCTTTTGGTGTGAAGAGATAAGTTTGATAGTGAATAACAGCTTCTTACT 1024
 Db 205 TACACATCTTTTGGTGTGAAGAGATAAGTTTGATAGTGAATAACAGCTTCTTACT 146
 Qy 1025 TCCTCAGCTCTTAAACATTAGATCCCTTAGTATTCATTCATATCATTCGCTGCC 1084
 Db 145 TCCTCAGCTCTTAAACATTAGATCCCTTAGTATTCATTCATATCATTCGCTGCC 86
 Qy 1085 AAAACAGTGTGAACACGCGGTGATTCAGGATTATCCACGATTATGAATATTTT 1144
 Db 85 AAAACAGTGTGAACACGCGGTGATTCAGGATTATCCACGATTATGAATATTTT 26
 Qy 1145 TTGGGAAAACACTCAATGCTGAG 1169
 Db 25 TTGGGAAAACACTCAATGCTGAG 1
 RESULT 3
 AM292343/C
 LOCUS
 DEFINITION UI-H-B12-8gw-a-10-0-UI.S1 NCI CGAP_Sub4 Homo sapiens cDNA clone
 IMAGE:272554.3', mRNA sequence.
 ACCESSION AM292343
 VERSION AM292343.1 GI:6698979
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 456)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 On Jun 5, 1998 this sequence version replaced gi:3188431.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. cDNA library preparation: M.B. Soares Lab Clone distribution:
 NCI-CGAP clone distribution information can be found through the
 I.M.A.G.E. Consortium/LNL at:
 www-bio.llnl.gov/dbp/image/image.html
 Seq primer: M13 Forward
 Polya=yes.
 Location/Qualifiers
 1..456
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:272554"
 /clone_11b="NCI-CGAP_Sub4"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker. Site 1: Not I; Site 2: Eco RI. The
 NCI-CGAP_Sub4 library is a subtracted library derived from
 the NCI-CGAP_Sub2 library which is a subtracted library
 derived from the NCI-CGAP_Sub1 library, which is a
 subtracted library derived from B1. B1 constitutes a
 mixture of 21 normalized or subtracted NCI-CGAP
 libraries: NCI-CGAP_C04, NCI-CGAP_P122, NCI-CGAP_P128,
 NCI-CGAP_C010, NCI-CGAP_C016, NCI-CGAP_K1d5,
 NCI-CGAP_K1d12, NCI-CGAP_K1d3, NCI-CGAP_K1d11,
 NCI-CGAP_L1m2, NCI-CGAP_Br2, NCI-CGAP_C08, NCI-CGAP_C1L1,
 NCI-CGAP_Lu24, NCI-CGAP_Br23, NCI-CGAP_Lu5,
 NCI-CGAP_Lu24, NCI-CGAP_Lu19, NCI-CGAP_G04, NCI-CGAP_G06,
 NCI-CGAP_Br25. These 21 libraries were pooled and a
 single-stranded DNA preparation of the resulting mixture
 was used as a tracer in a subtractive hybridization with
 a driver whose composition is detailed below.

REFERENCE
1 (bases 1 to 571)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
On Jun 5, 1998 this sequence version replaced gi:3187434.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.illn.gov/dbfp/image/image.html.

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FEATURES
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    1. .571
    Insert Length: 918      Std Error: 0.00
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    High quality sequence stop: 425.
    Location/Qualifiers

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FEATURES	Location/Qualifiers
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/tissue_type="carcinoid"
/abd_host="DH10B"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Juv was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonids
1414920-1417591 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Ronaldo."
BASE COUNT      172 a
ORIGIN           97 c   106 g   194 t      2 others

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/tissue_type="carcinoid"
/abd_host="DH10B"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Juv was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonids
1414920-1417591 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Ronaldo."
BASE COUNT      172 a
ORIGIN           97 c   106 g   194 t      2 others

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/tissue_type="carcinoid"
/abd_host="DH10B"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Juv was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonids
1414920-1417591 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Ronaldo."
BASE COUNT      172 a
ORIGIN           97 c   106 g   194 t      2 others

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Db 208 ATCGAGAAAAACATGATGTTACAGTTCCTAATTGAAACCACTGACTATATTCTGTC 149

Qy 1239 AAGCCAGACACACACATGATGTAAGAAAGCTGATTTTACTGACGCT 1298
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Db 148 AAGCCAGACACACACATGATGTAAGAAAGCTGATTTTACTGACGCT 89

Qy 1299 GATGTCGAGAAACAAACCAAGGAATA 1326
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Db 88 GTATGTGAGAAAAACAAACCAAGCTCAGA 61

RESULT 5
AM292342/c 403 bp mRNA EST 16-JAN-2000
LOCUS UI-H-BI2-aggw-a-09-0-01.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone
DEFINITION IMAGE:2725552 3', mRNA sequence.
ACCESSION AM292342
VERSION AM292342.1 GI:6698978
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 403)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
TITLE Unpublished (1997)
JOURNAL On Jun 5, 1998 this sequence version replaced gi:3188430.
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
The sequence contained an oligo-dr track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LINL at:
www.bio.lnlnl.gov/bbrp/image/image.html
Seq primer: M13 forward
POLA=yes.

FEATURES
Source Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:2725552"
/clone_1="NCI_CGAP_Sub4"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI. The
NCI-CGAP Sub4 library is a subtracted library derived from
the NCI-CGAP Sub2 library which is a subtracted library
derived from the NCI-CGAP Sub1 library, which is a
subtracted library derived from B1. B1 constitutes a
mixture of 21 normalized or subtracted NCI-CGAP
libraries: NCI-CGAP-Co4, NCI-CGAP-Pr22, NCI-CGAP-Pr28,
NCI-CGAP-Co10, NCI-CGAP-Co16, NCI-CGAP-Kid5,
NCI-CGAP-Kid12, NCI-CGAP-Kid3, NCI-CGAP-Pr28,
NCI-CGAP-Lym2, NCI-CGAP-Brn23, NCI-CGAP-Lus,
NCI-CGAP-Le42, NCI-CGAP-Br2, NCI-CGAP-CoB, NCI-CGAP-CLL1,
NCI-CGAP-Lu24, NCI-CGAP-Lu19, NCI-CGAP-GC4, NCI-CGAP-GC6,
NCI-CGAP-Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI-CGAP-Kid3 pool 1: LLM 3334-3337, 3662-3683,
3798-3803 (IMAGE Clonides 132276-132911,
1456008-1456775, 1500552-150855) NCI-CGAP-Kid5 pool 1:
LLM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonides
132912-1325831, 1471368-1472903, 1492104-1493255)
NCI-CGAP-Lus pool 1: LLM 3575-3582, 3851-3854 (IMAGE
Clonides 1414920-1417991, 1520904-1522339) NCI-CGAP-GC4
pool 1: LLM 3164-3167, 3716-3720, 3733-3735 (IMAGE

Clonides 1257096-1258631, 1469064-1470982,
1475592-1476743) NCI-CGAP-Pr22 pool 1: LLM 2457-2459,
2758-2759, 3062-3068 (IMAGE Clonides 985608-986759,
1101192-1101959, 1217928-1220651) NCI-CGAP-Co10 pool 1:
LLM 2644-2653, 2871-2872 (IMAGE Clonides 1057416-1061255,
1144584-1145351). Subtraction was performed as previously
described (Bonardo, Lennon & Soares (1996): Normalization
and Subtraction: Two Approaches To Facilitate Gene
Discovery. Genome Research 6, 791-806.)
TAG-LIB-NCI-CGAP-Lus
TAG-TISSUE-Lung
TAG_SEQ-CANC"

BASE COUNT 118 a 63 c 80 g 142 t
ORIGIN

Query Match 29.4%; Score 395; DB 79; Length 403;
Best Local Similarity 100.0%; Pred. NO. 1.1e-86;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 797 TCAAGTCAGTGGCTCCACGCGCTTTTAAAGAAATCCTGGAACCAATTTGTATTAATG 856
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Db 403 TCAAGTCAGTGGCTCCACGCGCTTTTAAAGAAATCCTGGAACCAATTTGTATTAATG 344
|||||

Qy 857 GAAACAAATACCTGACTGTGAAATGTCAAAACCTACCCAGTGTCTTCTCCAAAAGCT 916
|||||

Db 343 GAAACAAATACCTGACTGTGAAATGTCAAAACCTACCCAGTGTCTTCTCCAAAAGCT 284
|||||

Qy 917 TTTCAGAAAGAAATTTACCTCTCCGGGTACACATCTGTGGAATTAACATCTTT 976
|||||

Db 283 TTTCAGAAAGAAATTTACCTCTCCGGGTACACATCTGTGGAATTAACATCTTT 224
|||||

Qy 977 TTGCTCTGAAGAGATAAATTGATATGTAATACAGCTTCTACTTCTCCAGTCTT 1036
|||||

Db 223 TTGCTCTGAAGAGATAAATTGATATGTAATACAGCTTCTACTTCTCCAGTCTT 164
|||||

Qy 1037 TAACATTAGATCCCTAGTATGATTCATTCATATCATATGCTGCTCCAAAACAGTCTGG 1096
|||||

Db 163 TAACATTAGATCCCTAGTATGATTCATTCATATCATATGCTGCTCCAAAACAGTCTGG 104
|||||

Qy 1097 AACAACGCTGATCCAGGATTCACATGATTAATGTAATTTTGGGAAACAC 1156
|||||

Db 103 AACAACGCTGATCCAGGATTCACATGATTAATGTAATTTTGGGAAACAC 44
|||||

Qy 1157 TTCAAATGCTGAGAAAAAATATATGAGAAAAA 1191
|||||

Db 43 TTCAAATGCTGAGAAAAAATATATGAGAAAAA 9
|||||

RESULT 6
AA308713 383 bp mRNA EST 18-APR-1997
LOCUS AA308713
DEFINITION EST179523 HCC cell line (metastasis to liver in mouse) II Homo
sapiens cDNA 5' end similar to interferon, alpha/Beta receptor
(GI:560455), mRNA sequence.
ACCESSION AA308713
VERSION AA308713.1 GI:1961043
KEYWORDS EST.
WORDS AA308713.1
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 383)
Adams M.D., Kerlavague A.R., Fleischmann R.D., Fulmer R.A.,
Bult C.J., Lee N.H., Kirkness E.F., Weissbrock K.G., Gocayne J.D.,
White O., Sutton G., Blake J.A., Brandon R.C., Man-vel C.,
Clayton R.A., Cline T.R., Cotton M.D., Earle-Hughes J., Fine L.D.,
Fitzgerald L.M., Fitzhugh W.M., Fritchman J.L., Geoghegan N.S.,
Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle P.S., Jr.,
Kelley J.M., Kelley J.C., Liu L.-I., Mammoses S.M., Merrihew J.M.,
Moreno-Palmandres R.F., McDonald L.A., Nguyen D.T., Pellierino S.M.,
Phillips C.A., Ryder S.E., Scott J.L., Saudek D.M., Shirley R.,
Small K.V., Spriggs T.A., Uterback T.R., Weidman J.F., Li X.,

TITLE

Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dumke,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A.,
He,W.M., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meltsner,P.S., Olsen,H.,
Raymond,L., Wei,L.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

JOURNAL
MEDLINE

Nature 377 (6547 Suppl.), 3-174 (1995)
12140200

COMMENT

On Sep 12, 1996 this sequence version replaced gi:1392985.
Other ESTs: TNC171186
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/cdb/ng1/ng1.html>)
Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers
1. 383
/organism="Homo sapiens"
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/clone_lib="HCC cell line (metastasis to liver in mouse)"
/tissue_type="colon"
/cell_type="KM12C"
/note="Vector: pBluescript SK-; Site:1: EcoRI; Site:2:
XhoI"

BASE COUNT 111 a 75 c 91 g 104 t 2 others
ORIGIN

Query Match 27.2%; Score 365.8; DB 31; Length 383;
Best Local Similarity 98.7%; Pred. No. 1.6e-79;
Matches 378; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 16 GCGGCTCCAGATGATGTCCTCTGCGGCGGAGAGACCTAGTGTGCGCGTGG 75
DB 1 GCGGCTCCAGATGATGTCCTCTGCGGCGGAGAGACCTAGTGTGCGCGTGG 60
QY 76 GCCCATGGGTGTGTCGCGAGCCGAGGTGAAAAATCTAAATCTCTCAAAAAGTAG 135
DB 61 GCGCATGGGTGTGTCGCGAGCCGAGGTGAAAAATCTAAATCTCTCAAAAAGTAG 120
QY 136 AGCTCGCATCATGATGACAACTTATCTGAGGTGGAACAGAGCGATGAGTCTGCG 195
DB 121 AGCTCGCATCATGATGACAACTTATCTGAGGTGGAACAGAGCGATGAGTCTGCG 180
QY 196 GGAATGATCTTTTCATGATATCAAAAACTGGATGATGATGATGATGATGATGAT 255
DB 181 GGAATGATCTTTTCATGATATCAAAAACTGGATGATGATGATGATGATGATGAT 240
QY 256 CTGGGTGTCAAGATATAGTACCAAAATGCAACTTTCTCTCAAGCTGAATGTTT 315
DB 241 CTGGGTGTCAAGATATAGTACCAAAATGCAACTTTCTCTCAAGCTGAATGTTT 300
QY 316 ATGAAGAAATTAATTCGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 375
DB 301 ATGAAGAAATTAATTCGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 376 -TTGACTCATTTACCACTTTTCG 397
DB 361 TTGACTCATTTACCACTTTTCG 383

RESULT 7

AA258750

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

COMMENT

AA258750 380 bp mRNA EST 17-MAR-1997
zr62b09.r1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:667961 5'
similar to gb:J03171 INTERFERON-ALPHA RECEPTOR PRECURSOR (HUMAN);
mRNA sequence.
AA258750.1 GI:1893873
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 380)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucada,T., Le,M., Lennon,G., Matis,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevisan,E., Waterston,R., Williamson,A., Woldmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
On Sep 12, 1996 this sequence version replaced gi:1392980.
Contact: Willson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 Et from Amersham
High quality sequence stop: 360.

FEATURES

source

Location/Qualifiers
1. 380
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:667961"
/clone_lib="Soares_NbHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site:1: Not I;
Site:2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2bHMP, pregnant uterus
NBHMP, and fetal heart NBHMP) were mixed, and ss circles
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of 1 M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

BASE COUNT

ORIGIN

Query Match 25.4%; Score 341.2; DB 30; Length 380;
Best Local Similarity 98.9%; Pred. No. 1.7e-73;
Matches 354; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 6 GGGATCTGGGGGCTCCAGATGATGTCCTCTGCGGCGGAGAGACCTAGTGTCTC 65
DB 1 GGGATCTGGGGGCTCCAGATGATGTCCTCTGCGGCGGAGAGACCTAGTGTCTC 59
QY 66 GTGCGCGTGGGCGCCAGAGGTGTGTCGCGAGCCGAGGTGAAAAATCTAAATCTCT 125
DB 60 GTGCGCGTGGGCGCCAGAGGTGTGTCGCGAGCCGAGGTGAAAAATCTAAATCTCT 119
QY 126 CAAAAGTAGAGGTGACATCATAGTACCACTTATCTAGGTGGAACAGAGCGAT 185
DB 120 CAAAAGTAGAGGTGACATCATAGTACCACTTATCTAGGTGGAACAGAGCGAT 179
QY 186 GAGTCTGTGGGAGATGACTTTTCATTCGATATCAAAAACTGGGATGATTAATTGG 245

|||||
Db 180 GAGTCGCGGAAATGTCATTCATCGATATCAAAAAACGCGATGATATGG 239
Oy 246 ATAAATGTCGGGTGAGAAATATCTAGTACCAATGCACTTTCTCATCAG 305
Db 240 ATAAATGTCGGGTGAGAAATATCTAGTACCAATGCACTTTCTCATCAG 299
Oy 306 CTGAATGTTATGAGAAATTAATTCGTATAGAGAGAAAAAACAACCTCTT 363
Db 300 CTGAATGTTATGAGAAATTAATTCGTATAGAGAGAAAAAACAACCTCTT 357
RESULT 8
LOCUS AA447894 504 bp mRNA EST 04-JUN-1997
DEFINITION zll1a06.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:786130.5, similar to gb:J03171 INTERFERON-ALPHA RECEPTOR
PRECURSOR (HUMAN); mRNA sequence.
ACCESSION AA447894.1 GI:2161564
VERSION AA447894
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 504)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
TITLE On Sep 12, 1996 this sequence version replaced gi:1290666.
JOURNAL Contact: Wilson RK
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -28mJ rev2 ET from Amersham
High quality sequence stop: 464.
FEATURES
source
1..504
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="GDB:5983749"
/db_xref="taxon:9606"
/clone="IMAGE:786130"
/clone_id="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTACCAATGTCGAGCGCGCTTAATTTTCTTTTCTTTT 3']
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 168 a 90 c 85 g 161 t
ORIGIN
Query Match 20.7%; Score 277.4; DB 33; Length 504;
Best Local Similarity 99.6%; Pred. No. 7.4e-58;
Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1116 GATTATCCACGATTTATGAATATTTTGGGAAAACACTTCAATGCTGAGAGAAA 1175
Db 61 GATTATCCACGATTTATGAATATTTTGGGAAAACACTTCAATGCTGAGAGAAA 120
Oy 1176 ATATCGAGAAAAAACTGATGTTACAGTCCATATTTGAACCACTGATATTTGT 1235
Db 121 ATATCGAGAAAAAACTGATGTTACAGTCCATATTTGAACCACTGATATTTGT 180
Oy 1236 GTGAAGCCAGAGCAGCAGCATGATGAAAGCTGAAACGATGTTTATAGTAC 1295
Db 181 GTGAAGCCAGAGCAGCAGCATGATGAAAGCTGAAATGAACGATGTTTATAGTAC 240
Oy 1296 GCTGATGTCAGAAAAACAAACAGAAATACCTCTAAA 1334
Db 241 GCTGATGTCAGAAAAACAAACAGAAATACCTCTAAA 279
RESULT 9
LOCUS A1863225 444 bp mRNA EST 26-AUG-1999
DEFINITION t239a08.x1 NCI-CGAP Brn52 Homo sapiens cDNA clone IMAGE:2290934 3'
similar to gb:J03171 INTERFERON-ALPHA RECEPTOR PRECURSOR (HUMAN);
mRNA sequence.
ACCESSION A1863225
VERSION A1863225
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 444)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL On Dec 20, 1995 this sequence version replaced gi:1135299.
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bdrr/image/image.html
Seq primer: -40UP from G1BCO
High quality sequence stop: 420.
FEATURES
source
1..444
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2290934"
/clone_id="NCI-CGAP_Brn52"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/note="Organ: Brain; Vector: pCMV-SPORE6; Site_1: SalI;
Site_2: NotI; This library represents the normalized
version of NCI-CGAP Brn52. Cloned unidirectionally.
Primer: Oligo dT. Average insert size 1.19 Kb. Tumor
types include: meningioma, oligodendroglioma, astrocytoma
(grade II), medulloblastoma, oligocytoma (grade IV).
Constructed by Life Technologies."
BASE COUNT 140 a 85 c 137 t
ORIGIN
Query Match 20.2%; Score 271; DB 61; Length 444;
Best Local Similarity 100.0%; Pred. No. 2.7e-56;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AUTHORS	1 (bases 1 to 310) Lee,N.H., Glodex,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
TITLE	Rat Genome Project: Generation of a Rat EST (RESt) Catalog & Rat Gene Index
JOURNAL	Unpublished (1998)
COMMENT	Contact: Lee, NH ATCC The Institute for Genomic Research 912, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhlee@tigr.org Seq primer: M13-21.
FEATURES	Location/Qualifiers 1..310 /organism="Rattus sp." /db_xref="ATCC (Inhost):2033250" /db_xref="taxon:10118" /clone="R1CN21" /clone_1lb="Normalized rat placenta, Bento Soares" /clone_organa: placenta; Vector: pRT3Pac; Site_1: EcoRI; Site_2: NotI
SOURCE	
BASE COUNT	81 a 62 c 82 g 85 t
ORIGIN	

Query Match	Similarity	7.6%:	Score 128.8:	DB 43:	Length 310:
Best Local	Similarity	71.6%:	Pred. No. 2e-21:		
Matches 169:	Conservative	0:	Mismatches 67:	Indels	Gaps 0:
Oy	843	CATTGTATAATGAAACAATAACCTGACTGTGAAAAATGTCAAACACTACCCAGTGTGC	902		
Db	265	CATTGAGCAAAATGAAACCAATACCTCCGTGCAAAATGTCAGACATCACACACTGTGA	206		
Oy	903	TTTCCTCAAAAGCTTTCTCCAAAAAGGATTTACCTTCCTCCCGATCAAGCATCTGATGGA	962		
Db	205	TCTCTCCAGAGACTTTTCCACACAGGAACCTTCTTCTCCGCTGATCAAGCCTCAGATGGA	146		
Oy	963	AATAACACATCTTTTGGTCTGAAAGAGATTAAGTTTGATGACTGAATAACAAGCTTTCCTA	1022		
Db	145	AATAACAGCTCTTTTGGTCTGAAAGAGAACTTATGATCTTCAAAAATACACTCTCCTT	86		
Oy	1023	CTTCTCCAGCTTTTAATATAGATCCCTTGTGATTTATATCCATATCTATATCGG	1078		
Db	85	CCTCTCCGGTCATTGCTGTCTACCCCCCAGGGGAGCTCTTGCTTTATATGTCTAG	30		
RESULT 15					
LOCUS	CNS00396/c				
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC # BAR08K10 of RPI138 library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL063921				
VERSION	AL063921.1				
KEYWORDS	GI:4941778				
SOURCE	GSS.				
ORGANISM	fruit fly. Drosophila melanogaster				
REFERENCE	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
AUTHORS	1 (bases 1 to 1101)				
TITLE	Genoscope.				
JOURNAL	Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila				

RA Lowmyer P., Corral J.C., Detmer K., Lebeau M.M., Deaven L.,
 RA Lawrence H.J., Laryman C.;
 RT "A human Hox 1 homeobox gene exhibits myeloid-specific expression of
 RT alternative transcripts in human hematopoietic cells.";
 RL Nucleic Acids Res. 19:3443-3449(1991).
 RN [2]
 RP SEQUENCE OF 404-486 FROM N.A.
 RX MEDLINE: 90046832.
 RA Shen M.-F., Laryman C., Lowmyer P., Corral J.C., Detmer K.,
 RA Hauser C.A., Simonitch T.A., Hack F.M., Lawrence H.J.;
 RT "Lineage-restricted expression of homeobox-containing genes in human
 RT hematopoietic cell lines.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540(1989).
 RN [3]
 RP SEQUENCE OF 422-487 FROM N.A.
 RX MEDLINE: 90098876.
 RA Acampora D., D'Esposito M., Falcella A., Pannese M., Migliaccio E.,
 RA Morelli F., Stornaiuolo A., Nigro V., Simeone A., Boncinelli E.;
 RT "The human HOX gene family.";
 RL Nucleic Acids Res. 17:10385-10402(1989).
 RN [4]
 RP SEQUENCE OF 435-473 FROM N.A.
 RX MEDLINE: 94143486.
 RA Castronovo V., Kusaka M., Charlot A., Gielen J., Sobel M.;
 RT "Homeobox genes: potential candidates for the transcriptional control
 RT of the transformed and invasive phenotype.";
 RL Biochem. Pharmacol. 47:137-143(1994).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC BINDS TO THE DNA SEQUENCE 5'-AA[AT]TTTATAC-3'.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS: HOX-A10-1/PL1 (SHOWN HERE) AND
 CC HOX-A10-2/PL2, ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE ABD-B FAMILY OF HOMEBOX PROTEINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X58430: -; NOT ANNOTATED_CDS.
 DR EMBL: M10598: AA3606.1: -;
 DR EMBL: S69027: AAD14030.1: -;
 DR EMBL: S69029: AAD14031.1: -;
 DR PIR: S14930: S14930.
 DR PIR: S26402: S26402.
 DR PIR: A34425: A34425.
 DR HSSP: P02833: 1SAN.
 DR TRANSFAC: T01713: -;
 DR MIM: 142957: -;
 DR PRINTS: PR00024: HOMEBOX.
 DR PROSITE: PS00027: HOMEBOX_1: 1.
 DR PROSITE: PS50071: HOMEBOX_2: 1.
 DR PRAM: PF00046: homeobox; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation; Alternative splicing.
 FT DOMAIN 181 192 POLY-GLY.
 FT DOMAIN 219 223 POLY-PRO.
 FT DOMAIN 227 236 POLY-PRO.
 FT DOMAIN 366 371 POLY-ALA.
 FT DNA_BIND 422 481 HOMEBOX.
 FT VARSPIC 1 402 MISSING (IN ISOFORM HOX-A10-2).
 FT VARSPIC 403 405 DSL -> MCQ (IN ISOFORM HOX-A10-2).
 FT CONFLICT 435 435 L -> S (IN REF. 2).
 FT CONFLICT 437 437 L -> F (IN REF. 2).
 FT CONFLICT 473 473 R -> P (IN REF. 2).
 SO SEQUENCE 496 AA; 54733 MW; 77C6F67591652F0 CRC64;

Alignment_scores:

Quality:	59.00	Length:	24
Ratio:	3.105	Gaps:	1
Percent Similarity:	79.167	Percent Identity:	58.333

Alignment_block:

US-09-240-675-1_COPY_27_229 x HXAA_HUMAN

Align seg 1/1 to: HXAA_HUMAN from: 1 to: 496

```

15 CCTGGGGCGGCGAGCCCTAGTGTCTGTCGCCCGGCGCCATGGGTGTGT 64
|||||.....|  |||||  |||
350 Proglytsergtruprosertllargargargproproargtrp.leua 366
65 CCGGAGCCCGCGGTGGA 84
:::|||||.....|
366 laaiaaiaaiaaiaaarg 372

```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 31, 2000, 19:06:34 ; Search time 42.08 Seconds
(without alignments)
225.716 Million cell updates/sec

Title: US-09-240-675-2_COPY_27_427

Perfect score: 2141
Sequence: 1 GKNLSPQKVEVDIIDNFI.....AHTMDEKLKSSVSDAVCE 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2141	100.0	436	R14487	Soluble interferon
2	2141	100.0	436	R28495	Sequence of a soul
3	2141	100.0	557	R11958	Human alpha-interf
4	2141	100.0	557	R14488	Complete interfero
5	2141	100.0	557	R28496	Sequence of a soul
6	2141	100.0	557	R42635	Human interferon r
7	2137	99.8	557	R75356	Human IFN receptor
8	2136	99.8	434	W21805	Spliced-deleted in
9	2136	99.8	557	W21804	Transmembranal int
10	2132	99.6	436	R71123	IFN receptor extra
11	2084	97.3	436	W21806	Spliced-deleted in
12	220	10.3	325	W52296	CRFB4 protein. New
13	199	9.3	332	R75782	IFN-gamma receptor
14	180	8.4	553	W79159	Zcytor7 cytokine r
15	148	6.9	337	R71035	Human IFN-gamma ac
16	146	6.8	337	R73783	Human IFN-gamma rec
17	142	6.6	574	W97861	Human cytokine rec
18	131.5	6.1	211	W97864	Human cytokine rec
19	118	5.5	227	R14642	Gamma interferon r
20	118	5.5	231	R14641	Gamma interferon r
21	118	5.5	473	R55749	Extracellular doma
22	118	5.5	489	R07469	Plasmod. PBALDE hu
23	118	5.5	942	R70113	Gamma-IFN-R-GPB 13
24	118	5.5	1005	W83147	Rat receptor tyros
25	117.5	5.5	2214	W26357	Human LDL receptor
26	115.5	5.4	210	R14643	Gamma interferon r
27	113.5	5.3	1728	R13144	Deleted in Colorec
28	111.5	5.2	1571	W42087	Human Down syndrom
29	111.5	5.2	1910	W42086	Human Down syndrom
30	111	5.2	245	R62023	Soluble human inte
31	110	5.1	2213	W26356	Rabbit LDL recepto
32	109.5	5.1	575	R57139	Interleukin-10 rec
33	109.5	5.1	575	W41803	Mouse IL-10 recept
34	108	5.0	991	R85090	EPH-like receptor

35	107	5.0	426	1	W09822	Human Interleukin-
36	107	5.0	427	1	W24973	Human Interleukin-
37	107	5.0	753	1	W83927	Human T85 protein.
38	105.5	4.9	878	1	R78608	Murine IL-3 recept
39	105.5	4.9	1370	1	P60005	Sequence encoded b
40	104.5	4.9	596	1	R78616	Expression vector
41	104.5	4.9	600	1	R78610	Expression vector
42	104.5	4.9	600	1	R92526	Fas antigen #1. Im
43	104.5	4.9	1447	1	R68553	Deleted in colorec
44	103	4.8	17	1	R47008	IFN-alpha receptor
45	103	4.8	553	1	W35856	Human CD45 for use

ALIGNMENTS

RESULT 1
ID R14487 standard; Protein: 436 AA.
AC R14487;
DT 16-JAN-1992 (first entry)
DE Soluble interferon-alpha/beta receptor.
KM IFN: autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
PN FR2657881-A.
PD 09-AUG-1991.
PE 05-FEB-1990: 001298.
PR 05-FEB-1990: FR-001298.
PA (EUBI-) LAB EURO BIOTECNO.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Tovey MG, Uze G;
DR WPI: 91-319778/44.
DR N-PSDB: Q14239.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Claim 2; Page 43; 52pp; French.
CC The transmembrane and cytoplasmic domains of the native IFN receptor
CC have been deleted to obtain a soluble, circulating form of the
CC receptor. Potentially immunogenic epitopes have thus been eliminated.
CC Derivatives obtained by substitution or deletion of this sequence
CC are also claimed as are hybrid molecules comprising the soluble
CC receptor (or deriv.) and an immunoglobulin such as IgG1.
SQ See also Q14240.
SQ Sequence 436 AA:

Query Match 100.0%; Score 2141; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.3e-185;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKNLSPQKVEVDIIDNFIIRNRSDSGVNTFSFDYQKTGMNMIKLSGQNTSTPK 60
DB 27 GKNLSPQKVEVDIIDNFIIRNRSDSGVNTFSFDYQKTGMNMIKLSGQNTSTPK 86
QY 61 CNFSKLNLYEIEIKLRIRAEKENTSSWYEVDSFTFRKAQIGPPEVHLAEEDKAIYIH 120
DB 87 CNFSKLNLYEIEIKLRIRAEKENTSSWYEVDSFTFRKAQIGPPEVHLAEEDKAIYIH 146
QY 121 SPRTKSSVMALDGLSFTYSLLTWKNSGVEEIEINISHRKIKYKSPETTYLTKYKAL 180
DB 147 SPRTKSSVMALDGLSFTYSLLTWKNSGVEEIEINISHRKIKYKSPETTYLTKYKAL 206
QY 181 LTMKSGVSPVACIKTYENELPPENIEVSQONNYVLKMDYTAANNMFQVQMIHAFL 240
DB 207 LTMKSGVSPVACIKTYENELPPENIEVSQONNYVLKMDYTAANNMFQVQMIHAFL 266
QY 241 KRNPGRHLKWKQIPDCENYKIQCVFPQVFGKGIYLLRVQASDGNNTSFWSEIEIKFD 300
DB 267 KRNPGRHLKWKQIPDCENYKIQCVFPQVFGKGIYLLRVQASDGNNTSFWSEIEIKFD 326
QY 301 EIAFAFLPPFNIRSLSDSHIYIGAPKOSGNTPVYODPLIETIFNENTSNAEKITE 360

Db 327 EIOAFLLPVENIRSLSDSFHIIYIGAPKOSGNTPVIOYPLIYEIIFMENTSNAERKIIIE 386
QY 361 KKTDTVPNLKPLTYCYKARAHMTDEKLKSSVFSADACE 401
Db 387 KKTDTVPNLKPLTYCYKARAHMTDEKLKSSVFSADACE 427

RESULT 2

R28495
ID R28495 standard; Protein: 436 AA.
AC R28495;
DR 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the interferon (IFN) receptor
with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-interferon; beta-interferon.
OS Synthetic.
PN WO9218626-A.
PD 29-OCT-1992.
PF 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE.
TI Tovey M, Uze G;
DR WPI: 92-382110/46.
DR N-PSDB: Q30532.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
and beta - useful as immunosuppressants, for treating auto-immune
diseases and transplant rejection
PS Claim 2; Fig 1; 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
IFN-alpha and -beta is isolated by PCR, using appropriate
oligonucleotides as primers and cloned cDNA as template. For example,
bacteriophage lambda ZAP, containing the entire coding sequence of
the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
Q30534 and Q30535. R28496 represents the complete receptor. R28495
lacks the transmembrane and cytoplasmic domains. Both forms bind
IFN in the same way as antibodies so are immunosuppressants e.g. for
treating autoimmune diseases and graft rejection. They lack the
toxic side-effects of known immunosuppressants such as steroids.
SO Sequence 436 AA.

Query Match 100.0%; Score 2141; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.3e-185;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GKNLKSPOKVEVDIIDDNFILRMNRSDSEVGNTFSFDYOKTGMNMWIKLSGCONITSTK 60
Db 27 GKNLKSPOKVEVDIIDDNFILRMNRSDSEVGNTFSFDYOKTGMNMWIKLSGCONITSTK 86
QY 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEDSFTPRKAOIGPPEVHLEADKAIVIH 120
Db 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEDSFTPRKAOIGPPEVHLEADKAIVIH 146
QY 121 SPGRKDSVYMAALDGLSFTYSLIMKNSGVEERIEINYSRRKIYKLSPEPTYCLKVKAAL 180
Db 147 SPGRKDSVYMAALDGLSFTYSLIMKNSGVEERIEINYSRRKIYKLSPEPTYCLKVKAAL 206
QY 181 LTSKIKIGYSPVHCITKTTEENELPPENIEVSQONONYLKMWDYANNMFQVOMLAFL 240
Db 207 LTSKIKIGYSPVHCITKTTEENELPPENIEVSQONONYLKMWDYANNMFQVOMLAFL 266
QY 241 KRNPGNHLKXKQKIPDCENVTTCQCFPQNYFOGIGILLRVQASDGNNTSFSSEIKFPT 300
Db 267 KRNPGNHLKXKQKIPDCENVTTCQCFPQNYFOGIGILLRVQASDGNNTSFSSEIKFPT 326
QY 301 EIOAFLLPVENIRSLSDSFHIIYIGAPKOSGNTPVIOYPLIYEIIFMENTSNAERKIIIE 360
Db 327 EIOAFLLPVENIRSLSDSFHIIYIGAPKOSGNTPVIOYPLIYEIIFMENTSNAERKIIIE 386
QY 361 KKTDTVPNLKPLTYCYKARAHMTDEKLKSSVFSADACE 401
Db 387 KKTDTVPNLKPLTYCYKARAHMTDEKLKSSVFSADACE 427

RESULT 3
R11958
ID R11958 standard; Protein: 557 AA.
AC R11958;
DR 18-JUL-1991 (first entry)
DE Human alpha-interferon receptor protein.
KW Human alpha IFN; IFN agonists; antiviral; anti tumour agent;
OS Homo sapiens.
FH Key
FT peptide 1.27
PN WO9105862-A.
PD 02-MAY-1991.
PF 19-OCT-1990; F00758.
PR 20-OCT-1989; FR-013770.
PA (CNRS) CNRS CENT NAT RECH SCI.
PI Mogensen KE, Uze G, Lutfalla G, Gresser I;
DR WPI: 91-148740/20.
DR N-PSDB: Q11701.

PT New human alpha-interferon receptor protein - useful for testing
PT Interferon agonists and in treatment or diagnosis
PS Disclosure; fig 4; 30pp; French.
CC This recombinant human alpha interferon (IFN) receptor protein is
useful for the testing of IFN agonists and for treatment and diag-
nosis of viral diseases and tumours. Antibodies raised against
this protein can be used for blocking the receptor when required,
CC eg where overexpression of alpha-IFN is harmful. The Abs are
CC also useful for eg drug targeting. Variants of the protein,
CC having residue 164 (Thr) replaced by Arg and an Asp inserted
CC between residues 479 and 480, are also useful.
SO Sequence 557 AA.

Query Match 100.0%; Score 2141; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.3e-185;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GKNLKSPOKVEVDIIDDNFILRMNRSDSEVGNTFSFDYOKTGMNMWIKLSGCONITSTK 60
Db 27 GKNLKSPOKVEVDIIDDNFILRMNRSDSEVGNTFSFDYOKTGMNMWIKLSGCONITSTK 86
QY 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEDSFTPRKAOIGPPEVHLEADKAIVIH 120
Db 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEDSFTPRKAOIGPPEVHLEADKAIVIH 146
QY 121 SPGRKDSVYMAALDGLSFTYSLIMKNSGVEERIEINYSRRKIYKLSPEPTYCLKVKAAL 180
Db 147 SPGRKDSVYMAALDGLSFTYSLIMKNSGVEERIEINYSRRKIYKLSPEPTYCLKVKAAL 206
QY 181 LTSKIKIGYSPVHCITKTTEENELPPENIEVSQONONYLKMWDYANNMFQVOMLAFL 240
Db 207 LTSKIKIGYSPVHCITKTTEENELPPENIEVSQONONYLKMWDYANNMFQVOMLAFL 266
QY 241 KRNPGNHLKXKQKIPDCENVTTCQCFPQNYFOGIGILLRVQASDGNNTSFSSEIKFPT 300
Db 267 KRNPGNHLKXKQKIPDCENVTTCQCFPQNYFOGIGILLRVQASDGNNTSFSSEIKFPT 326
QY 301 EIOAFLLPVENIRSLSDSFHIIYIGAPKOSGNTPVIOYPLIYEIIFMENTSNAERKIIIE 360
Db 327 EIOAFLLPVENIRSLSDSFHIIYIGAPKOSGNTPVIOYPLIYEIIFMENTSNAERKIIIE 386
QY 361 KKTDTVPNLKPLTYCYKARAHMTDEKLKSSVFSADACE 401
Db 387 KKTDTVPNLKPLTYCYKARAHMTDEKLKSSVFSADACE 427

RESULT 4
R14488
ID R14488 standard; Protein: 557 AA.
AC R14488;

DR 16-JAN-1992 (first entry)
DE Complete interferon-alpha/beta receptor.
KW IFN, autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 437..457
FT domain /label= transmembrane
FT domain 458..557
FT domain /label= cytoplasmic
FN FR2657881.A.
PD 09-AUG-1991.
PE 05-FEB-1990; 001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECNO.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE.
PI Toyey M, Uze G.
DR WP1; 91-319778/44.
DR N-PSDB; Q14240.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Disclosure: Page 47; 52pp; French.
CC The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from transformed cells. Soluble deriv.s block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft rejection. See also Q14239.
CC Sequence 557 AA;

Query Match 100.0%; Score 2141; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.3e-185;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OS Synthetic.
FN WO9218626-A.
PD 29-OCT-1992.
PE 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE.
PI Toyey M, Uze G.
DR WP1; 92-382110/46.
DR N-PSDB; Q30533.
PT Water soluble polypeptide(s) strongly bind interferon (s) alpha and beta - useful as immunosuppressants, for treating autoimmune diseases and transplant rejection
PS Claim 3; Fig 2; 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos Q30534 and Q30535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the toxic side-effects of known immunosuppressants such as steroids.
CC Sequence 557 AA;

Query Match 100.0%; Score 2141; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.3e-185;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKNLSPQKVEVDIIDDNFILRMNRSDSVGNVTFSPDYQKGMNWKLSGCONITSTK 60
DB 27 GKNLSPQKVEVDIIDDNFILRMNRSDSVGNVTFSPDYQKGMNWKLSGCONITSTK 86
QY 61 CNFSSLKNTVEEIKLRRAKENTSSWYEVDSFTPFRAKQIGPEVHLEADKAIYIHI 120
DB 87 CNFSSLKNTVEEIKLRRAKENTSSWYEVDSFTPFRAKQIGPEVHLEADKAIYIHI 146
QY 121 SPGRKDSYMAALDGLSFTYSLIMKNSGVEERENIYSRHKIKYLSPEYTCCLKVAAL 180
DB 147 SPGRKDSYMAALDGLSFTYSLIMKNSGVEERENIYSRHKIKYLSPEYTCCLKVAAL 206
QY 181 LTSWKIGYSPVHCIKTIVENELPPENIEVSQONVYLVKMDTYANMTFOVOMLAFL 240
DB 207 LTSWKIGYSPVHCIKTIVENELPPENIEVSQONVYLVKMDTYANMTFOVOMLAFL 266
QY 241 KRNPGNHLKXKQKQIPDCENVTTCQVFPONVFOKGIYLLRVOASDGNNTSFWSEIKFDT 300
DB 267 KRNPGNHLKXKQKQIPDCENVTTCQVFPONVFOKGIYLLRVOASDGNNTSFWSEIKFDT 326
QY 301 EIOAFLLPVPENIRSLSDSFHIYIGAPKOSGNTPIYIDYPLIYEIIFEMNTSNAERKIIIE 360
DB 327 EIOAFLLPVPENIRSLSDSFHIYIGAPKOSGNTPIYIDYPLIYEIIFEMNTSNAERKIIIE 386
QY 361 KKTDTVPNLKPLTVYCVKARAHTMDEKLKSSVFSADVCE 401
DB 387 KKTDTVPNLKPLTVYCVKARAHTMDEKLKSSVFSADVCE 427

RESULT 5
R28496 standard; Protein; 557 AA.
AC R28496;
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-interferon; beta-interferon..

QY 1 GKNLSPQKVEVDIIDDNFILRMNRSDSVGNVTFSPDYQKGMNWKLSGCONITSTK 60
DB 27 GKNLSPQKVEVDIIDDNFILRMNRSDSVGNVTFSPDYQKGMNWKLSGCONITSTK 86
QY 61 CNFSSLKNTVEEIKLRRAKENTSSWYEVDSFTPFRAKQIGPEVHLEADKAIYIHI 120
DB 87 CNFSSLKNTVEEIKLRRAKENTSSWYEVDSFTPFRAKQIGPEVHLEADKAIYIHI 146
QY 121 SPGRKDSYMAALDGLSFTYSLIMKNSGVEERENIYSRHKIKYLSPEYTCCLKVAAL 180
DB 147 SPGRKDSYMAALDGLSFTYSLIMKNSGVEERENIYSRHKIKYLSPEYTCCLKVAAL 206
QY 181 LTSWKIGYSPVHCIKTIVENELPPENIEVSQONVYLVKMDTYANMTFOVOMLAFL 240
DB 207 LTSWKIGYSPVHCIKTIVENELPPENIEVSQONVYLVKMDTYANMTFOVOMLAFL 266
QY 241 KRNPGNHLKXKQKQIPDCENVTTCQVFPONVFOKGIYLLRVOASDGNNTSFWSEIKFDT 300
DB 267 KRNPGNHLKXKQKQIPDCENVTTCQVFPONVFOKGIYLLRVOASDGNNTSFWSEIKFDT 326
QY 301 EIOAFLLPVPENIRSLSDSFHIYIGAPKOSGNTPIYIDYPLIYEIIFEMNTSNAERKIIIE 360
DB 327 EIOAFLLPVPENIRSLSDSFHIYIGAPKOSGNTPIYIDYPLIYEIIFEMNTSNAERKIIIE 386
QY 361 KKTDTVPNLKPLTVYCVKARAHTMDEKLKSSVFSADVCE 401
DB 387 KKTDTVPNLKPLTVYCVKARAHTMDEKLKSSVFSADVCE 427

RESULT 6
R42635 standard; Protein; 557 AA.
AC R42635;
DT 20-APR-1994 (first entry)
DE Human interferon receptor.
KW IFN-R; extracellular domain; monoclonal antibody; viral infection; cell proliferation; allograft rejection; systemic lupus erythematosus; psoriasis; multiple sclerosis; Behcet's disease; aplastic anaemia; immunodeficiency; measles virus; interferon-alpha-beta.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..436

FT /label- extracellular_domain
 FT /note- "soluble, immunogenic form of IFN-R"
 PD EP-56387-A.
 PD 06-OCT-1993.
 PD 31-MAR-1992; 400902.
 PR 31-MAR-1992; EP-400902.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG;
 DR WPI: 95-312951/40.
 DR P-PSDB: R42635.
 PT Monoclonal antibody to human interferon type-I receptor - having
 PT neutralising activity against human type I interferon, used for
 PT therapy and diagnosis
 PS Disclosure: Fig 3: 21pp; English.
 CC Monoclonal antibodies produced against soluble forms of the human
 CC interferon alpha-beta receptor based on the full-length human IFN-R
 CC sequence are claimed. The antibodies are useful for treatment and
 CC prophylaxis of disorders involving cell proliferation and/or viral
 CC infection.
 CC Sequence 557 AA:
 SQ
 Query Match 100.0%; Score 2141; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 3.3e-185;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GKNLKSPOKVEVDIIDNFIILRNWRSDESGVNTFSFDYOKTGMDNMKISGCONITSTK 60
 DB 27 GKNLKSPOKVEVDIIDNFIILRNWRSDESGVNTFSFDYOKTGMDNMKISGCONITSTK 86
 QY 61 CNFSSKLNVYEIEIKLRIRAEKENTSSWYEVDSFTFPRKAQIGPPEVHLEADKAIVIH 120
 DB 87 CNFSSKLNVYEIEIKLRIRAEKENTSSWYEVDSFTFPRKAQIGPPEVHLEADKAIVIH 146
 QY 121 SPGTSDSYMALDGLSFTSYSLIIMKNSGVEERIENTISRRKIYKLSPEPTYCLKVKAL 180
 DB 147 SPGTSDSYMALDGLSFTSYSLIIMKNSGVEERIENTISRRKIYKLSPEPTYCLKVKAL 206
 QY 181 LTSWKIGVSPVHCITKTVENELPPENIEVSVOONVYLKMDTYANMTFOVOMLHAF 240
 DB 207 LTSWKIGVSPVHCITKTVENELPPENIEVSVOONVYLKMDTYANMTFOVOMLHAF 266
 QY 241 KRNPNHLYKMKQIPDCENKTKTCVFPQNVFOKGIYLLRVQASDGNNTSFWSEIEKFD 300
 DB 267 KRNPNHLYKMKQIPDCENKTKTCVFPQNVFOKGIYLLRVQASDGNNTSFWSEIEKFD 326
 QY 301 EIQAFLLPPVFNIRLSDSFHIYIGAPKOSGNTPVIOIDYPLIYEIIFMENTSNAEKIIE 360
 DB 327 EIQAFLLPPVFNIRLSDSFHIYIGAPKOSGNTPVIOIDYPLIYEIIFMENTSNAEKIIE 386
 QY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLKNSVFSDAVCE 401
 DB 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLKNSVFSDAVCE 427
 RESULT 7
 ID R75356 standard; Protein: 557 AA.
 AC R75356;
 DT 16-OCT-1995 (first entry)
 DE Human IFN receptor.
 KW IFN receptor; interferon receptor; interferon-alpha;
 OS Interferon-beta; monoclonal antibody; immunomodulator; AIDS.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT 1..436
 FT domain /label- Extracellular_domain
 PD W09507716-A.
 PD 23-MAR-1995.
 PD 16-SEP-1994; E03114.
 PR 17-SEP-1993; EP-402279.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benizri EJ, Tovey MG;

DR WPI: 95-131187/17.
 DR N-PSDB: Q86458.
 PT Compn. of monoclonal antibodies against interferon receptor -
 PT useful as immuno:modulator, eg. for treating AIDS
 PS Disclosure: Fig.3a-2b; 105pp; English.
 CC The amino acid sequence of human interferon class I receptor is
 CC given in R75356. A recombinant soluble form of the extracellular
 CC domain of this receptor (R71723) has been used to raise
 CC immunomodulatory monoclonal antibodies.
 CC Sequence 557 AA:
 SQ
 Query Match 99.8%; Score 2137; DB 1; Length 557;
 Best Local Similarity 99.8%; Pred. No. 7.6e-185;
 Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GKNLKSPOKVEVDIIDNFIILRNWRSDESGVNTFSFDYOKTGMDNMKISGCONITSTK 60
 DB 27 GKNLKSPOKVEVDIIDNFIILRNWRSDESGVNTFSFDYOKTGMDNMKISGCONITSTK 86
 QY 61 CNFSSKLNVYEIEIKLRIRAEKENTSSWYEVDSFTFPRKAQIGPPEVHLEADKAIVIH 120
 DB 87 CNFSSKLNVYEIEIKLRIRAEKENTSSWYEVDSFTFPRKAQIGPPEVHLEADKAIVIH 146
 QY 121 SPGTSDSYMALDGLSFTSYSLIIMKNSGVEERIENTISRRKIYKLSPEPTYCLKVKAL 180
 DB 147 SPGTSDSYMALDGLSFTSYSLIIMKNSGVEERIENTISRRKIYKLSPEPTYCLKVKAL 206
 QY 181 LTSWKIGVSPVHCITKTVENELPPENIEVSVOONVYLKMDTYANMTFOVOMLHAF 240
 DB 207 LTSWKIGVSPVHCITKTVENELPPENIEVSVOONVYLKMDTYANMTFOVOMLHAF 266
 QY 241 KRNPNHLYKMKQIPDCENKTKTCVFPQNVFOKGIYLLRVQASDGNNTSFWSEIEKFD 300
 DB 267 KRNPNHLYKMKQIPDCENKTKTCVFPQNVFOKGIYLLRVQASDGNNTSFWSEIEKFD 326
 QY 301 EIQAFLLPPVFNIRLSDSFHIYIGAPKOSGNTPVIOIDYPLIYEIIFMENTSNAEKIIE 360
 DB 327 EIQAFLLPPVFNIRLSDSFHIYIGAPKOSGNTPVIOIDYPLIYEIIFMENTSNAEKIIE 386
 QY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLKNSVFSDAVCE 401
 DB 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLKNSVFSDAVCE 427
 RESULT 8
 ID W21805 standard; Protein: 434 AA.
 AC W21805;
 DT 23-SEP-1997 (first entry)
 DE Spliced-deleted interferon alpha-receptor form 1.
 KW Interferon alpha-receptor; IFNAR.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT 1..427
 FT domain /label- Extracellular_domain
 FT /note- "comprises amino acids 1-427 of the
 FT transmembranal IFNAR"
 FT 428..434
 FT domain /label- S_domain
 PD AU9475977-A.
 PD 11-MAY-1995.
 PD 20-OCT-1994; 075977.
 PR 24-OCT-1993; IL-107378.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (ABRA/) ABRAMOVICH C.
 PI Abramovich C, Ratovitski E, Revel M;
 DR WPI: 95-200634/27
 PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Example 2; Fig 7; 46pp; English.
 CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 1
 CC (W21805) is characterised by a new domain (S) which follows an

CC end-deleted extracellular domain when compared to transmembrane
CC IFNAR (W21804). There is no transmembrane domain. The amino acid
CC sequence is predicted from a cDNA clone (see also T73520) Obtd.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 and 2 (see also W21806) probably regulate
CC the response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating the activity of the multiple IFN
CC subtypes. They can be expressed in host cells and used to inhibit,
CC modulate or modify the activities of IFNs alpha and beta in cells,
CC tissues and organisms, or for diagnostic purposes.
SQ Sequence 434 AA;

Query Match 99.8%; Score 2136; DB 1; Length 434;
Best Local Similarity 99.8%; Pred. No. 6.5e-185;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GKNLSPQKVEVDIIDDNFILRMNRSDSGVNFSPDYOKTGMDNMIKLSGCONITSTK 60
DB 27 GKNLSPQKVEVDIIDDNFILRMNRSDSGVNFSPDYOKTGMDNMIKLSGCONITSTK 86
QY 61 CNFSSLKLNVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPEVHLEADKAIVYHI 120
DB 87 CNFSSLKLNVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPEVHLEADKAIVYHI 146
QY 121 SPGRKDSVMALDGLSTFYSLLIMKNSGVEERIENTSRHKIKYLSPEPTYCLKVKAAL 180
DB 147 SPGRKDSVMALDGLSTFYSLLIMKNSGVEERIENTSRHKIKYLSPEPTYCLKVKAAL 206
QY 181 LFSWKIGVYSPVHCIKTTVENELPPENIEVSQVONQVYLKMDTYANMTFOVOMLAFL 240
DB 207 LFSWKIGVYSPVHCIKTTVENELPPENIEVSQVONQVYLKMDTYANMTFOVOMLAFL 266
QY 241 KRPNGNHLKWKQIIPDCENKVTQCVFPOVFOKGIYLLRVOASDGNNTSFWSEIKFDT 300
DB 267 KRPNGNHLKWKQIIPDCENKVTQCVFPOVFOKGIYLLRVOASDGNNTSFWSEIKFDT 326
QY 301 EIOAFLLPVPENIRSLDSFHIYIGAPKOSGNTPVIOIDYPLIYEIIFWENTSNAERKITE 360
DB 327 EIOAFLLPVPENIRSLDSFHIYIGAPKOSGNTPVIOIDYPLIYEIIFWENTSNAERKITE 386
QY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLKNSVFSADVCE 401
DB 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLKNSVFSADVCE 427

RESULT 9

W21804
ID W21804 standard; Protein; 557 AA.
AC W21804;
DT 23-SEP-1997 (first entry)
DE Transmembrane Interferon alpha-receptor.
KW Interferon alpha-receptor; IFNAR.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..436
FT /label= Extracellular_domain
FT /label= 437
FT /label= Transmembrane_domain
FT /label= 458
FT domain /label= Intracellular_domain
FT A09475977-A.
FN 11-MAY-1995.
PD 20-OCT-1993; 075977.
PE 24-OCT-1993; IL-107378.
PR (YEDA.) YEDA RES & DEV CO LTD.
PA (ABRA.) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M;
DR WPI: 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PS Inhibiting, modulating or modifying the activities of interferon(s)
CC Human transmembrane Interferon alpha receptor (IFNAR) (W21804)

CC Includes a 21-amino acid transmembrane region. Novel, splice-
CC deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected
CC that lack this transmembrane domain. These, soluble non-membrane
CC bound polypeptides can be expressed in host cells and used to
CC inhibit, modulate or modify the activities of interferons alpha
CC and beta in cells, tissues and organisms, or for diagnostic
CC purposes.
SQ Sequence 557 AA;

Query Match 99.8%; Score 2136; DB 1; Length 557;
Best Local Similarity 99.8%; Pred. No. 9.4e-185;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GKNLSPQKVEVDIIDDNFILRMNRSDSGVNFSPDYOKTGMDNMIKLSGCONITSTK 60
DB 27 GKNLSPQKVEVDIIDDNFILRMNRSDSGVNFSPDYOKTGMDNMIKLSGCONITSTK 86
QY 61 CNFSSLKLNVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPEVHLEADKAIVYHI 120
DB 87 CNFSSLKLNVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPEVHLEADKAIVYHI 146
QY 121 SPGRKDSVMALDGLSTFYSLLIMKNSGVEERIENTSRHKIKYLSPEPTYCLKVKAAL 180
DB 147 SPGRKDSVMALDGLSTFYSLLIMKNSGVEERIENTSRHKIKYLSPEPTYCLKVKAAL 206
QY 181 LFSWKIGVYSPVHCIKTTVENELPPENIEVSQVONQVYLKMDTYANMTFOVOMLAFL 240
DB 207 LFSWKIGVYSPVHCIKTTVENELPPENIEVSQVONQVYLKMDTYANMTFOVOMLAFL 266
QY 241 KRPNGNHLKWKQIIPDCENKVTQCVFPOVFOKGIYLLRVOASDGNNTSFWSEIKFDT 300
DB 267 KRPNGNHLKWKQIIPDCENKVTQCVFPOVFOKGIYLLRVOASDGNNTSFWSEIKFDT 326
QY 301 EIOAFLLPVPENIRSLDSFHIYIGAPKOSGNTPVIOIDYPLIYEIIFWENTSNAERKITE 360
DB 327 EIOAFLLPVPENIRSLDSFHIYIGAPKOSGNTPVIOIDYPLIYEIIFWENTSNAERKITE 386
QY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLKNSVFSADVCE 401
DB 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLKNSVFSADVCE 427

RESULT 10

R71723
ID R71723 standard; Protein; 436 AA.
AC R71723;
DT 16-OCT-1995 (first entry)
DE IFN receptor extracellular domain.
KW IFN receptor; Interferon receptor; Interferon-alpha;
KW Interferon-beta; monoclonal antibody; immunomodulator; AIDS.
OS Homo sapiens.
PN M09507716-A.
PD 23-MAR-1995.
PE 16-SEP-1994; E03114.
PR 17-SEP-1993; EP-402279.
PA (EUBI.) IAB EURO BIOTECHNOLOGIE SA.
PI Benizri EJ, Tovey MG;
DR WPI: 95-131187/17.
DR N-PSDB: 086457.
FT Compn. of monoclonal antibodies against Interferon receptor -
PT useful as immuno-modulator, eg. for treating AIDS
PS Disclosure; Fig. 2A-2B; 105pp; English.
CC A recombinant soluble form of the human interferon class I receptor
CC protein extracellular domain, given in R71723, was expressed in
CC either E. coli or COS cell hosts. The protein was used to raise
CC immunomodulatory monoclonal antibodies.
SQ Sequence 436 AA;

Query Match 99.6%; Score 2137; DB 1; Length 436;
Best Local Similarity 99.3%; Pred. No. 1.5e-184;
Matches 398; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GKNLSPQKVEVDIIDDNFILRMNRSDSVGNVTFSPDYOKTGMDNMIKLSGCONITSTK 60
DB 27 GKNLSPQKVEVDIIDDNFILRMNRSDSVGNVTFSPDYOKTGMDNMIKLSGCONITSTK 86
OY 61 CNFSSLKLNVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLAEADKAIVIH 120
DB 87 CNFSSLKLNVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLAEADKAIVIH 146
OY 121 SPGKDSVMALDGLSTFTSYSLILKNSGVEERINISRKIKYLSPEITCYLKYAAL 180
DB 147 SPGKDSVMALDGLSTFTSYSLILKNSGVEERINISRKIKYLSPEITCYLKYAAL 206
OY 181 LTSWKIGYSPVHCIKTTVENELPPENIEVSQONVYLVKMDYTYANMTFOVOMLHAF 240
DB 207 LTSWKIGYSPVHCIKTTVENELPPENIEVSQONVYLVKMDYTYANMTFOVOMLHAF 266
OY 241 KRNPNHLYKKKQIPDCENKTTQCVFPQNVFOKGIYLLRVQASDGNNTSFWSEIKFDT 300
DB 267 KRNPNHLYKKKQIPDCENKTTQCVFPQNVFOKGIYLLRVQASDGNNTSFWSEIKFDT 326
OY 301 EIOAFLLPVPVNIIRSLDSFHIYIGAPKOSGNTPIYIDYPLIYEIIFEMTNSNAERKIE 360
DB 327 EIOAFLLPVPVNIIRSLDSFHIYIGAPKOSGNTPIYIDYPLIYEIIFEMTNSNAERKIE 386
OY 361 KRTDVTVPNLKPLTVYCVKARAHMTDEKLNKSSVSDAVCE 401
DB 387 KRTDVTVPNLKPLTVYCVKARAHMTDEKLNKSSVSDAVCE 427

RESULT 11
W21806
ID W21806 standard; Protein: 496 AA.
AC W21806;
DT 23-SEP-1997 (first entry)
DE Spliced-deleted interferon alpha-receptor form 2.
KM Interferon alpha-receptor; IFNAR.
OS Homo sapiens.
FH Key location/Qualifiers
FT domain 1, 419
FT /label= Extracellular-domain
FT /note= "comprises amino acid residues 1-413 and
FT 422-427 of transmembrane IFNAR"
FT domain 420, 496
FT /label= Intracellular domain
FT /note= "comprises amino acids 481-557 of
FT transmembrane IFNAR"
FT
FT
PD A09475977-A.
PN 11-MAY-1995.
PF 20-OCT-1994; 075977.
PR 24-OCT-1993; IL-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PI (ABRAVA) ABRAMOVICH C, Ratovitski E, Revel M,
DR WPI: 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Example 3; Fig 7: 46pp; English.
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2
CC (W21806) is characterised by a double deletion when compared to
CC transmembrane IFNAR (W21804). The extracellular domain is
CC shortened by 6 amino acid residues and is followed by a truncated
CC intracellular domain. There is no transmembrane region. The amino
CC acid sequence is predicted from a cDNA clone (see also J73521) obtd.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 (see also W21805) and 2 may regulate the
CC response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating IFN activities. They can be expressed
CC in host cells and used to inhibit, modulate or modify the
CC activities of IFNs alpha and beta in cells, tissues and organisms,
CC or for diagnostic purposes.
CC Sequence 496 AA.

```

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Query Match 97.3%; Score 2084; DB 1; Length 496;
Best Local Similarity 97.8%; Pred. No. 3, 9e-180;
Matches 392; Conservative 0; Mismatches 1; Indels 8; Gaps 1;

OY 1 GKNLSPQKVEVDIIDDNFILRMNRSDSVGNVTFSPDYOKTGMDNMIKLSGCONITSTK 60
DB 27 GKNLSPQKVEVDIIDDNFILRMNRSDSVGNVTFSPDYOKTGMDNMIKLSGCONITSTK 86
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DB 267 KRNPNHLYKKKQIPDCENKTTQCVFPQNVFOKGIYLLRVQASDGNNTSFWSEIKFDT 326
OY 301 EIOAFLLPVPVNIIRSLDSFHIYIGAPKOSGNTPIYIDYPLIYEIIFEMTNSNAERKIE 360
DB 327 EIOAFLLPVPVNIIRSLDSFHIYIGAPKOSGNTPIYIDYPLIYEIIFEMTNSNAERKIE 386
OY 361 KRTDVTVPNLKPLTVYCVKARAHMTDEKLNKSSVSDAVCE 401
DB 387 KRTDVTVPNLKPLTVYCVKARAHMTDEKLNKSSVSDAVCE 419

RESULT 12
W52296
ID W52296 standard; Protein: 325 AA.
AC W52296;
DT 23-JUN-1998 (first entry)
DE CRFB4 protein.
KM CRFB4; Interleukin-10; IL-10; IL-10 receptor; allograft rejection;
KM vaccine; photosensitivity; inflammation; autoimmune disease;
KM septic shock; immune response; organ rejection; gene therapy.
OS Homo sapiens.
PN W09802542-A1.
PD 22-JAN-1998.
PF 17-JUL-1997; U12455.
PR 17-JUL-1996; US-683743.
PA (DYNE-) UNIV NEW JERSEY.
PI Kotenko SV, Pestka S;
DR WPI: 98-110590/10.
DR N-PSDB: V19874.
PT New recombinant DNA - comprises sequences encoding interleukin-10
PT and CRFB4 linked to operator, useful, e.g. preventing allograft
PT rejection
PS Claim 2; Page 7; 79pp; English.
CC This sequence is the human CRFB4 sequence, DNA encoding it is used in the
CC recombinant DNA (I) of the invention. (I) comprises a sequence (S1)
CC encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2)
CC encoding CRFB4, both operably linked to expression control sequences.
CC Cells containing (I) may be used to identify agonists/antagonists of
CC IL-10. Agonists are potentially useful, e.g. for preventing allograft
CC rejection, as vaccine adjuvants, for treatment of photosensitivity,
CC inflammation, autoimmune disease and septic shock, while antagonists are
CC potentially useful for increasing immune responses against tumors,
CC viruses, bacteria and parasites (especially intracellular pathogens) and
CC for preventing organ rejection. A vector containing (I) is used to
CC restore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses
CC a dysfunctional IL10R and is able to bind IL-10 but not to transduce a
CC signal. Antisense CRFB4 sequences (especially ribozymes), can inhibit
CC IL-10 activity in cells. Antibodies specific for CRFB4 are used to
CC measure and localise CRFB4, for diagnosis of defective IL-10 activity.
CC Fragments of (I) are used as primers or probes to assay CRFB4-specific

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Search completed: June 1, 2000, 00:40:12
Job time: 20018 sec

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QY 122 PGT-----DSVMALDGLSTVSLIWNKSSGVEERIENIYSRKIYK--LSPET 170
DB 157 APEKRNKPEDLPVSMQOYISNLKYNVSLNTKSNRTWSQCVN-----HTLVLMLEPNT 212
QY 171 TYCLKVAALLITSMKIGVSPVHCITKTVENE-----LPPENIEVSQONQY 218
DB 213 LYCVHESFVGPFRRAOPSEKQCARLTKDQSSSEFKAIIFWVLP-----ISITV----- 264
QY 219 VLKMDYVANTFOV-OMLHAFILKRNPGNHLKWKQIIPDCENVKTQCVFPQNVFQKGIY 277
DB 264 -----FLFSVVGYSIYRIHKGKHPANLI-----LIGNEFDKRF 301
QY 278 LLRQASDGNNTSWSEIKFDEI---QAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 334
DB 302 V-----PAEKIYINFTLINISDQSKSHQDMSLKGSSDVSLSND-----POPSGNLR 349
QY 335 VIQDYPLIYK-----IFWENTSNAEKIIEKTDV--TVPNLKPLTY 376
DB 350 PPOEEVKHKGYSALHMEIFCDSEENTEGTSTQOESLSTRTIPDKTVIEX 401
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RESULT 15

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R71035
ID R71035 standard: Protein; 337 AA.
AC R71035;
DT 11-OCT-1995 (first entry)
DE Human IFN-gamma accessory factor-1.
KM Interferon-gamma; Af-1; tumour.
OS Homo sapiens.
PN W09505847-A.
PD 02-MAR-1995.
PF 22-AUG-1994; U09438.
PR 20-AUG-1993; US-110119.
PA (UYNE-) UNIV NEW JERSEY.
PI Cook JR, Donnelly RJ, Emanuel S, Kolenko S, Mariano TM;
PI Pestka S, Schwartz B, Soh J;
DR MPI; 95-106679/14.
DR N-PSDB; Q84697.
PT Suppressing tumours in mammals with accessory factor 1 (Af-1) -
PT for interferon gamma, specifically induction of class I HLA
PT antigens. Including use of Af-1 DNA in gene therapy
PS Disclosure; Fig 21a; 114pp; English.
CC The sequence is that of human interferon-gamma accessory factor-1.
CC Incorporation of Af-1 into immune and tumour cells re-establishes
CC normal function with elimination of malignant cells.
SQ Sequence 337 AA;
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Query Match 6.98; Score 148; DB 1; Length 337;

Best Local Similarity 22.28; Pred. No. 1.4e-05;

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Matches 62; Conservative 49; Mismatches 104; Indels 64; Gaps 13;

QY 4 LKSPQKVEVDIIDNFIKRW-----NRSDSVGNVTFSFDYOKTGMDNWKLS----- 52
DB 30 LPAPQHPKIRLYNAEOYLSWEPVALSNSTRPVYQVQFKYTDK-----WFTADIMSIGV 84
QY 52 GCONITSTKCNFS-----LKLNYEEIKLRIRAKENT-SSWYEVDSTFPRKAQI 102
DB 85 NCTQITATECDFTLAASAGFPMDFNV-----TLRLRAELGALHSAM/TMPFQHYRNVTV 140
QY 103 GPPEVHLE--AEDKAIVIHISPGTKDSVMALDGLSTVSLIWNKSSGVEERIENIYS 159
DB 141 GPPE-NIEVTPGEGSLIIRFSSPFIADTSPAF---FCYVHYWE--KGGIQOVKQPF 193
QY 160 RHKTY--KLSPETTYCLKVKAALLTS---WKIGVSPVHCITKTVENELPPENIEVS 213
DB 194 SNSISLDNLKPSRYCLOVQOLMLNKSNIIFRGHLSISCYETMADASTELQOVILISV 253
QY 214 -----QONQYVLKMDYTYANMTFOVQ 234
DB 254 GTFSLSLVLAGACFFVLVKYRGLIKYWFHPPTPIQIE 292
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 00:00:26 ; Search time 23.82 Seconds

(without alignments)
243,048 Million cell updates/sec

Title: US-09-240-675-2_COPY_27_427

Perfect score: 2141
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Gapop 10.0, Gapext 0.5

Searched: 145308 seqs, 14437401 residues

Total number of hits satisfying chosen parameters: 145308

Minimum DB seq length: 0

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Post-processing: Minimum Match 08
Listing first 45 summaries

Database :

Issued Patents AA:*
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4: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep.*
5: /cgn2_6/prodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2141	100.0	434	1	US-08-328-256-11 Sequence 11, Appl
2	2141	100.0	436	2	US-08-307-588-2 Sequence 2, Appl
3	2141	100.0	557	1	US-08-328-256-10 Sequence 10, Appl
4	2141	100.0	557	1	US-08-471-654-2 Sequence 2, Appl
5	2141	100.0	557	2	US-08-466-974-2 Sequence 2, Appl
6	2141	100.0	557	2	US-08-471-654-2 Sequence 2, Appl
7	2141	100.0	557	2	US-08-307-588-4 Sequence 4, Appl
8	2089	97.6	496	1	US-08-328-256-12 Sequence 12, Appl
9	490.5	22.9	202	4	PCT-US94-14277-3 Sequence 3, Appl
10	438.5	20.3	200	4	PCT-US94-14277-4 Sequence 4, Appl
11	220	10.3	325	2	US-08-683-743-4 Sequence 4, Appl
12	199	9.3	332	4	PCT-US94-14277-2 Sequence 4, Appl
13	192	9.0	223	4	PCT-US94-14277-6 Sequence 6, Appl
14	180	8.4	553	2	US-08-943-087-14 Sequence 14, Appl
15	180	8.4	553	2	US-08-943-087-15 Sequence 15, Appl
16	180	8.4	553	2	US-08-943-087-16 Sequence 16, Appl
17	180	8.4	553	2	US-08-943-087-18 Sequence 18, Appl
18	180	8.4	553	2	US-08-943-087-20 Sequence 20, Appl
19	180	8.4	553	2	US-08-943-087-22 Sequence 22, Appl
20	180	8.4	553	2	US-08-943-087-24 Sequence 24, Appl
21	180	8.4	553	2	US-08-943-087-26 Sequence 26, Appl
22	180	8.4	553	2	US-08-943-087-28 Sequence 28, Appl
23	180	8.4	553	2	US-08-943-087-30 Sequence 30, Appl
24	180	8.4	553	2	US-08-943-087-32 Sequence 32, Appl
25	180	8.4	553	2	US-08-943-087-34 Sequence 34, Appl
26	180	8.4	553	2	US-08-943-087-36 Sequence 36, Appl
27	180	8.4	553	2	US-08-943-087-38 Sequence 38, Appl
28	180	8.4	553	2	US-08-943-087-40 Sequence 40, Appl
29	180	8.4	553	2	US-08-943-087-42 Sequence 42, Appl

30	180	8.4	553	2	US-08-943-087-44 Sequence 44, Appl
31	180	8.4	553	2	US-08-943-087-46 Sequence 46, Appl
32	180	8.4	553	2	US-08-943-087-48 Sequence 48, Appl
33	172.5	8.1	221	2	US-08-943-087-56 Sequence 56, Appl
34	167.5	7.8	221	2	US-08-943-087-54 Sequence 54, Appl
35	166.5	7.8	221	2	US-08-943-087-50 Sequence 50, Appl
36	165.5	7.7	221	2	US-08-943-087-52 Sequence 52, Appl
37	163.5	7.6	221	2	US-08-943-087-60 Sequence 60, Appl
38	160.5	7.5	221	2	US-08-943-087-58 Sequence 58, Appl
39	146	6.8	337	4	PCT-US94-14277-8 Sequence 8, Appl
40	142	6.6	574	2	US-08-906-713-2 Sequence 2, Appl
41	118	5.5	489	4	PCT-US93-11110-1 Sequence 1, Appl
42	118	5.5	489	5	5221789-1 Patent No. 5221789
43	118	5.5	1005	2	US-08-469-537A-103 Sequence 103, App
44	117.5	5.5	2214	1	US-08-727-034-7 Sequence 7, Appl
45	110	5.1	2213	1	US-08-727-034-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-328-256-11
Sequence 11, Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RANOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-256-11
Query Match 100.0%; Score 2141; DB 1; Length 434;
Best Local Similarity 100.0%; Pred. No. 9.4e-214;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GKNLSPQKVEVDIIDNFTILKRNRSDESGVNTSFDYQKGMQWIRLSCQNTITSK 60

Db 27 GKNLKSPOKVEVDIIDNFIILRNRSDESIGNVTFSEFDYQKGTGMNMIKLSGCCNITSTK 86
Qy 61 CNFSSLKLANYEELIKLIRAKENTSSWYEDSFTFPRKAQIGPPEVHLAEADKAIYIH 120
Db 87 CNFSSLKLANYEELIKLIRAKENTSSWYEDSFTFPRKAQIGPPEVHLAEADKAIYIH 146
Qy 121 SPGKDSVMALDGLSFTYSLLIMKSSGVEERIEINYSRHKIKLSPETTYCLAKYKAL 180
Db 147 SPGKDSVMALDGLSFTYSLLIMKSSGVEERIEINYSRHKIKLSPETTYCLAKYKAL 206
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Db 207 LTSKIGVSPVHCITKTVENELPPENIEVSQNONVYLKMDYTYANMTFOVOMLHAF 266
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Db 267 KRNGNHLKWKQIPDCENVTTCQVFPQNVFQKGIYLLRVQASDGNNTSFMSSEIKFDT 326
Qy 301 EIQAFLLPVFNIRSLSDSFHITGAPKOSGNTPIODYPLIYEIIFMENTSNAERKIE 360
Db 327 EIQAFLLPVFNIRSLSDSFHITGAPKOSGNTPIODYPLIYEIIFMENTSNAERKIE 386
Qy 361 KKTDTVPNLKPLTYVCVKARAHMTDEKLNKSSVFSDAVCE 401
Db 387 KKTDTVPNLKPLTYVCVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 2
US-08-307-588-2
Sequence 2, Application US/08307588
Patent No. 5919453
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
TITLE OF INVENTION: INTERFERON
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/GUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-588-2

Query Match 100.0%; Score 2141; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 9.5e-214;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GKNLKSPOKVEVDIIDNFIILRNRSDESIGNVTFSEFDYQKGTGMNMIKLSGCCNITSTK 60
Qy 27 GKNLKSPOKVEVDIIDNFIILRNRSDESIGNVTFSEFDYQKGTGMNMIKLSGCCNITSTK 86
Db 61 CNFSSLKLANYEELIKLIRAKENTSSWYEDSFTFPRKAQIGPPEVHLAEADKAIYIH 120
Qy 87 CNFSSLKLANYEELIKLIRAKENTSSWYEDSFTFPRKAQIGPPEVHLAEADKAIYIH 146
Db 121 SPGKDSVMALDGLSFTYSLLIMKSSGVEERIEINYSRHKIKLSPETTYCLAKYKAL 180
Qy 147 SPGKDSVMALDGLSFTYSLLIMKSSGVEERIEINYSRHKIKLSPETTYCLAKYKAL 206
Db 181 LTSKIGVSPVHCITKTVENELPPENIEVSQNONVYLKMDYTYANMTFOVOMLHAF 240
Qy 207 LTSKIGVSPVHCITKTVENELPPENIEVSQNONVYLKMDYTYANMTFOVOMLHAF 266
Db 241 KRNGNHLKWKQIPDCENVTTCQVFPQNVFQKGIYLLRVQASDGNNTSFMSSEIKFDT 300
Qy 267 KRNGNHLKWKQIPDCENVTTCQVFPQNVFQKGIYLLRVQASDGNNTSFMSSEIKFDT 326
Db 301 EIQAFLLPVFNIRSLSDSFHITGAPKOSGNTPIODYPLIYEIIFMENTSNAERKIE 360
Qy 327 EIQAFLLPVFNIRSLSDSFHITGAPKOSGNTPIODYPLIYEIIFMENTSNAERKIE 386
Db 361 KKTDTVPNLKPLTYVCVKARAHMTDEKLNKSSVFSDAVCE 401
Qy 387 KKTDTVPNLKPLTYVCVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 3
US-08-328-256-10
Sequence 10, Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVIJSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197

TELEFAX: 207-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-256-10

Query Match 100.0%; Score 2141; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.4e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKLLKSPQKVEVDIIDNFIKRNRSDESGVNTFSFDYOKTGMNWKISGCONITSTK 60
DB 27 GKRLKSPQKVEVDIIDNFIKRNRSDESGVNTFSFDYOKTGMNWKISGCONITSTK 86
QY 61 CNFSSKLNYEIEIKLRIRAEKENTSSWYEVDSFTPRKAQIGPPEVHLEADKAIVIH 120
DB 87 CNFSSKLNYEIEIKLRIRAEKENTSSWYEVDSFTPRKAQIGPPEVHLEADKAIVIH 146
QY 121 SPQTKSVYVMDLGLSFTYSLIMKNSSGVEERIEINYSRHKIKYKSPETTYCLKYKAL 180
DB 147 SPQTKSVYVMDLGLSFTYSLIMKNSSGVEERIEINYSRHKIKYKSPETTYCLKYKAL 206
QY 181 LFSMKIGVSPVHCITTYENELPPENIEVSQONNYVLKMDTYANNMFOYQMLHAF 240
DB 207 LFSMKIGVSPVHCITTYENELPPENIEVSQONNYVLKMDTYANNMFOYQMLHAF 266
QY 241 KRNPGNHLKWKQIPDCENKTTQCVFPQNVFGKGYLLRVQASDGNNTSFMSEIEIKFDT 300
DB 267 KRNPGNHLKWKQIPDCENKTTQCVFPQNVFGKGYLLRVQASDGNNTSFMSEIEIKFDT 326
QY 301 EIOAFLLPVFNIRSLDSFHIYIGAPKOSGNTPVYODYPLIYEIIFWENTSNAERKII 360
DB 327 EIOAFLLPVFNIRSLDSFHIYIGAPKOSGNTPVYODYPLIYEIIFWENTSNAERKII 386
QY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSADACE 401
DB 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSADACE 427

RESULT 4
US-08-471-454-2
Sequence 2, Application US/08471454
Patent No. 5731169
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,454
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN DR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-454-2

Query Match 100.0%; Score 2141; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.4e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKLLKSPQKVEVDIIDNFIKRNRSDESGVNTFSFDYOKTGMNWKISGCONITSTK 60
DB 27 GKRLKSPQKVEVDIIDNFIKRNRSDESGVNTFSFDYOKTGMNWKISGCONITSTK 86
QY 61 CNFSSKLNYEIEIKLRIRAEKENTSSWYEVDSFTPRKAQIGPPEVHLEADKAIVIH 120
DB 87 CNFSSKLNYEIEIKLRIRAEKENTSSWYEVDSFTPRKAQIGPPEVHLEADKAIVIH 146
QY 121 SPQTKSVYVMDLGLSFTYSLIMKNSSGVEERIEINYSRHKIKYKSPETTYCLKYKAL 180
DB 147 SPQTKSVYVMDLGLSFTYSLIMKNSSGVEERIEINYSRHKIKYKSPETTYCLKYKAL 206
QY 181 LFSMKIGVSPVHCITTYENELPPENIEVSQONNYVLKMDTYANNMFOYQMLHAF 240
DB 207 LFSMKIGVSPVHCITTYENELPPENIEVSQONNYVLKMDTYANNMFOYQMLHAF 266
QY 241 KRNPGNHLKWKQIPDCENKTTQCVFPQNVFGKGYLLRVQASDGNNTSFMSEIEIKFDT 300
DB 267 KRNPGNHLKWKQIPDCENKTTQCVFPQNVFGKGYLLRVQASDGNNTSFMSEIEIKFDT 326
QY 301 EIOAFLLPVFNIRSLDSFHIYIGAPKOSGNTPVYODYPLIYEIIFWENTSNAERKII 360
DB 327 EIOAFLLPVFNIRSLDSFHIYIGAPKOSGNTPVYODYPLIYEIIFWENTSNAERKII 386
QY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSADACE 401
DB 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSADACE 427

RESULT 5
US-08-466-974-2
Sequence 2, Application US/08466974
Patent No. 5861258
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P. C.
STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,974
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-974-2

Query Match 100.0%; Score 2141; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.4e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GKNLSPKQKVEVDIDDFILRMNRSDESGVNTFSFDYOKTGMNWKIKSGCONITSTK 60
DB 27 GKNLSPKQKVEVDIDDFILRMNRSDESGVNTFSFDYOKTGMNWKIKSGCONITSTK 86
QY 61 CNFSLKLNVEEIKLRRAEKENTSSWYEVDSFTFPRKAOIGPEVHLEAEKAIYIHI 120
DB 87 CNFSLKLNVEEIKLRRAEKENTSSWYEVDSFTFPRKAOIGPEVHLEAEKAIYIHI 146
QY 121 SPGTRDSVMALDGLSFTYSLIMKNSGVEERLENIYSRHKIKYKLSPEYTYCLKYKAL 180
DB 147 SPGTRDSVMALDGLSFTYSLIMKNSGVEERLENIYSRHKIKYKLSPEYTYCLKYKAL 206
QY 181 LTSKIGVSPVHCIKTIVENELPPENIEVSQONQNTVLMKYTYANMTFOVOMLHAFI 240
DB 207 LTSKIGVSPVHCIKTIVENELPPENIEVSQONQNTVLMKYTYANMTFOVOMLHAFI 266
QY 241 KRNPNHLYKMKOIPDCENKTTQCVFPQNVFOKGIYLLRVQASDGNNTSFWSEIEIKFDI 300
DB 267 KRNPNHLYKMKOIPDCENKTTQCVFPQNVFOKGIYLLRVQASDGNNTSFWSEIEIKFDI 326
QY 301 EIOAFLLPVPFNIRSLSDSFHIYIGAPKOSGNTPIYDIYPLIYEIIFWENTSNAERKIIIE 360
DB 327 EIOAFLLPVPFNIRSLSDSFHIYIGAPKOSGNTPIYDIYPLIYEIIFWENTSNAERKIIIE 386
QY 361 KRTDVTPLNKLPLTYCYVKARAHMTDELNTSSVSFSDAVCE 401
DB 387 KRTDVTPLNKLPLTYCYVKARAHMTDELNTSSVSFSDAVCE 427

RESULT 6
US-08-471-453-2
Sequence 2, Application US/08471453
Patent No. 5886153

GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,453
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-453-2

Query Match 100.0%; Score 2141; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.4e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GKNLSPKQKVEVDIDDFILRMNRSDESGVNTFSFDYOKTGMNWKIKSGCONITSTK 60
DB 27 GKNLSPKQKVEVDIDDFILRMNRSDESGVNTFSFDYOKTGMNWKIKSGCONITSTK 86
QY 61 CNFSLKLNVEEIKLRRAEKENTSSWYEVDSFTFPRKAOIGPEVHLEAEKAIYIHI 120
DB 87 CNFSLKLNVEEIKLRRAEKENTSSWYEVDSFTFPRKAOIGPEVHLEAEKAIYIHI 146
QY 121 SPGTRDSVMALDGLSFTYSLIMKNSGVEERLENIYSRHKIKYKLSPEYTYCLKYKAL 180
DB 147 SPGTRDSVMALDGLSFTYSLIMKNSGVEERLENIYSRHKIKYKLSPEYTYCLKYKAL 206
QY 181 LTSKIGVSPVHCIKTIVENELPPENIEVSQONQNTVLMKYTYANMTFOVOMLHAFI 240
DB 207 LTSKIGVSPVHCIKTIVENELPPENIEVSQONQNTVLMKYTYANMTFOVOMLHAFI 266
QY 241 KRNPNHLYKMKOIPDCENKTTQCVFPQNVFOKGIYLLRVQASDGNNTSFWSEIEIKFDI 300
DB 267 KRNPNHLYKMKOIPDCENKTTQCVFPQNVFOKGIYLLRVQASDGNNTSFWSEIEIKFDI 326
QY 301 EIOAFLLPVPFNIRSLSDSFHIYIGAPKOSGNTPIYDIYPLIYEIIFWENTSNAERKIIIE 360

DB 327 EIOAFLLPVPFNIRSLSDSFHIYIGAPKOSGNTPVIODYPLIYEITFMENTSNAERKIIIE 386
OY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVE 401
DB 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVE 427

RESULT 7
US-08-307-588-4
; Sequence 4, Application US/08307588
; Patent No. 5919453
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MAGUIRE, Deborah
; APPLICANT: PLAVEC, Ivan
; APPLICANT: TOVEY, Michael G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,588
; FILING DATE: 05-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00770
; FILING DATE: 30-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92400902.0
; FILING DATE: 31-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 17283/117/CUPL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-307-588-4

Query Match 100.0%; Score 2141; DB 2: Length 557;
Best Local Similarity 100.0%; Pred. No. 14e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 GKNLSPKQKVEVDIIDNFIILRNRSDESNGNTFSFDYOKTGMDNMIKLSGCONITSTK 60
DB 27 GKNLSPKQKVEVDIIDNFIILRNRSDESNGNTFSFDYOKTGMDNMIKLSGCONITSTK 86
OY 61 CNRSSKLNYEERIKIRAEKENTSSWYVDSTPPRKAQIGPEVHLAEADKAIYIHI 120
DB 87 CNRSSKLNYEERIKIRAEKENTSSWYVDSTPPRKAQIGPEVHLAEADKAIYIHI 146
OY 121 SPGTGDSVMMALDGLSTYSLILMKNSSGVGERENTENYSHKIKYKLSPEPTYCKVYAAAL 180
DB 147 SPGTGDSVMMALDGLSTYSLILMKNSSGVGERENTENYSHKIKYKLSPEPTYCKVYAAAL 206

OY 181 LITSMKIGVSPVHCITTYENELPPENIEVSQONONYLKMDTYANTFOVQMLHAFL 240
DB 207 LITSMKIGVSPVHCITTYENELPPENIEVSQONONYLKMDTYANTFOVQMLHAFL 266
OY 241 KRNPGHNLKMKQIPDCENKTKQCVFPQNFQKGIYLLRVQASDGNNTSFMSEELKFDI 300
DB 267 KRNPGHNLKMKQIPDCENKTKQCVFPQNFQKGIYLLRVQASDGNNTSFMSEELKFDI 326
OY 301 EIOAFLLPVPFNIRSLSDSFHIYIGAPKOSGNTPVIODYPLIYEITFMENTSNAERKIIIE 360
DB 327 EIOAFLLPVPFNIRSLSDSFHIYIGAPKOSGNTPVIODYPLIYEITFMENTSNAERKIIIE 386
OY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVE 401
DB 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVE 427

RESULT 8
US-08-328-256-12
; Sequence 12, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: ABRAMOVICH, Carolina
; APPLICANT: RAYOVITSKI, Edward
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NETMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,256
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107378
; FILING DATE: 24-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: REVEL-13
; REFERENCE/DOCKET NUMBER: 25,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-328-256-12

Query Match 97.6%; Score 2089; DB 1: Length 496;
Best Local Similarity 98.0%; Pred. No. 2.9e-208;
Matches 393; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

DB 1 GKNLSPKQKVEVDIIDNFIILRNRSDESNGNTFSFDYOKTGMDNMIKLSGCONITSTK 60
DB 27 GKNLSPKQKVEVDIIDNFIILRNRSDESNGNTFSFDYOKTGMDNMIKLSGCONITSTK 86

Qy	61	CNFSLKANTYEEIKLRIRAKENKTSWYEDSTPPRKMOIGPPEVHLAEADKAIYIH	130
Db	87	CNFSLKANTYEEIKLRIRAKENKTSWYEDSTPPRKMOIGPPEVHLAEADKAIYIH	166
Qy	121	SPGRDYSYMAALDGLSTFYSLILKRNKSGVEERIENTYSRKIKYKLSPEPTYCLAKYAAAL	180
Db	147	SPGRDYSYMAALDGLSTFYSLILKRNKSGVEERIENTYSRKIKYKLSPEPTYCLAKYAAAL	206
Qy	181	LTSRKIGVSPVHOKITVENELPPENIEVSYONQNVYLMKWDYANMFEVOYOMLAFL	240
Db	207	LTSRKIGVSPVHOKITVENELPPENIEVSYONQNVYLMKWDYANMFEVOYOMLAFL	266
Qy	241	KRNQGNHLYKKKQIIPDCGNVYTTQCVFPQNTFOGKGYLLRQVABDGNNTSFWSSEIKFDT	300
Db	267	KRNQGNHLYKKKQIIPDCGNVYTTQCVFPQNTFOGKGYLLRQVABDGNNTSFWSSEIKFDT	328
Qy	301	EIOAFLLPPVNNISLSDSFHIIYIGAPKQSGNTFVIDOYPLIYIEIIPMENTSNARKIIE	360
Db	327	EIOAFLLPPVNNISLSDSFHIIYIGAPKQSGNTFVIDOYPLIYIEIIPMENTSNARKIIE	366
Qy	361	KKTIDYVNLKPLIYCYKARAHMDELKNSVSFDSADYE	401
Db	387	KKTIDYVNLKPLIYCYKARAHMDE-----SDAVCE	419

```

RESULT      9
PCT-US94-14277-3
: Sequence 3, Application PC/TUS9414277
GENERAL INFORMATION:
APPLICANT: Aguet, Michel
APPLICANT: Boniani, Ruth
APPLICANT: Hemmi, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-3

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Query Match	22.98;	Score 490.5;	DB 4;	Length 202;
Best Local Similarity	48.58;	Pred. No. 4e-43;		
Matches 98;	Conservative 34;	Mismatches 69;	Indels 1;	Gaps 1;

[illegible]

RESULT 10
 PCT-US94-14277-4
 Sequence 4: Application PC/TUS9414277
 GENERAL INFORMATION:
 APPLICANT: Agnet, Michel
 APPLICANT: Bonni, Ruth
 APPLICANT: Hemmi, Silvio
 TITLE OF INVENTION: Receptor Subunit Polypeptides
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/14277
 FILING DATE: 07-DEC-1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/164596
 FILING DATE: 09-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: 866PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5530
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 200 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 PCT-US94-14277-4

Query Match	20.58;	Score 438.5;	DB 4;	Length 200;
Best Local Similarity	44.08;	Pred. NO. 9.7e-38;		
Matches 88;	Conservative 35;	Mismatches 68;	Indels 9;	Gaps 3.

[illegible]


```

APPLICANT: Bohm, Ruth
APPLICANT: Hemmi, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-6

Query Match      9.08; Score 192; DB 4; Length 223;
Best Local Similarity 29.68; Pred. No. 4.2e-12;
Matches 64; Conservative 37; Mismatches 83; Indels 32; Gaps 12;

QY 4 LKSPQXVEVDIIDNFIILRNRSDES-----VGNVTFSEFDYKGTGMD-NMVKL--SGCQ 54
DB 10 LARLANRLHLYNDEQLTWEPSSNDPRVYQVEYSF-----IDGSHRLLEPCT 63
QY 55 NITSTKCNFS--LKLNYE-EIKLIRAKEN-TSSWYEVDSFTPRKAOIGPPE-VH 108
DB 64 DITFKCDLGGGRLKLFPHFTVFLVRAKRGULTSKWGLPEFOHENTVGPKNIS 123
QY 109 LEADKAVIHISPGTDSVMALDGLSFTYSLIMKNSGVVERIENIYSRHKIY--KL 166
DB 124 VTPKGSIVYHFSPPFD----VFHGATFOYLVHYWEKSETOQOVEDGPEKSNISVLGNL 178
QY 167 SPETTYCLKVKAAL-LTSMKI---GVYSPVHCITTT 198
DB 179 KPIRYVCLQTEROLILKNKIRPHGLLSNVSCHETT 214

RESULT 14
Sequence 2, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:
APPLICANT: Lok, S.I.
APPLICANT: Kuo, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Parrish, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G.
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-943-087-2
```

```

Query Match      8.48; Score 180; DB 2; Length 553;
Best Local Similarity 20.68; Pred. No. 3.2e-10;
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

QY 4 LKSPQXVEVDIIDNFIILRNRSDES--VGNVTFSEFDYKGTGMD-NMVKL--SGCQ 62
DB 37 LKPRANITFLSIMKKNVLTQTPPEGLOGVAVTYVYFIRGAKMKLNKSCRNINRYCD 96
QY 63 FSSIKLVNVEIKLRIRL-EKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAVIYHIS 121
DB 97 LSAETSDYEHQYAKYKVAIWGTRCSKMAESGRYPPELTOIGPEVALTTDEKSSISVL 156
QY 122 PGTK-----DSVMALDGLSFTYSLIMKNSGVVERIENIYSRHKIY--LSPET 170
DB 157 APEKWRNPEDLVSMQOITSNKLINVSYVNTSNRTWSQCVN-----HVLVLTWLEPNT 212
QY 171 TYCLKVKAALLTSMKIGVYSPVHCITTYENE-----LPPENIEVSQONMY 218
DB 213 LYCVHVESFVGPBPRAOPSEKOCARTLKQOSEFAKIIFFVYLP-----ISITV 264
QY 219 VLKMDYIYAMTYQV-QMLHAFILKRNPNHLYKMKQIIPDCENKTKTQCVPPQVFOKGIY 277
DB 264 ----FLFSVYSGYSIRYIHVGKREKHPANLI-----LTYGNEFDPRFF 301
QY 278 LIRVQASDGNNTSFWSEIKFDEI---QALLPVPFNIRLSDSFHIYIGARKSGNTP 334
DB 302 V----PAKIVINFITINISDDSKISHODSLGKSSDVSLND-----PQSGNLR 349
QY 335 VIQDYPLIYEI-----LEWNTSNAEKRIIEKKTGV--TVPNLKPLTVY 376
DB 350 PPOGEVEVKHLYASHLMEIFCDSEENTEGTSPTQOESLSRTIPDPKTVLEY 401

RESULT 15
US-08-943-087-14
```

Sequence 14, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jeimberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Fairan, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-14

Query Match 8.4%; Score 180; DB 2; Length 553;

Best Local Similarity 20.6%; Pred. No. 3.2e-10;

Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

QY 4 LKSPQVEVDIIDNFIILRNRSDESVC--NTESFDYOKTGMDNWKILSGCONITSTKCN 62
DB 37 LRPANITILSLIMKKNVLOMTPEGLQYKAVITVVOFYIGQKKWLKSKCNINRTYCD 96
QY 63 FSLKLNVEIEIKLIRI--EKENTSSMYEVSFTPPRKAQIGPEVHLEAEKAVIHIS 121
DB 97 LSAETSDYEHQYAKYKALMGTKCSMAESGRFPFLFQIGPEVALTTDEKISIVLT 156
QY 122 PGTK-----DSVMALDGLSFTYSLIMKNSSGVEERINISRKRIY--LSPET 170
DB 157 APEKMRNPEDLPLVSMQIYSNLKYNVSVLNTKSNRTWSQCVTN---HTLVLTWLEPNT 212
QY 171 TYCLKYKALLLSMKIGVSPVHCITVENE-----LPPENIEVSQONKY 218
DB 213 LCVHVESVPPGPRRAQSEKOCARTLKDQSEFRAKIIFWVLP-----ISITV----- 264
QY 219 VLKMDYTYANMTQV--QMLHAFLEKRNPGNHLKWKQIPDCENKTTQCVFPQNVFQGIY 277
DB 264 -----FLFSVMGYSIYRIHVGEKHPANLI-----LTYGNEFDKRF 301

QY 278 LLRVQASDGNNTSFWSEIEKFDTEI---QAFLLPVFNIRSLDSFHIYIGAPKOSGNTP 334
DB 302 V---PAEKIVINFTLNTSDSKISHQDMSLGRSDVSLSND-----PQPSGNLR 349
QY 335 VIDDYPLIYEI-----IFMENTSNAEKIIEKTDV--TVPNLKPLTVY 376
DB 350 PQDEEVKHLGYASHLMELFCDESENTBGTSTQOESISRTIPDKTVIEX 401

Search completed: June 1, 2000, 04:17:53
Job time: 15447 sec

Mon Jun 5 12:56:16 2000

us-09-240-675-2_copy_27_427.modif.ra

GenCore version 4.5
Copyright (c) 1993 - 2000 Compen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2000, 00:37:00 ; Search time 64.83 seconds

(without alignments)
362,649 million cell updates/sec

Title: US-09-240-675-2_COPY_27_427

Perfect score: 2141

Sequence: 1 GKNLSPQKVEVDIIDDNF.....ARTDRLKNSVFSDAVCE 401

Scoring table: BLOSUM62

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 08

Database : PIR_63:**

1: PIR1:**
2: PIR2:**
3: PIR3:**
4: PIR4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2141	100.0	557	2 A3694	interferon alpha/b
2	1384.5	64.7	560	2 S27387	interferon alpha r
3	966	45.1	590	2 A45283	interferon alpha/b
4	225	10.5	273	2 G01418	cytokine receptor
5	220	10.3	325	2 A47003	cytokine receptor
6	217.5	10.2	349	2 JC6311	interferon recepto
7	199	9.3	332	2 A49947	interferon gamma r
8	148	6.9	337	2 I38500	interferon gamma r
9	123.5	5.8	1443	2 I50600	neogenin - chicken
10	123	5.7	1375	2 T13822	frizzled gene prot
11	123	5.7	1326	2 T13823	frizzled gene prot
12	122.5	5.7	1451	2 S42167	190K protein - hum
13	118	5.5	489	2 A31555	interferon gamma r
14	118	5.5	981	2 S51604	receptor-like tyro
15	118	5.5	1005	2 S49015	receptor tyrosine
16	117.5	5.5	1283	2 A36080	insulin receptor p
17	117.5	5.5	1427	2 I31669	tumor suppressor p
18	117.5	5.5	1585	2 T19121	probable protein-t
19	117	5.4	817	2 A48721	titin, muscle - ch
20	115.5	5.4	658	2 T16040	hypothetical prote
21	115	5.4	26926	1 I38344	titin, cardiac mus
22	113	5.3	1450	2 A46027	165K myofibrillar
23	113	5.3	1615	2 B49502	protein-tyrosine-p
24	113	5.3	1767	2 A49502	protein-tyrosine-p
25	111.5	5.2	1896	2 T08851	Down syndrome cell
26	111	5.2	6831	2 T27934	hypothetical prote
27	111	5.2	6839	2 S57242	twitchin - Caenorh
28	111	5.2	7160	2 T27935	hypothetical prote
29	110.5	5.1	1898	2 S46216	leucocyte antigen-p
30	110	5.1	1912	2 A56178	protein-tyrosine-p

31	109.5	5.1	575	2 A49667	interleukin-10 rec
32	109	5.1	416	2 T25036	hypothetical prote
33	108.5	5.1	2033	2 T09123	hybrid receptor so
34	108.5	5.1	2215	2 T00348	Lf11 protein - mou
35	108	5.0	991	2 T78843	receptor protein-t
36	107.5	5.0	1372	2 A34157	insulin receptor p
37	105.5	4.9	878	1 A40091	interleukin-3 rece
38	105.5	4.9	1825	2 T32828	hypothetical prote
39	105	4.9	56	2 S41602	interferon alpha r
40	104.5	4.9	1447	2 A54100	tumor suppressor p
41	104	4.9	896	1 A35782	cytokine receptor
42	104	4.9	1239	1 A32579	neuroglial - fruit
43	104	4.9	2311	1 TVCHSR	kinase-related pro
44	103.5	4.8	896	2 I56563	interleukin-3 rece
45	103.5	4.8	1499	2 I50212	protein-tyrosine-p

ALIGNMENTS

RESULT 1

A32694

Interferon alpha/beta receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 22-Oct-1999

C:Accession: A32694; S17112

R:Uze, G.; Lutfalla, G.; Gresser, I.

Cell 60, 225-234, 1990

A:Title: Genetic transfer of a functional human interferon alpha receptor into mouse

A:Reference number: A32694; MUID:90124632

A:Accession: A32694

A:Molecule type: mRNA

A:Residues: 1-557 <UZE>

A:Cross-references: GB:J03171; NID:q184645; PID:NAA52730.1; PID:q306914

R:Lutfalla, G.

submitted to the EMBL Data Library, July 1991

A:Description: The structure of the human interferon alpha/beta receptor gene.

A:Reference number: S17112

A:Accession: S17112

A:Molecule type: DNA

A:Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUT>

A:Cross-references: EMBL:X60459; NID:q32671

C:Genetics:

A:Gene: GDB:IFNAR1; IFNAR; IFRC

A:Cross-references: GDB:120078; OMIM:107450

A:Map position: 21q22.1-21q22.1

A:Initons: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3

C:Keywords: cytokine receptor; glycoprotein; transmembrane protein

F:1-21/Domain: transmembrane #status predicted <TRN1>

F:437-455/Domain: transmembrane #status predicted <TRN2>

F:50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydrate

Query Match 100.0%; Score 2141; DB 2; Length 557;

Best Local Similarity 100.0%; Pred. No. 4, 2e-154;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GKNLSPQKVEVDIIDDNFILRMNSDESVDGVTSPFYOKTGMMNWKLSGCONITSTK 60		
DB	27	GKNLSPQKVEVDIIDDNFILRMNSDESVDGVTSPFYOKTGMMNWKLSGCONITSTK 86		
QY	61	CNFFSLKLVNVEIKLIRAEKENTSSWYEVDSFPFKRAOIGPPEVLEADKAIIVHI 120		
DB	87	CNFFSLKLVNVEIKLIRAEKENTSSWYEVDSFPFKRAOIGPPEVLEADKAIIVHI 146		
QY	121	SPGTRDSVWMLDGLSFTYSLIMKNSGVEERIEINYSRHKIYKLSPEYTCGLVKVKAAL 180		
DB	147	SPGTRDSVWMLDGLSFTYSLIMKNSGVEERIEINYSRHKIYKLSPEYTCGLVKVKAAL 206		
QY	181	LTSKILGYSPVPHCIKTIVENLPPENIEVSQONVYKMDYTYAMTQVQVLAFL 240		
DB	207	LTSKILGYSPVPHCIKTIVENLPPENIEVSQONVYKMDYTYAMTQVQVLAFL 266		


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0Y 61 CNFSLKLNVEEIKLIRKEKE-7SMYVQSFPERKQAGPREVLHEADKAIYH 119
Db 86 CEFSLDTNVIKQFVRABEGNSJSSMAEVPDPIFPTAHKSPREVLHEADKAILH 145
0Y 120 ISPTKDSVMALDGLSFTYSLLIMKSSGVEERINITYSRHKIYKLSPEPTYCCLKVKA 179
Db 146 ISPPGOGNNMALEKPEFESTIRIMQWSSSDKTIINSTYYVEIPBLLPETTYCLEYAI 205
0Y 180 LLTSMKIGVYSPVHCKITTVENELPREPENIEVSQONQNYLKWY-7YANMTFOYOMLHA 238
Db 206 HPSLKHSNYSVQICISTYANKKRPVGNLQVDAQGSYVLKMDYIASADVLEFRQWMLPG 265
0Y 239 FLKRNPNHLYKWKQOIPDCENKVTQCVFQONTFOKGIYLLRQVQSDGNNTSFWSEIKF 298
Db 266 YSKSSSGSHSKMXPPIPTCANVOYTHCVFSQDTPYTGTFELHVAEGEHNHTFSWSEIKFI 325
0Y 299 DTELQAFLLPPVFNIRBSLSPSHYIGAPRQSGNTPIQDYLPIYALFIMENTSNAEKRI 358
Db 326 DSOHNLPRPPVIVLTMASDTLLVYVQCDSTDD-----GLNTEILFIMENTSNNKISM 378
0Y 359 IEKKTDTVPLKPLTVYCYKARAHNTDEKLNSSVPOADVE 401
Db 379 EKQDPETLKNLQPLVYCYQARV-LFRALLNTSINSEKICE 420

```

RESULT 4
G01418
cytokine receptor family II, member 4 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #ext_change 17-Jul-1996
C:Accession: G01418
R:Jutfalla, G.
submitted to the EMBL Data Library, April 1994
A:Reference number: G06935
A:Accession: G01418
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-273 <LUT>
A:Cross-references: EMBL:U08988; NID:g571295; PID:g5711296
C:Genetics:
A:Gene: GDB:CRFB4; CRF2-4
A:Cross-references: GDB:138168; OMIM:123889
A:Map position: 21q22.1-21q22.2
A:introns: 17/1; 58/2; 111/1; 166/3; 216/1

Query Match	10.5%	Score 225	DB 2	Length 273	
Best Local Similarity	30.0%	Pred. No. 7.2e-10			
Matches 61	Conservative	43	Mismatches 87	Indels 12	Gaps 7
QY	7	PKQVEVDIIDDDFILMNRNDSVGNVYTFSDQKGMNDMIKLSGCONITTSKCNFSSL	66		
DB	24	PENVRNRNSNFNKLQWESPAFAKGNLTAYQ----	LSYRIQDKCONMTLTLECDFFSS	79	
QY	67	KLNVEEILRLRAE-KENTSSWYEDSTTFPKAIGPPEVHLEEDKRAIVH-ISPCT	124		
DB	79	-LSKYGDDHLRLRAEADSDSDVYN--TCCPDDDTTIGPGMVEVLDLSLHFRFLAPKI	136		
QY	125	KDSV--MMALDGL--SEYTSLLIMKNSSGVEERIEINYSRHKIKLSPTETCYCLVKAAL	181		
DB	137	ENDEYEWTKMKNNYSNMTYVQYWKKNGTDEDFQITTPQYDPEVLANLEPMTTYCQVGVGFLP	196		
QY	182	TSMKIGVYSPVHCITKTVENELP	204		
DB	197	DRNKAGWSEPVCEQTTTDETVP	219		

RESULT 5
A47003
cytokine receptor family class II protein CCRF-4 precursor - human
C:Species: Homo sapiens (man)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1994
C:Accession: A47003

R: Lutfalla, G, Gardiner, K., Uze, G.
Genomics 16, 366-373, 1993
A: Title: A new member of the cytokine receptor gene family maps on chromosome 21 at
A: Reference number: A47003; MID:93300310
A: Accession: A47003
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-325 <LUT>
A: Cross-references: GB:217227; NID:g933378; PID:g933379
C: Genetics:
A: Map position: 21q
C: keywords: transmembrane protein

[illegible]

```

RESULT      6
JC63j11
Interferon receptor-class II cytokine receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: JC63j11
R:Gibbs, V.C.; Pennica, D.
Gene 186, 97-101, 1997
A:Title: CR2-4: isolation of cDNA clones encoding the human and mouse proteins
A:Reference number: JC63j11
A:Accession: JC63j11
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-349 <GIB>
A:Cross-references: GB:U53696

```

	Query Match	10.24:	Score 217.5:	DB 2:	Length 349:
Best Local Similarity	28.44:	Pred. No. 3.7e-09:			
Matches 60:	Conservative 45:	Mismatches 79:	Indels 27:	Gaps 9:	
OY	7	POKEVVDIIDDFILRNKRSDSVGNVFSESDYO--KTGMDMIKLSGCONITSTKCNFS	64		
DB	24	PEKVAMNSVNFENKILQWVEVPAPPKNLNFTAQYESYRSPD-----CKRATSTQCDPS	77		
OY	65	SLKLVNVEIKRIKIAE--KENTSSRYEVDSTFPFKKAOGPVEVHLAEADKRIYHIIS--	122		
DB	78	--HLSKYDDYIVRYVAELADEHSEVNVN--TCEVVDITJIGPEMOKESTIAESLELTFSPAP	134		
OY	122	-----PGTRDSYMAALDGL--SFYSLIKVNSGVEERIEIENIYSHKRIYKLSPTETCYCL	174		
DB	135	QIENEPET-----WTLKNIYDSMAVRQYQMKNGKTNEMKFGVSPYDSEVLRNLDEPMTTYCI	189		
OY	175	KYKALLTSMKIGVSPVHCITTYENENLPP	205		
DB	190	QVQGFLLDQNRTEGWESEPIC--ERTGNDITPP	219		

RESULT 7
A49947
Interferon gamma receptor beta subunit - mouse
N:Alternate names: IFN-gamma R beta chain, IFN-gamma R species-specific cofactor; type 1
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A49947
R:Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M.
Cell 76, 803-810, 1994
A:Title: A novel member of the interferon receptor family complements functionality of the
A:Reference number: A49947; MUID:94170381
A:Accession: A49947
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-332 <HEX>
A:Cross-references: GH:569336; NID:9545841; PIDN:AAB30165.1; PID:9545842
A:Experimental source: early B-cell line Y16
A:Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIPI:145656)
C:Keywords: cytokine receptor

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Query Match          9.3%: Score 199: DB 2: Length 332;
Best Local Similarity 30.1%: Pred. No. 8.6e-08;
Matches 65; Conservative 38; Mismatches 81; Indels 32; Gaps 12;

QY 4 LKSPQKEVVDIDDDNFILMNRSDS-----VGNTSEFSDYQKTGMD-NWIKL--SGGQ 54
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 29 LAAPLNPRHLHXNDEQILTWEPSPSSNDPRPVYQVEYSF-----IDGSHRLLEPNCT 82
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 55 NITSRKCNSS---LKLANYE-EIKLRIRAEKEN-TSSSYEVDSETPFKKAIGPPE-VH 108
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 83 DITETKCDLGGGRLLKLPFTVFLVRAKKGNLSKSWGLGEPHOHNVNTVGPBKINIS 142
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 109 LEADKKAIVIHISPGTKDSVMALDGLSFTYSLLIWKNSGVEERLENITYSKKIY--KL 166
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 143 VAPGKSLVIHSPRPD-----VFHGATFOYLVIHYEKSETOEQVEGEPKNSIYLGNL 197
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 167 SPETTYCLKVKAAL-LTSWKI---GYSPVHCLIKTT 198
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 198 KPRVYCLOTEAOQLINKKKIRPHGLLSNVSCHETT 233
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 8
138500
Interferon gamma receptor accessory factor-1 precursor - human
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 05-Nov-1999
C:Accession: I38500; I38501
R:Sch. J.; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S.
Cell 76, 793-802, 1994
A:Title: Identification and sequence of an accessory factor required for activation of T
A:Reference number: A49946; MUID:94170380
A:Accession: I38500
A:Molecule type: mRNA
A:Residues: 1-337 <RES>
A:Cross-References: EMBL:U05875; NID:g463549; PIDN:AAA16955.1; PID:g463550
A:Experimental source: clone pSKI
A:Accession: I38501
A:Molecule type: mRNA
A:Residues: 1-63, '0', 65-337 <RE2>
A:Cross-References: EMBL:U05877; NID:g463551; PIDN:AAA16956.1; PID:g463552
A:Experimental source: clone pJS3
C:Genetics:
A:Map position: 21
C:Keywords: cytokine receptor

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Query Match      6.98; Score 148; DB 2; Length 337;  
Best Local Similarity 22.2%; Pred. No. 0.00062;  
Matches    62; Conservative   49; Mismatches 104; Indels   64; Gaps   13.  
  
QY      4 LKSPQKEVDIIDNFIILKR-----NRSDSGNGNTFSEFDIOKTOMDMWIKLS----- 52  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```

```

Db 30 LPAPDHPRILRYLNNOYVLSMEPVALSNSSTRVYRVYQFKYTDK-----WETADIMSIGV 84
OY 52 GCONITSKCNFSS-----LKNLYEEKLIIRAKENT--SWEYVDSFPRKAOI 102
Db 85 NCTQTATCECTFASPSPAGFPMDFNV---TLERLRGLALGHSAMVMPFOHRYNTV 140
OY 103 GPPEVHLE--AEDKAIYIHISPGTKDSVMALDGLSEFTYSLLIMKNSGVEERIEIYIS 159
Db 141 GPPE-NIEWPGBESLIIRFSSPFDIADTSAF---FCYVYHWE--KGGIQOVKQPR 193
OY 160 RHKIY--KLSEPTYCLKVKALILTS---WKIGIVSPVHCIKTYVENELPRPENIEVS 213
Db 194 SNSISLDNLKRSRYCLOVOQAOLIMKNSNIRVGHLSNISCYETPMADASTELQOVLISV 253
OY 214 -----QONONYLKLMDYTYAANTPQOV 234
Db 254 GTFSLSLSTVLACGFFVLKYRGILKMYFHHPRPSIPLOIE 292

```

RESULT 9
150600
neogenin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
A:Accession: 150600
R:Vilmetter, J.; Kayem, J.F.; Roman, J.M.; Dreyer, W.J.
J. Cell Biol. 127, 2009-2020, 1994
A:Title: Neogenin, an avian cell surface protein expressed during terminal neuronal d
A:Reference number: A5193; MUID:95105243
A:Accession: 150600
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1443 <VIE>
A:Cross-references: EMBL:U07644; NID:9641965; PID:9641966

```

Query Match      5.8% Score 123.5 DB 2 Length 1443;
Best Local Similarity 22.0% Pred. No. 0.32;
Matches    89; Conservative   60; Mismatches 194; Indels   61; Gaps 19;

QY      6 SPQKVEVDIIDNEFI-LRWNR--SDESGVNTFFSEDYOKTGMDNMIKSLGCONITSTKCN 62
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     427 ARDVAATLVSRIFRLMTRTPVSDPGGNLTIISFYTEG----INREVEN-TSRPE 481

QY      63 FSSKLNTYEETKLIIRKEKENTSSNYEYDSTTTPRKAIOGPPEVHLHEDAKIYIHISP 122
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     482 TQVMIONLMPEVTVYERVAQNKHGGE--SSAPLKVAI-OPEVOLPPADNIRAYAGS 537

QY      123 GKRDYSWML---DLSPFTSYLLIMKNSSGYEEIRENIYSRHKIYKLSPEPTCYCLKVA 178
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     538 PPSVYTWTETPISNGEIQNKLYIMEKGQDSODVAVGLSYTTIGLKKYTEISRVA 597

QY      179 ALLTSWKIGVSPVHCIKTTVENELPPENIEVSQN-QNYVLKMDYIANNTFVOYQLH 237
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     598 --YNKHGPSVTQDVVVRLTSDVPSPAOPNLTLIARNSKSIMLHQOPPA----- 646

QY      238 AFLKRNGHNL-----YKKKQIPDCENVKTQTCCPVONFQ--KGI-----YLRVQASD 285
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     646 -----GTHSQITTYGRIKYRKSVRSKSVITSYGTOQLFOLIEGBERTENFRAAMT 698

QY      286 GNNT--SFWSSEIKFDETIEIAFLPPV--FNISLSDSFHIYIGAPKQSCNTPIYIDY 339
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     699 VNGTGATOWVAEMFEESLDLDESRAPEVPSLSHVPLTYSI-VVSWTPRENONI-VVRGY 756

QY      340 PLILEIIEWENTSNAER-KIIEKKTDVYVNPNLKPLTYVCVKARA 382
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     757 ALGTGTG---GSPHAOTIKVDKORYYLENDPPSHYITTLKA 796

```

RESULT 10
T13822
frazzled gene protein - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T13822
 R:Kolodziej, P.A.; Timpe, L.; Mitchell, K.J.; Goodman, C.S.; Fried, S.; Jan, L.Y.; Jan, C.
 Cell 87, 197-204, 1996
 A:Title: Frazzled encodes a Drosophila member of the DCC immunoglobulin subfamily and is
 A:Reference number: 217780
 A:Accession: T13822
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1375 <KOL>
 A:Cross-references: EMBL:U71001; NID:g1621114; PID:g1621115; PIDN:AAC47314.1
 C:Genetics:
 A:Gene: frazzled
 C:Function:
 A:Map position: 2
 A:Description: may function in vivo as a receptor or component of a receptor mediating N

Query Match 5.7%; Score 123; DB 2; Length 1375;
 Best Local Similarity 16.3%; Pred. No. 0.33;
 Matches 101; Conservative 68; Mismatches 184; Indels 268; Gaps 22;

QY 1 GKLNKS-----PQVEVDIIDNFI-LRW-----NNSDESVG 31
 DB 448 GKPLDSGLQARLPSPQPDVAQIVKSRFVTLNWEPLQAGDVVYVYVYKNNSEERQK 507
 QY 32 NTFSPFYQKTGMNDWIKLSGCQNTSTKCNFS-----LKLNVYEIKLR-----78
 DB 508 MWTSHDDQOVNIQSLPGRTYQFRVEANTFSGASAPLEVSTQPEVNIAGPPRNFEG 567
 QY 78 -IRAENTSSWE-----PEVHLE-AEDKAIYIHISPTKDSVMALD 133
 DB 568 YARSHKEIYKWEPTVTNGEILKRYVYSENDGADLYHDSALVLEAVLELRPHTDVYI 627
 QY 93 SFTPFRAQIG-----PREVHLE-AEDKAIYIHISPTKDSVMALD 133
 DB 628 SVVPEFNNGMGDSAEIRKVTFSSTPEPPNNVTLEVTSSSITVHWPPEAEDRNGOIT 687
 QY 134 GLSTYSLLIKNKGVEERIEINYSRKIKYKSPETTYCLKYKAL-----TSWKIG 187
 DB 688 GYKIRYRK--FKDAPQYKSTPANT-RYFELSNLDRAEYQKIAAMTVNGSGPTEENRA 744
 QY 188 VSPVHCIKTTVENELP-----PENIEVQONONYLVKW 222
 DB 745 -----NLENDLDETQVPGKPIWISHPGANNIALHMGPPQHPEIKI--RNYVLGW 793
 QY 223 -----DY-----225
 DB 794 GRGIPDENTIELKTERYHILKNLESNDYVSLRARNYKGDGPPIYDNIKTREDEPYDA 853
 QY 225 -----TYANMTFOVOMLHAFLEKRN-----PGNHLKWKQIPD 256
 DB 854 PTPLEVPVGLRAITWSSSIYVYWDITMLKNKHVTDNRHYTVSYGIGSNRRY-----909
 QY 257 CENVKTQCVFPOVNFQKGIYLLRVOASDGNNTSFSEIEIKFDEIOAFLLPVPFNIRSL 316
 DB 909 -HNTTDLNCHI-NDLRPTQYEFPAVKYVKGRRSSMSVSLNSTQVNPVTPP-----960
 QY 317 SDSFHIYIGAPKOSGNTPIQDYP-----LYEIIEMNTSNAER-----KIEEKT 363
 DB 960 ---REVTVRLDEMPPTVYQWIPKHTLGOITGYINITYTDTTKRSDMSVEAFAGEET 1016
 QY 364 DVTVPNLKPLTVYCVKARAHT 384
 DB 1017 MLMPLNLKPLTYTYFKVQART 1037

RESULT 11
 T13823
 frazzled gene protein, log isoform - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T13823

R:Kolodziej, P.A.; Timpe, L.; Mitchell, K.J.; Goodman, C.S.; Fried, S.; Jan, L.Y.; Jan, C.
 Cell 87, 197-204, 1996
 A:Title: Frazzled encodes a Drosophila member of the DCC immunoglobulin subfamily at
 A:Reference number: 217780
 A:Accession: T13823
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1526 <KOL>
 A:Cross-references: EMBL:U71002; NID:g1621116; PID:g1621117; PIDN:AAC47315.1
 C:Genetics:
 A:Gene: frazzled
 C:Function:
 A:Map position: 2

Query Match 5.7%; Score 123; DB 2; Length 1526;
 Best Local Similarity 16.3%; Pred. No. 0.38;
 Matches 101; Conservative 68; Mismatches 184; Indels 268; Gaps 22;

QY 1 GKLNKS-----PQVEVDIIDNFI-LRW-----NNSDESVG 31
 DB 599 GKPLDSGLQARLPSPQPDVAQIVKSRFVTLNWEPLQAGDVVYVYVYKNNSEERQK 658
 QY 32 NTFSPFYQKTGMNDWIKLSGCQNTSTKCNFS-----LKLNVYEIKLR-----78
 DB 659 MWTSHDDQOVNIQSLPGRTYQFRVEANTFSGASAPLEVSTQPEVNIAGPPRNFEG 718
 QY 78 -IRAENTSSWE-----PEVHLE-AEDKAIYIHISPTKDSVMALD 133
 DB 719 YARSHKEIYKWEPTVTNGEILKRYVYSENDGADLYHDSALVLEAVLELRPHTDVYI 778
 QY 93 SFTPFRAQIG-----PREVHLE-AEDKAIYIHISPTKDSVMALD 133
 DB 779 SVVPEFNNGMGDSAEIRKVTFSSTPEPPNNVTLEVTSSSITVHWPPEAEDRNGOIT 838
 QY 134 GLSTYSLLIKNKGVEERIEINYSRKIKYKSPETTYCLKYKAL-----TSWKIG 187
 DB 839 GYKIRYRK--FKDAPQYKSTPANT-RYFELSNLDRAEYQKIAAMTVNGSGPTEENRA 895
 QY 188 VSPVHCIKTTVENELP-----PENIEVQONONYLVKW 222
 DB 896 -----NLENDLDETQVPGKPIWISHPGANNIALHMGPPQHPEIKI--RNYVLGW 944
 QY 223 -----DY-----225
 DB 945 GRGIPDENTIELKTERYHILKNLESNDYVSLRARNYKGDGPPIYDNIKTREDEPYDA 1004
 QY 225 -----TYANMTFOVOMLHAFLEKRN-----PGNHLKWKQIPD 256
 DB 1005 PTPLEVPVGLRAITWSSSIYVYWDITMLKNKHVTDNRHYTVSYGIGSNRRY-----1060
 QY 257 CENVKTQCVFPOVNFQKGIYLLRVOASDGNNTSFSEIEIKFDEIOAFLLPVPFNIRSL 316
 DB 1060 -HNTTDLNCHI-NDLRPTQYEFPAVKYVKGRRSSMSVSLNSTQVNPVTPP-----1111
 QY 317 SDSFHIYIGAPKOSGNTPIQDYP-----LYEIIEMNTSNAER-----KIEEKT 363
 DB 1111 ---REVTVRLDEMPPTVYQWIPKHTLGOITGYINITYTDTTKRSDMSVEAFAGEET 1167
 QY 364 DVTVPNLKPLTVYCVKARAHT 384
 DB 1168 MLMPLNLKPLTYTYFKVQART 1188

RESULT 12
 S42167
 190K protein - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
 C:Accession: S42167
 R:Vinkemeier, U.; Obermann, W.; Weber, K.; Fuerst, D.O.
 J. Cell Sci. 106, 319-350, 1993
 A:Title: The globular head domain of titin extends into the center of the sarcomeric
 A:Reference number: S42166; KUID:94095665

RESULT 15

S49015

receptor tyrosine kinase Eph-1 - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999

C/Accession: S49015; S51602

R/Maisonpierre, P.C.; Battezueta, N.X.; Yancopoulos, G.D.

Oncogene 8, 3277-3288, 1993

A/Title: Eph-1 and Eph-2: two novel members of the Eph receptor-like tyrosine kinase fam

A/Reference number: S49015; MUID:9406777

A/Accession: S49015

A>Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1005 <MA1>

A/Cross-references: EMBL:S68024

A/Note: the authors translated the codon GAC for residue 170 as Glu

A/Accession: S51602

A>Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-305, 'G', 359-1005 <MA2>

A/Cross-references: EMBL:S68026

A/Note: the authors translated the codon GAC for residue 170 as Glu

C/Keywords: ATP; transmembrane protein

F/675-941/Domain: protein kinase homology <KIN>

F/683-691/Region: protein kinase ATP-binding motif

Query Match 5.58; Score 118; DB 2; Length 1005;

Best Local Similarity 20.18; Pred. No. 0.51;

Matches 92; Conservative 51; Mismatches 165; Indels 150; Gaps 21;

```
OY 1 GKNLSPQKVEVDII--DDNF-----ILRMNSDESGVNT--SFQYOKTGMDNW 47
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 165 GRNKKNDNOYIKIDITADESTEDLDGRVMTNTEVDRVGPLSKKGYLAQDVG---- 221
OY 48 IKLSGCONITST-----KCNFSLKLNYYEIKLIRAEKENTSSWYEVDSFTFPRKAQI 102
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 221 ----ACIALVSVRYKKCPSEVRHLAVFPD----TITGADSSQLLEVSGSCVNHSTVD 271
OY 103 GPPEVHLEAEKAIYIHISPGTKDSVMALDGLSTYSLLIMKNSGVEERIENT-YSRH 161
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 272 DPKMHCSAECEWLV---PIGKCMC-----KAGYEKKNGTCQVCRP 309
OY 162 KIYKSPETTYCLKVKALLSMKIGVYSPVH-----CIKTVENELRP----- 206
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 310 GFFKASPHSQTCSCPP-----HSTHEASTSCVCEKDYFRRESDPPTMACTRP 359
OY 206 ---PENIEVSVONQNYVLKM-----DYTYANMTFOVOWLAFLKRNPGNHLKMK 252
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 360 PSAPRNIAISNVNETSVEFLEWIPADTGSGKDVSYIILCKCN-SHAGVCECGGHR--- 416
OY 253 QIPDCENVKTTQCVFPQVNFQKGIYLLRVQASDGNNTSFMSEIKFDTEIOAFLPPVFN 312
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 416 -----YLPQOIGLKNTSVMADPLAHTNYTF-----EIEA-----YNG 448
OY 313 IRSLSDSFHIYIG---AFKOSGNTPVIG-----DYP-----LIYEILF 347
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 449 VSDLSPTGRQYVSVVTTNQAAPSFVTNVKKGKIAKNSISLSKQEDPRPNGIILLEYELKY 508
OY 348 WENTSNAERKIIIE-KKTDVTVPNLKLPLTVYCVKARAHT 384
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 509 FEKQDETSTYIIKSKETITTAEGLKPAASVYVFQIRART 546
```

Search completed: June 1, 2000, 04:35:09
Job time: 14289 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2000, 00:40:17 ; Search time 34.71 Seconds

(without alignments)
351,842 Million cell updates/sec

Title: us-09-240-675-2_copy_27_427

Perfect score: 2141
Sequence: 1 GRNLSPOKVEVDIIDNFI.....AHTMDEKLNKSSVSDAYCE 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 08
Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2141	100.0	557	1 INRL_HUMAN	P17181 homo sapien
2	1384.5	64.7	560	1 INRL_BOVIN	Q04790 bos taurus
3	1382.5	64.6	560	1 INRL_SHEEP	Q28589 ovis aries
4	966	45.1	590	1 INRL_MOUSE	P33896 mus musculus
5	220	10.3	325	1 CRP_HUMAN	Q08334 homo sapien
6	148	6.9	337	1 INGS_HUMAN	P38484 homo sapien
7	122.5	5.7	1451	1 MYM1_HUMAN	P52179 homo sapien
8	118	5.5	489	1 INGR_HUMAN	P15260 homo sapien
9	118	5.5	1005	1 EPAS_RAT	P54757 rattus norv
10	117.5	5.3	1383	1 INSR_RAT	P15127 rattus norv
11	113	5.3	1450	1 MPST_CHICK	Q02173 gallus gall
12	111.5	5.2	1447	1 DCC_MOUSE	P70211 mus musculus
13	110	5.1	1912	1 PTPN_HUMAN	P23468 homo sapien
14	109.5	5.1	575	1 IL10R_MOUSE	Q61727 mus musculus
15	108	5.0	1037	1 EPAS_HUMAN	P54756 homo sapien
16	107.5	5.0	1372	1 INSR_MOUSE	P15208 mus musculus
17	107	5.0	427	1 IL13_HUMAN	P78552 homo sapien
18	105.5	4.9	878	1 IL13_MOUSE	P26934 mus musculus
19	104.5	4.9	1447	1 DCC_HUMAN	P43146 homo sapien
20	104	4.9	896	1 CYR2_MOUSE	P26955 mus musculus
21	104	4.9	1239	1 NRG_DROME	P20241 drosophila
22	102.5	4.8	1897	1 PTPN_HUMAN	P10566 homo sapien
23	101	4.7	1304	1 CD45_HUMAN	P08575 homo sapien
24	99.5	4.6	677	1 SPOT_HAEM	P43811 haemophilus
25	99.5	4.6	897	1 CYR2_HUMAN	P32927 homo sapien
26	98.5	4.6	1345	1 YHO0_YEAST	P38800 saccharomyc
27	98.5	4.6	1615	1 RRP0_TMY	P03566 tobaccos mos
28	98.5	4.6	3135	1 S230_PLAFO	Q08372 plasmodium
29	97.5	4.6	306	1 K128_YEAST	P06242 saccharomyc
30	97.5	4.6	1256	1 FINC_CHICK	P11722 gallus gall
31	97.5	4.6	1382	1 INSR_HUMAN	P06213 homo sapien
32	96.5	4.5	515	1 INR1_HUMAN	P48551 homo sapien
33	96.5	4.5	2029	1 LAR_DROME	P16521 drosophila
34	96	4.5	662	1 IL12R_HUMAN	P42701 homo sapien

35	95.5	4.5	925	1 PMP2_CAEL	P91341 caenorhabdit
36	95.5	4.5	2280	1 YCF2_TOBAC	P09976 nicotiana t
37	95	4.4	918	1 IL6B_HUMAN	P40189 homo sapien
38	94.5	4.4	1068	1 YCF0_MARPO	P12221 marchantia
39	94	4.4	917	1 IL6B_MOUSE	Q00560 mus musculus
40	94	4.4	2628	1 HAGA_PORCI	Q51845 porphyronom
41	93.5	4.4	620	1 YMO0_YEAST	Q03162 saccharomyc
42	93.5	4.4	847	1 CD22_HUMAN	P20273 homo sapien
43	93.5	4.4	1091	1 C1C2_RAT	P54290 rattus norv
44	93	4.3	1097	1 LIFR_HUMAN	P42702 homo sapien
45	93	4.3	1101	1 P11G_HUMAN	P48736 homo sapien

ALIGNMENTS

```

RESULT 1
ID INRL_HUMAN
AC P17181;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DE 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
GN IFNAR1 OR IFNAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP MEDLINE: 90124632.
RA Uze G., Lutfalla G., Gresser I.;
RT "Genetic transfer of a functional human interferon alpha receptor
RT into mouse cells: cloning and expression of its cDNA.";
RL Cell 60:225-234(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE: 92129376.
RA Lutfalla G., Gardiner K., Proudhon D., Vleth E., Uze G.;
RT "The structure of the human interferon alpha/beta receptor gene.";
RL J. Biol. Chem. 267:2802-2809(1992).
RN [3]
RP PHOSPHORYLATION BY TYK2.
RA MEDLINE: 95059042.
RA Colamonici O., Yan H., Domanski P., Handa R., Smalley D.,
RA Mullerstein J., Witte M., Krishnan K., Krolewski J.;
RT "Direct binding to and tyrosine phosphorylation of the alpha subunit
RT of the type I interferon receptor by pl35tyk2 tyrosine kinase.";
RL Mol. Cell. Biol. 14:8133-8142(1994).
CC - FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC - TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND
CC EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.
CC - PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.
CC - SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC - SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@sdb-sdb.ch).
DR EMBL: J03171; AA52730.1; -
DR EMBL: X60459; CAA42992.1; -
DR PIR: A32694; A32694.
DR PIR: S17112; S17112.
DR MIM: 107450; -

```


KW Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;
 KW Phosphorylation.
 FT SIGNAL 1 27
 FT CHAIN 28 557
 FT
 FT DOMAIN 28 436
 FT TRANSMEM 437 457
 FT DOMAIN 458 557
 FT DISULFID 79 87
 FT DISULFID 199 220
 FT MOD_RFS 466 466
 FT MOD_RFS 481 481
 FT CARBOHYD 50 50
 FT CARBOHYD 58 58
 FT CARBOHYD 81 81
 FT CARBOHYD 88 88
 FT CARBOHYD 110 110
 FT CARBOHYD 172 172
 FT CARBOHYD 254 254
 FT CARBOHYD 313 313
 FT CARBOHYD 314 314
 FT CARBOHYD 376 376
 FT CARBOHYD 416 416
 FT CARBOHYD 433 433
 FT VARIANT 168 168
 FT
 FT CONFLICT 17 17
 FT SEQUENCE 557 AA: 63525 MW: 0F6744C8A1ADBE73 CMC64;
 G -> A (IN REF. 2).
 /FTID=VAR.002717.

Query Match
 Best Local Similarity 100.0%; Score 2141; DB 1; Length 557;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKNLSPKQVEVDITDDNFILRNNSDSVGNVTSFDTQKGMNWKLSGCCNITSTK 60
 DB 27 GKNLSPKQVEVDITDDNFILRNNSDSVGNVTSFDTQKGMNWKLSGCCNITSTK 86
 QY 61 CNFSSLKINVEEIKLRIRAEKENTSSWYEVDSFTPKRAQIGPEVHLEADKAIYHI 120
 DB 87 CNFSSLKINVEEIKLRIRAEKENTSSWYEVDSFTPKRAQIGPEVHLEADKAIYHI 146
 QY 121 SPGRDSVMMALDGLSFTYSLIMKNSGVEERINITYSRHKYKLSPEYTCVKYKAL 180
 DB 147 SPGRDSVMMALDGLSFTYSLIMKNSGVEERINITYSRHKYKLSPEYTCVKYKAL 206
 QY 181 LTKMIGIVSPVHCIKTYENELPPENIEVSQONQNYLKKDYTYAMTQVQVLAFL 240
 DB 207 LTKMIGIVSPVHCIKTYENELPPENIEVSQONQNYLKKDYTYAMTQVQVLAFL 266
 QY 241 KRNPNHLYKMKQIPDCEVKTQCVFQONVFOKGIYLLRVOASDGNNTSFSEERKFD 300
 DB 267 KRNPNHLYKMKQIPDCEVKTQCVFQONVFOKGIYLLRVOASDGNNTSFSEERKFD 326
 QY 301 EIQAFLPPVENIRSLDSFHIYIGAPQSGNTPIQDPLIYEIIEFMENTSNAERKIE 360
 DB 327 EIQAFLPPVENIRSLDSFHIYIGAPQSGNTPIQDPLIYEIIEFMENTSNAERKIE 386
 QY 361 KKTDTVPRLKPLTYCYKARAHMTDEKLNKSSVSFSDANCE 401
 DB 387 KKTDTVPRLKPLTYCYKARAHMTDEKLNKSSVSFSDANCE 427

RESULT 2
 INRL_BOVIN STANDARD: PRT: 560 AA.
 AC 004790;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
 GN IFNARI OR IFNAR.
 OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG.
 RX MEDLINE: 93076908.
 RA Mouchel-Vleish E., Luftalla G., Mogenssen K.E., Uze G.;
 RT "Specific antiviral activities of the human alpha interferons are
 RT determined at the level of receptor (IFNAR) structure."
 RL FEBS Lett. 313:255-259(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93057725.
 RA Lim J.-K., Langer J.A.;
 RT "Cloning and characterization of a bovine alpha interferon receptor."
 RL Biochim. Biophys. Acta 1173:314-319(1993).
 CC -I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 CC -I- I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
 CC SUBUNITS THEMSELVES.
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC
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 CC
 CC EMBL: X56443; CAA48484.1; -;
 DR EMBL: L05320; AAA02571.1; -;
 DR PIR: S33770; S33770.
 DR PIR: S27387; S27387.
 DR PIR: PF00041; fn3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 560
 FT
 FT DOMAIN 25 437
 FT TRANSMEM 438 458
 FT DOMAIN 459 560
 FT DISULFID 76 84
 FT DISULFID 199 220
 FT CARBOHYD 47 47
 FT CARBOHYD 55 55
 FT CARBOHYD 85 85
 FT CARBOHYD 109 109
 FT CARBOHYD 172 172
 FT CARBOHYD 254 254
 FT CARBOHYD 313 313
 FT CARBOHYD 377 377
 FT CARBOHYD 434 434
 FT CONFLICT 422 422
 FT SEQUENCE 560 AA: 63818 MW: 66D76B72861E1D11 CRC64;
 F -> V (IN REF. 2).

Query Match
 Best Local Similarity 64.7%; Score 1384.5; DB 1; Length 560;
 Matches 258; Conservative 62; Mismatches 78; Indels 5; Gaps 5;

QY 3 NLKSPQVEVDITDDNFILRNNSDSVGNVTSFDTQKGMNWKLSGCCNITSTKCN 62
 DB 27 NLK-PENVEIHTIDDNFLLRNNSDSVGNVTSFDTQKGMNWKLSGCCNITSTKCN 85
 QY 63 FSSSLKLNVEEIKLRIRAEK-ENTSSWYEVDSFTPKRAQIGPEVHLEADKAIYHI 120
 DB 86 FSSVELEVEFKILIRAEKENTSSWYEVDSFTPKRAQIGPEVHLEADKAIYHI 145
 QY 121 SPGRDSVMMALDGLSFTYSLIMKNSGVEERINITYSRHKYKLSPEYTCVKYKAA 179

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Db      146  SEPTGKDSIMAMMDRSSFRSVYIMKSSSLERTETVYPEDKITLSPETICLVAKKE 205
Oy      180  ILTSMKIGVSVVHCCKTIVENELPPENIEVSONQNYLAKDITYANMTVOVLAHF 239
Db      206  LKLSQSVGVGYSPVYCINTTERHKVSPENIQIADQOIYVLKMDYENATQAOVLRAF 265
Oy      240  LKRNPNHLKYKKOIPDCENVKTTCVFPONFQKGIYLLRVAQSPGNNTSFSEIKPD 299
Db      266  FKKIGNSHDKMKQIPNCENVSTHCVFFREYSSRIYVRARASNGNTSFSEKEKN 325
Oy      300  TELQALFLPVPVNSLS-DSEHIYIGAPKQSGQNPVIDYDPLVEIIFEWNTSNAERI 358
Db      326  TELKTIIFPPLVSVKTDSDSLHVSQAEESEENKSMVNDLPLEYEVIFEWNTSNAERY 385
Oy      359  IEKKTQVTVPNLKLPLTVYCVKARAHMMDGAEKLSVSEFANOE 401
Db      366  LEKRTNFIPTDLKPLTVYCVKARALIEHDRNRKNGSSFSDTJCE 428

RESULT
3
INRL--SHEEP
ID      INRL_SHEEP      STANDARD:      PRT:      560 AA.
AC      028589; 095206;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-FEB-2000 (Rel. 39, Last annotation update)
DE      INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
DE      (INTERFERON ALPHA/BETA RECEPTOR-1).
GN      IFNAR1 OR IFNAR.
OS      Ovis aries (Sheep).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC      Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Caprinae; Ovis.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-ENDOMETRIUM;
RX      MEDLINE: 97135690.
RA      Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
RT      "Structure of an ovine interferon receptor and its expression in
RT      endometrium.";
RL      J. Mol. Endocrinol. 17:207-215(1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE-ENDOMETRIUM;
RX      MEDLINE: 98006426.
RA      Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;
RT      "Molecular cloning of ovine and bovine type I interferon receptor
RT      subunits from uteri, and endometrial expression of messenger
RT      ribonucleic acid for ovine receptors during the estrous cycle and
RT      pregnancy.";
RL      Endocrinology 138:4757-4767(1997).
CC      -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC      I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC      INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC      SUBUNITS THEMSELVES.
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
CC      CONCEPTUS AT DAY 15 OF PREGNANCY.
CC      -1- SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.
CC      -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC      or send an email to license@isb-slb.ch).
PR      EMBL; X95939; CA65183.1; -.
PR      EMBL; U65978; AAB84231.1; -.
PR      PFM; PF00041; f03; 1.

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Query Match	Best Local Similarity	Score	DB 1	Length	560
Matches 256; Conservative 65; Mismatches 77; Indels 5; Gaps 5	64.6%; 63.5%;	1382.5;			
Query	3	NLSKQKVEVDIIDNFIILRNKNSDESGVNTFFSDYCKTGMDNKLKSGCQNTISTKCN	62		
Db	27	NLKS-ENVEIHIIIDNFIILRNKNSDESGVNTFFSDYCKTGMDNKLKSGCQNTISTKCN	85		
Qy	63	FSSKL-LVYEEIKRIRAEK-ENMSWYEVSTFPFRAQIGPPEVHLAEADKAVIHI	120		
Db	86	FSSVSLKLVFEIEIRIRAEBSGNTSTVEPFPFLAQIGPPEVHLAEADKALII	145		
Qy	121	S-PGKSDVMALDLSEFTSLILKNSGVEERLENIYSRRKIYKLPETTYCLKVKA	179		
Db	146	SPGEGEDSIMALDKSSFRISVVIKKNSSLEERETVYPEDKIYKLPSEIYCLKVKA	205		
Qy	180	LITSKIKIVSPVHCIKTTVENELPPENIEVSONQNTVLEKMDTYANMTFOVOMLAF	239		
Db	206	LRLQSVGCVSPVCIINTTERHKVSPENVOINVNOQAVLKMDFYESTTFOAGWLA	265		
Qy	240	LKRNGNLIYKWKQIPDDENKITTCQVFPQVFOGIIYILRQVQASDGNSTFWSSEIKAD	299		
Db	266	LKKIPGKSNMKWQIPDDENKITTCQVFPQVFOGIIYILRQVQASDGNSTFWSSEIKAD	325		
Qy	300	TEIOAFLLPAPENINISL-DSFHFIYIGPKOSGNPVYODVPLIYEIIFMENTSNARKI	358		
Db	326	TEVAPLIPPIYKSKSTIDDSLHVSVSSESENNSVQDLPLVEVFEVMENTSNARKI	385		
Qy	359	IEKTDVTPNKLPLTYCVKARAHMDEKLKNSVFSADCE	401		
Db	386	LEKRTDFEPNKLPLTYCVKARAHMDEKLKNSVFSADCE	428		
RESULT 4					
INRL_MOUSE	INRL_MOUSE	STANDARD;	PRT;	590 AA.	
AC	P33896;				
DT	01-FEB-1994 (Rel. 28, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	15-FEB-2000 (Rel. 39, Last annotation update)				
DE	INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).				
GN	IFNAR OR IFNAR OR IFNAR.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC	Euteleia; Rodentia; Sciurognathii; Muridae; Murinae; Mus.				
RP	[1]				
RP	SEQUENCE FROM N.A.				


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DB 24 PENVBNMSVNFKNILQWESPAFAKGNLFTTAQY-----LSYRIFODKCMNTTTECDSS- 79
QY 67 KLVNYEIKIRIRAE-KENTSSWYEVDSFTPPFRAAIGPPEVHLEA-EDKAIYIHISPGT 124
DB 79 -LSYRGHTIRAEFAEDSDWVNI-TFCPVDDTIIGPGMQVEVLADSLHMFAPKI 136
QY 125 KDSY-MALDGL--SFYSLILWKNSSGVEERIENTISRKIKYLSSETTYCKVKAAL 181
DB 137 ENEYETWTKNKNYSWNTNVOYWKNGTDEKFOITPOYDFEVLRLNLEPMYTCVQVRGFLP 196
QY 182 TSWKIGVSPVHCITVENELP 204
DB 197 DRKAGSESPVCEQTHDETVP 219

RESULT 6
INGS_HUMAN
ID INGS_HUMAN STANDARD: PRT: 337 AA.
AC P38484;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA
DE RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).
GN IFNGR2 OR IFNG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG FIBROBLAST;
RC MEDLINE: 94170380.
RA Wang J., Donnelly R.J., Kolenko S., Mariano T.M., Cook J.R.,
RA Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.;
RT Identification and sequence of an accessory factor required for
RT activation of the human interferon gamma receptor."
RL Cell 76:793-802(1994).
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR
CC SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF
CC THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO
CC INTERACT WITH GAF, JAK1, AND/OR JAK2.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC -----
DR EMBL: U05875; AAA16955.1; -
DR EMBL: U05877; AAA16956.1; -
DR MIM: 147569; -
DR PFAM: PF00041; fn3; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT CHAIN 1 27
FT SIGNAL 1 27
FT DOMAIN 28 337
FT DOMAIN 28 247
FT TRANSMEM 248 268
FT DOMAIN 269 337
FT CARBOHYD 56 56
FT CARBOHYD 85 85
FT CARBOHYD 110 110
FT CARBOHYD 137 137
FT CARBOHYD 219 219
FT CARBOHYD 231 231
FT VARIANT 64 64
FT R -> O.
FT /FRID-VAR.002718.
SQ SEQUENCE 337 AA: 37834 MW: 18661B10AD90E509 CRC64:

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Query Match 6.9%; Score 148; DB 1; Length 337;
Best Local Similarity 22.2%; Pred. No. 0.00032;
Matches 62; Conservative 49; Mismatches 104; Indels 64; Gaps 13;

QY 4 LKSPQVEVDIIDDNFILW-----NRSDSEYGVNTSEFDYQKGMNWILS----- 52
DB 30 LPAPQHPKIRLVNAEQVLSWEPVALSNSTRPVYRQFRTDSK-----WFTADISIGV 84
QY 52 GCONITSTFCNFS-----LKLNYEIKIRIRAEKENT-SSWYEVDSFTPPFKAQI 102
DB 85 NCTQITATECDTIAASPSAGFPDENV-----TLRLAEGLALHSANVYIPWFOHNTV 140
QY 103 GPPEVHLEA---AEDKAIYIHISPGTSDYVMAALDGLSFTYSLILWKNSSGVEERIENTIS 159
DB 141 GPPE-NIEVTPGEGSLIRFSSPFDIADSTAF---FCYYHYWE--KGIQYKGPFR 193
QY 160 RKRTY--KLSPETTYCKVKAALLTS---WKIGVSPVHCITVENELPPEPNTIEVS 213
DB 194 SNSISIDNLKPSFRVYCLQVQADLLWKNISIFRGHLSNISCYETADASTELQVILLISV 253
QY 214 -----ONQNVVLKMDYTANMFQVQ 234
DB 254 GTFSLSLVLAGACFFLVLYLKYRGLIKYWHTPPSIPLQIE 292

RESULT 7
INGS_HUMAN
ID INGS_HUMAN STANDARD: PRT: 1451 AA.
AC P52179;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE MYOHEXIN 1 (190 KD TITIN-ASSOCIATED PROTEIN) (190 KD CONNECTIN-
DE ASSOCIATED PROTEIN).
GN MYOM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKETAL MUSCLE;
RC MEDLINE: 94095665.
RA Vinemeyer U., Obermann W., Weber K., Fuerst D.O.;
RT The globular head domain of titin extends into the center of the
RT sarcomeric M band. cDNA cloning, epitope mapping and immunoelectron
RT microscopy of two titin-associated proteins."
RL J. Cell Sci. 106:319-330(1993).
CC -1- FUNCTION: MAJOR COMPONENT OF THE VERTEBRATE MYOFIBRILLAR M BAND.
CC BINDS MYOSIN, TITIN, AND LIGHT MEROMYOSIN. THIS BINDING IS DOSE
CC DEPENDENT.
CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 7 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC -----
DR EMBL: X69090; CAA48833.1; -
DR MIM: 603508; -
DR PFAM: PF00041; fn3; 5.
DR PFAM: PF00047; fn3; 3.
DR PRINTS: PR00014; FNTYPEPIT.
KW Immunoglobulin domain; Muscle protein; Thick filament; Repeat.
FT DOMAIN 46 81
FT REPEAT 46 51
FT REPEAT 52 57
FT REPEAT 58 63
FT REPEAT 64 69
FT REPEAT 64 69

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FT REPEAT 70 75 5.
FT REPEAT 76 81 6.
FT DOMAIN 156 289 FIBRONECTIN TYPE-III.
FT DOMAIN 290 384 FIBRONECTIN TYPE-III.
FT DOMAIN 385 511 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 512 612 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 613 711 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 712 816 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 817 917 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 918 1023 FIBRONECTIN TYPE-III.
FT DOMAIN 1024 1137 FIBRONECTIN TYPE-III.
FT DOMAIN 1138 1239 FIBRONECTIN TYPE-III.
FT DOMAIN 1240 1352 FIBRONECTIN TYPE-III.
FT DOMAIN 1353 1451 FIBRONECTIN TYPE-III.
SO SEQUENCE 1451 AA; 162452 MW; 35293FE6GFFFD10 CRC64;

Query Match 5.7%; Score 122.5; DB 1; Length 1451;
Best Local Similarity 19.8%; Pred. No. 0.18;
Matches 91; Conservative 66; Mismatches 181; Indels 121; Gaps 21;

QY 17 DNFLRNRRSDSYGN--VFSPDYOKTGMNWKLSGQNTSTKCNFSLKNTYEET 74
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 388 DYIISMKQPAVDGSPILGYFDKCEVGTDSM-----SQCDTFVKFAPEPV 436
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 75 KL-----RIRAEKENTSM-----YEVDSFPRKAQIGPEVHLEADKAVIHIS 121
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 437 GLIGRSYIFRVRANKGIGFPRSEAVAALDPAERAKRSP--LSTLDWTIVYEE 493
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 122 PGTKDSVMMALDGLSFT-----YSLIWK-----NSSGEERIENTYS----- 160
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 494 EPSEGVGPPDLSVATATSYVLSMKPRQGRHEGIMFVEGCEGENTMORVNTL 553
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 160 -----RHKYKLSPEPTYCLKVKKALLTSWKIGVSPVCHIKTTV-----ENELP 204
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 554 PVKSPRALFDLAEGKSCYCFRVRC-----SNSAGVEPESEAEVTVGDKLDIPKAPGKII 609
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 205 PRENIEVSQNONVYVKMD-----YTYAMTQOVOMLHFLKRNPGNLYKWK 252
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 610 PSRNDTSTV-----VVSWEESKDAKELVGYTEAVNAGSGKWEPC--NNNPVKTHRF-- 660
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 253 QIPDCENVYTCQVFPQNVFQKGIYLLRYOASDGNNTSFSEIKFTDIEQAFLLP-- 310
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 660 ---TEHGLVTGGS-----YIFRRAVNAAGLSYSDSE--ALEVKAIAIPSPSP 704
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 310 --VFNRISLSDSFHYIGAPKOSGNTPVLYQDYPLIYEIT-----FWENTSNAEKRIIEKK 362
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 705 CQITCLESPRDSMWLGWKQPKDTGGAETGYVYNTREVLDGVPKWR--EANYKAVREE 761
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 363 TDVTPNKLPLTVYCVKKAHNMDEKLKSSVFSDAVCE 401
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 762 A-YKISLNKENVYQFOVAAHNAAGLAPSAVSECFKE 799
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
INCR_HUMAN STANDARD: PRT: 489 AA.
AC P15260;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119).
GN IFNGR1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89003065.
RA Aguet M., Dembic Z., Meriin G.;
RT "Molecular cloning and expression of the human interferon-gamma
RT receptor.";
RL Cell 55:273-280(1988).

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RN [2]
RP DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.
RX MEDLINE: 93183911.
RA Stueder D., Friedlein A., Fountoulakis M., Lahm H.-W., Garotta G.;
RT "Alignment of disulfide bonds of the extracellular domain of the
RT interferon gamma receptor and investigation of their role in
RT biological activity.";
RL Biochemistry 32:2423-2430(1993).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.
RX MEDLINE: 95342235.
RA Walter M.R., Windsor W.T., Nagabhushan T.L., Lundell D.J., Lunn C.A.,
RA Zaudovy P., Nadula S.K.;
RT "Crystal structure of a complex between interferon-gamma and its
RT soluble high-affinity receptor.";
RL Nature 376:230-235(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 COMPLEX WITH ANTIBODY.
RX MEDLINE: 98035727.
RA Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A.,
RA Winkler F.K., Robinson J.A.;
RT "Neutralizing epitopes on the extracellular interferon gamma receptor
RT (IFNGAMR) alpha-chain characterized by homolog scanning mutagenesis
RT and x-ray crystal structure of the A6 fab-IFNGAMR1-108 complex.";
RL J. Mol. Biol. 273:882-897(1997).
CC -1- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
CC INTERFERON-GAMMA DIMER.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC -----
CC EMBL: J03143; AAA52731.1; -
CC PIR: A31555; A31555.
CC DR PDB: 1JRH; 25-MAR-98.
CC DR MM: 107470; -
CC DR MM: 209950; -
CC KW Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;
CC Immunoglobulin domain; 3D-structure.
CC FT SIGNAL 1 17
CC FT CHAIN 18 489 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
CC FT DOMAIN 18 245 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 246 266 POTENTIAL.
CC FT DOMAIN 267 489 CYTOPLASMIC (POTENTIAL).
CC FT DISULFID 77 85
CC FT DISULFID 122 167
CC FT DISULFID 195 200
CC FT DISULFID 214 235
CC FT CARBOHYD 34 34 POTENTIAL.
CC FT CARBOHYD 79 79 POTENTIAL.
CC FT CARBOHYD 86 86 POTENTIAL.
CC FT CARBOHYD 179 179 POTENTIAL.
CC FT CARBOHYD 240 240 POTENTIAL.
CC SO SEQUENCE 489 AA; 54404 MW; DCF9E57AD8F47400 CRC64;

Query Match 5.5%; Score 118; DB 1; Length 489;
Best Local Similarity 22.2%; Pred. No. 0.093;
Matches 50; Conservative 39; Mismatches 102; Indels 34; Gaps 10;

QY 201 NELPPENIEVSQNONVYVKMDTYANM--TFQVOMLHAFKRNPGNHLKRNQIPDCE 258
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 27 SSVPTPTVETIESYNNPVIWEYQIMPOVVFIVE-----VANYGVKNSRW--IDACI 78
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```


DR PFAM: PF00041; fn3; 6.
 DR PFAM: PF00047; 1g; 4.
 DR PRINTS: PR00014; FNTYPE11.
 KW Glycoprotein; Immunoglobulin domain; Transmembrane; Signal;
 KW Anti-oncogene; Alternative Initiation; Alternative Splicing.
 FT SIGNAL 1 25
 FT CHAIN 26 1447
 FT CHAIN 85 1447
 FT CHAIN 26 1097
 FT TRANSMEM 1098 1122
 FT DOMAIN 1123 1447
 FT DOMAIN 54 124
 FT DOMAIN 154 219
 FT DOMAIN 254 317
 FT DOMAIN 345 407
 FT DOMAIN 426 522
 FT DOMAIN 525 618
 FT DOMAIN 619 716
 FT DOMAIN 722 816
 FT DOMAIN 840 940
 FT DOMAIN 941 1042
 FT DISULFID 61 117
 FT DISULFID 161 212
 FT DISULFID 261 310
 FT DISULFID 352 400
 FT CARBOHYD 60 94
 FT CARBOHYD 94 124
 FT CARBOHYD 299 329
 FT CARBOHYD 318 318
 FT CARBOHYD 478 478
 FT CARBOHYD 628 628
 FT CARBOHYD 702 702
 FT VARSPLIC 819 838
 FT SEQUENCE 1447 AA; 158298 MW; 0D1F1097C22D559F CRC64;
 5.2%; Score 111.5; DB 1; Length 1447;
 Best Local Similarity 21.4%; Pred. No. 1.2;
 Matches 106; Conservative 63; Mismatches 174; Indels 153; Gaps 29;

Query Match 5.2%; Score 111.5; DB 1; Length 1447;
 Best Local Similarity 21.4%; Pred. No. 1.2;
 Matches 106; Conservative 63; Mismatches 174; Indels 153; Gaps 29;
 6 SPQKVEVDIIDNFI-LRNNRSDSEYGN-TSPFYQKGMNMIKLSGCCNITSTKCNF 63
 431 ABRDVLPLVSSRFVFLSRPPAEKGNITFTFFSRGDRERALTNP----- 483
 64 SLKLT--NVEEIKRIRAEKENTSSWEVDSFPPFKA-----QIGPEVHLEAEDKA 115
 483 GSDLVGLNKLKPEAMTFNVAVIN--EKPGSSOPIKVATPELOVGPVENLHA----- 537
 116 IVIHISPGTKDSVMA---LDGLSFTYSLLIMKSSGVEERIENTYSHKIKYKLSPEPT 171
 537 --VSTSP-TSILITWEPAYANGPVQGYRLFCTEYSTGEQNIENVGLSYKLEGLKKEFE 593
 172 YCLAKYAAALLTSKIKGVYSPVHCIKTTVENELPPENIEVSQN-----Q 216
 594 YTLRFLA--YNRYPGVSTDDITVTLSVPSAPPNISLEVANSRSIKVSMLEPPSGTQ 651
 217 N-----YVLK-----MDITYAN-----TFQV-----QW 235
 652 NGFITTKYKIRHKTRRGEMETLEPNNLM-YLTGTEKXSQSFQVSAMTVNGTGPSPMW 710
 236 LHAFLKRNQGNMLYKWKQIIPDCEN---KTQCVFPQ-----NVEQGIYLLRVAQS 284
 711 --YTAETPENDLDE--SQVPDQSSSLHVRPQTCIMSTWPLPNIVVRG--YIIQYGVG 765
 285 DGNNTSFNSEEIKFDEIQAFLLPFPENRSLSDSFHII-----GAP-KOSGWT 333
 766 -----SPYAEYAVVDSKQ-----YSTERLESSSHYVYISLKAENNAEGVPLYESATT 814
 334 PVIOD-----YPLIYEIIFMENTSNAERKIEKKTDTVPNLKPLTYVCV-----KAR 381
 815 RSTIDPDPDYPLDDF-----PTSG-----PDVSTPMLPVPVGVAAVALTHEAVR 861
 382 AHMDEKLKSSVFS 397

Db 862 VSWADNSVPRKORTSD 877
 RESULT 13
 ID PTP_HUMAN STANDARD; PRT; 1912 AA.
 AC P23468;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP-DELTA).
 GN PTPRD.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP MEDLINE; 95204468.
 RA Pulido R., Krueger N.X., Serra-Pages C., Salto H., Streuli M.;
 RT "Molecular characterization of the human transmembrane
 protein-tyrosine phosphatase delta. Evidence for tissue-specific
 expression of alternative human transmembrane protein-tyrosine
 phosphatase delta isoforms.";
 RT J. Biol. Chem. 270:6722-6728(1995).
 RL [2]
 RP SEQUENCE OF 390-1912 FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE; 91006018.
 RA Krueger N.X., Streuli M., Salto H.;
 RT "Structural diversity and evolution of human receptor-like protein
 tyrosine phosphatases.";
 RT EMBO J. 9:3241-3252(1990).
 RL [1]
 CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O -
 CC -1- PROTEIN TYROSINE + ORTHOPHOSPHATE
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS ARE FOUND IN DIFFERENT
 CC TISSUES DUE TO ALTERNATIVE SPLICING.
 CC -1- PFM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
 CC FROM THE TRANSMEMBRANE SEGMENT.
 CC -1- SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (3 IG-
 CC LIKE DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS),
 CC AND A CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L36929; AAC41749.1; -;
 DR EMBL; X54133; CA38068.1; -;
 DR PIR; S12052; S12052.
 DR HSSP; P18052; IYFO.
 DR MIM; 601598; -;
 DR PRINTS; PR00014; FNTYPE11.
 DR PRINTS; PR00700; PRTYPPHASE.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS00386; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 DR PFAM; PF00041; fn3; 8.
 DR PFAM; PF00047; fn3; 3.
 DR PFAM; PF00102; Y-phosphatase; 2.
 DR Hydrolyase; Receptor; Glycoprotein; Signal; Transmembrane; Duplication;
 KW Immunoglobulin domain; Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 21 1912
 FT CHAIN 21 1265
 FT TRANSMEM 1266 1290
 FT DOMAIN 1291 1912
 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 23 115 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 118 225 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 232 318 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 320 414 FIBRONECTIN TYPE-III.
FT DOMAIN 417 513 FIBRONECTIN TYPE-III.
FT DOMAIN 516 606 FIBRONECTIN TYPE-III.
FT DOMAIN 609 708 FIBRONECTIN TYPE-III.
FT DOMAIN 711 822 FIBRONECTIN TYPE-III.
FT DOMAIN 825 916 FIBRONECTIN TYPE-III.
FT DOMAIN 918 1017 FIBRONECTIN TYPE-III.
FT DOMAIN 1020 1137 FIBRONECTIN TYPE-III.
FT DOMAIN 1375 1618 PROTEIN-TYROSINE PHOSPHATASE.
FT DOMAIN 1519 1912 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 1553 1553 BY SIMILARITY.
FT ACT_SITE 1844 1844 CLEAVAGE (POTENTIAL).
FT SITE 1175 1178 CLEAVAGE (POTENTIAL).
FT CARBOHYD 254 254 POTENTIAL.
FT CARBOHYD 299 299 POTENTIAL.
FT CARBOHYD 724 724 POTENTIAL.
FT CARBOHYD 832 832 POTENTIAL.
FT VARSPLC 181 189 MISSING (IN KIDNEY ISOFORM).
FT VARSPLC 226 229 MISSING (IN KIDNEY ISOFORM).
FT VARSPLC 775 783 MISSING (IN KIDNEY ISOFORM).
FT VARSPLC 609 1137 MISSING (IN RETAL BRAIN ISOFORM).
FT MUTAGEN 1178 1178 R->A: 2.5-FOLD REDUCTION IN CLEAVAGE.
SQ SEQUENCE 1912 AA: 214759 MW: 3A8BCBD32182E36 CRC64;

Query Match 5.1%; Score 110; DB 1; Length 1912;
Best Local Similarity 22.9%; Pred. No. 2.2; Mismatches 96; Gaps 11;
Matches 60; Conservative 24; Indels 96; Gaps 11;

OY 166 LSEPTCYCLVKA-----ALLTSM--KIGV 188
DB 790 LQETSYSLVATVATGDKARSKPLVSTGAVPKRLVNHQMTALLIQHPVYD 849
OY 189 YSVHCKTIV-ENELPPNIEVSQNONVYVKMDYTNAMTFQVOMLAFKRNQNH 247
DB 850 FGLQGYRLKFGKRDMPPLTLEFSEKEDFTADLHKHGSAYVFR--LSARKVGFGE 906
OY 248 LYMKQIPDCENVTQCVFQNVFQKGYLLRYQASDGNSTPSESEIFDEIQAFLL 307
DB 907 MKVEISIP--EVPPTG---FPQMLHSGTSTVQVLS-----WO----- 941
OY 308 PVFNIRISDSSEHYIYGAPKQSGNTPVIODYPLIYEIIFMENTS-----AEKIIIEKK 362
DB 941 PVLAEKN-----GIIRKYLIVRDI-----NIPLLPMQOLIVPAD 976
OY 363 TDVTVNLKPLVYCYKARAH 384
DB 977 TMTLTGLKPDYTYDVYKRAHT 998

RESULT 14
110R_MOUSE STANDARD; PRT; 575 AA.
ID 110R_MOUSE
AC 061727;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
GN IL10RA OR IL10R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X AJ F1; TISSUE=HEMATOPOIETIC;
RX MEDLINE; 94068585.
RA Ho A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.:
RT "A receptor for interleukin 10 is related to interferon receptors."
Proc. Natl. Acad. Sci. U.S.A. 90:11261-11271(1993).
CC -1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC or send an email to license@isb-sdb.ch).
CC EMBL: 112120; AAA16156.1;
DR MGD; MGI:96538; IL10RA.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 16
FT CHAIN 17 575
FT DOMAIN 241 262
FT TRANSMEM 263 575
FT DISULFID 204 225
FT CARBOHYD 50 50
FT CARBOHYD 66 66
FT CARBOHYD 113 113
FT CARBOHYD 182 182
FT CARBOHYD 238 238
SQ SEQUENCE 575 AA: 64248 MW: 820B9CD576F686B7 CRC64;

Query Match 5.1%; Score 109.5; DB 1; Length 575;
Best Local Similarity 20.0%; Pred. No. 0.5;
Matches 75; Conservative 46; Mismatches 129; Indels 125; Gaps 16;

OY 1 GKRLKSPQKVEVDIIDNFIKRM-----NRSDESVGNVTFSPDYOKTGDMNFKLSGCCNI 56
DB 23 GTELPSPSTVWEARFQHIILMKRPNOSSESTYIEVAL-----KQGNSTWMDIHICRA 78
OY 57 TSTCKNFSSKLIVYEE--IKLRIRA--EKENTSSVYEYDS--FTPFKKAQIQPEVHLEA 111
DB 79 QALSCDLTFTFLDILHRSYGYRARRAVNDSQYSMTTETRETFT----- 123
OY 112 EDKATVTHISPTKQSV--WALDGLSTYSLLIMKNSSEVERENIENYSRHKIYKLS--- 168
DB 123 VDEVIL-----TVDSVTLKAMDGIYGIHPRPRTIFPAGDEYQGVFNDLHVYKISIK 176
OY 168 -----PEI-----TYCLKYAALLTSKIGVSPVHKIKTTVENELRP 205
DB 177 ESELKNATRKVKQETFTLTPVIGVRKFCVKVLRLESIRINKAEMSEEOCLITTYOY--- 234
OY 206 PENIEVSQNONVYVKMDYTNAMTFQV-----QMLHAFKRNPGNHLK 250
DB 234 -----FTVYNLSILVISMILFGILVCLVQW-----YIRHFG----- 267
OY 251 WKQIPDCENVTQCVFQNV-----VFQKGYLLRYQASDGNNTS--FWS 293
DB 267 --KLPTVLVFKKPHDFEFPANPLCPETPDALHIVDLEVPKYSLELRDSVLHGSTDSGFGS 324
OY 294 EEIKFDTEIQAFILP 308
DB 325 GKPSLQTESQPLLP 339

RESULT 15
EPAS_HUMAN STANDARD; PRT; 1037 AA.
ID EPAS_HUMAN
AC P34736;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR EHK-1) (EPH HOMOLOG KINASE-1) (RECEPTOR PROTEIN-
DE TYROSINE KINASE HEK7).
GN EPHAS OR EHK1 OR HEK7.
OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euthera; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Mescher G.C.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 25-1037 FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 95206782.
RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
Basu R., Weicher A.A.;
RT *cDNA cloning and tissue distribution of five human EPH-like receptor
protein-tyrosine kinases.*
RL Oncogene 10:897-905(1995).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC -1- PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS
CC SYSTEM.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; X95425; CA64700.1; -
DR EMBL; L36644; AAA74245.1; -
DR HSSP; P00523; 2PTK.
DR MIM; 600004; -
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP_1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM_1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PFAM; PF00041; fn3; 2.
DR PFAM; PF00069; kinase; 1.
DR PFAM; PF00536; SAM; 1.
DR PFAM; PF01404; EPH_Lbd; 1.
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
FT SIGNAL 1 24
FT CHAIN 25 1037 EPHRIN TYPE-A RECEPTOR 5.
FT DOMAIN 25 573 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 574 594 POTENTIAL.
FT DOMAIN 595 1037 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 675 936 PROTEIN KINASE.
FT NP_BIND 681 689 ATP (BY SIMILARITY).
FT BINDING 707 707 ATP (BY SIMILARITY).
FT ACT_SITE 800 800 BY SIMILARITY.
FT CARBOHYD 264 264 POTENTIAL.
FT CARBOHYD 299 299 POTENTIAL.
FT CARBOHYD 369 369 POTENTIAL.
FT CARBOHYD 423 423 POTENTIAL.
FT CARBOHYD 436 436 POTENTIAL.
FT CARBOHYD 461 461 POTENTIAL.
FT VARSPIC 597 619 SCCECGGRASSICAVAPILLIV -> R (IN ISOFORM
FT SEQUENCE 1037 AA; 114784 MM; FC2C46C959AFB699 CRC64;
2).

Query Match 5.0%; Score 108; DB 1; Length 1037;
Best Local Similarity 20.3%; Pred No.1.4; Indels 162; Gaps 23;
Matches 94; Conservative 49; Mismatches 159;
QY 1 GKNLSPQVEVDII--DDNF-----ILRMNRSDSEVGNV---PSFDYQKTGMNW 47
DB 163 GRNIRKNQYIKIDITLADSDSFELDGDVYMKLNFVRDVGPLSKGFLAFQDVG---- 219
QY 48 IKLSCGNTST-----KCNFSLKLVNVEEIKIRAKEMTSSMYVEDSTFPRKAI 102
DB 219 ---ACIALVSVYVYKVKCPVVRHLAVPD-----TITGAUSSOLLEVSQCVNHSVTD 269
QY 103 GPPEVHLEADKAIVIHISPGTKDSYMMALDGLSFTYSLLIMKNSGVEERIENI-YSRH 161
DB 270 EPRKMHCSAGEVLY---PIGKMC-----KAGYEKNKTOGVCP 307
QY 162 KIYKLSPEPTYCLKVKAALLTSKIGVSPVH-----CIKTVENELP----- 206
DB 308 GPRKASPHIQSC-----GKCPHSTHEASTSCVCEKDYRRSDPTMACTRP 357
QY 206 ---PENIEVSQONVYLR-----DYTY-----ANMTFOVMLHAFKRNPN 246
DB 358 PSAPRNALISVNETSVFLEWIPPADTGGKRDVSYTACKKCN-----HAGVCECGG 410
QY 247 HLYKWKQIPDCENVKTQCVFQPNVFOKGIYLLRVOASDGNNTSFWSEIKFETLQAF 306
DB 411 HV---RILPQSGIKNTS-----VMMVLLAHNTYTF-----ELEA--- 444
QY 307 LPVFNIRSLDSFHIYIG---APKSGNTPVIO-----DYP-----L 341
DB 444 ---VNGVSDLSPGARQVSVNTTNGAAPSPVNVKKGIRAKNSISLSWQEDPRPNCIL 500
QY 342 IYELLFEMNTSNAEKRIE-KKIDVYVFNKPLTYCVKRAHT 384
DB 501 EYEIKHFEKDOETSYTIKSKETITTAEGIKPASVYVFOIRART 544

Search completed: June 1, 2000, 04:38:50
Job time: 14313 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 00:39:48 ; Search time 69.16 Seconds

(without alignments)
402.010 Million cell updates/sec

Title: US-09-240-675-2_COPY_27_427

Perfect score: 2141
Sequence: 1 GKNKSPQKVEVDIIDNFT.....AHTWDEKLKNSVFSADACE 401

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTOZOA:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	668.5	31.2	569	13	O9YHMO
2	216.5	10.1	349	11	O61190
3	199	9.3	332	11	O63953
4	183.5	8.6	341	13	O9YGC8
5	133.5	6.2	918	13	O9W6U9
6	127.5	6.0	508	13	O9YHV9
7	125	5.8	1493	11	P97798
8	123.5	5.8	1443	13	O90610
9	123	5.7	1375	5	O94537
10	123	5.7	1526	5	O94538
11	121	5.7	1461	4	O92859
12	121	5.7	1461	4	O00340
13	117.5	5.5	1427	13	O91562
14	117.5	5.5	1585	5	O17859
15	117.5	5.5	2214	4	O92673
16	117	5.5	817	13	O07784
17	116.5	5.4	1264	5	P91767
18	115.5	5.4	658	5	O09946
19	115	5.4	26926	4	O10466
20	114	5.3	1377	11	P97603

21	113	5.3	1767	5	O24495
22	112	5.2	572	6	O29117
23	111.5	5.2	1445	11	O63155
24	111.5	5.2	1571	4	O60459
25	111.5	5.2	1896	4	O60458
26	111	5.2	6048	5	O23020
27	111	5.2	6831	5	O23550
28	111	5.2	7160	5	O23551
29	110.5	5.2	484	4	O14936
30	110.5	5.2	1898	11	O64604
31	110	5.1	2213	6	O95209
32	109	5.1	416	5	O18094
33	109	5.1	427	4	O95646
34	109	5.1	873	13	O98949
35	108.5	5.1	1040	13	O9W675
36	108.5	5.1	2033	11	O54711
37	108.5	5.1	2215	11	O88307
38	107	5.0	1651	4	O9Y6N7
39	105.5	4.9	1825	5	O61210
40	105	4.9	1948	4	O13332
41	104	4.9	1239	5	O61541
42	104	4.9	1302	5	O61542
43	103.5	4.8	896	11	O64146
44	103.5	4.8	1499	13	O90815
45	103	4.8	777	4	O9Y2H6

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	569 AA.
O9YHMO				
AC	O9YHMO			
DT	01-MAY-1999 (TREMBLrel. 10, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DE	01-MAY-1999 (TREMBLrel. 10, Last annotation update)			
DE	INTERFERON ALPHA/BETA RECEPTOR 1.			
GN	IFNAR1.			
OS	Gallus gallus (chicken).			
CC	Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;			
CC	Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-LIVER:			
RA	RESCOU, J., GARDINER K., MONNERON D., UZE G., LUTFALLA G.;			
RT	"Comparative genomic analysis of the interferon/interleukin-10			
RL	receptor gene cluster.";			
RL	Genome Res. 0:0-0(1999).			
KW	EMBL: AF082664; AAD13669.1; ..			
DR	Receptor.			
SO	SEQUENCE	569 AA;	6405 MW;	F99BC099 CRC32;

Query Match 31.2%; Score 668.5; DB 13; Length 569;

Best Local Similarity 38.0%; Pred. No. 8,9e-46;
Matches 158; Conservative 77; Mismatches 154; Indels 27; Gaps 12;

OY	3	NKSPQKVEVDIIDNFTLRNNSDESVGVTFSDYQ-----KTGMDNWKISGCONIT	57
DB	31	NKSPQKVEVDIIDNFTLRNNSDESVGVTFSDYQ-----KTGMDNWKISGCONIT	89
OY	58	STKSNFSSLMKLYEELKLRRAE-KENTSSWYVDSFTFRKQIOTPPVHLAEKAI	116
DB	90	HTEDFSSAITRAYDTHIRIRERREKSPWSIFEMIPETIAQIGPELALQSINGAI	149
OY	117	VHISPTKDSV--MMLDGLSFYSLILKNSGVEERLENIYSRKIKYLSPEYYCL	174
DB	150	KINSPPEANOVKRMW-LISVFKNYIVINDNSNV--EKRSITIPDIVINDLAPETYYCL	207
OY	175	KYKALITSKRIGYVSVCIKITVE--NELPPENIEVSQVONNYLKWDTYV-ANNTFO	232
DB	208	KVQATVLEDKGIFSPICIKITRKVNDILCPTNVVFLNKKFYLLMDNHNHEHTYT	267

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OY 223 VOMLHAFILKRNPGHNLHYKMGKIDPPCEANWTKQC-----VPEQONVFOKGIYLLRVOASDGN 287
Db 268 VOYLGLYKLNLYDYISSKWQVSGCENTSTKCNLSUYKFTS-----ASYIFRQAMNEY 323
OY 288 NTSFMSSEIKFDTLEAOFLPPVFNIRSLSDSFHYIIGAPKOSGNTPTVYIDYPLIETIIF 347
Db 324 SKSCLSKVEVDPPPTNIGPPGVKVDLSVDLLHFKIRPPGPGPKIMSDLYDSFQILY 383
OY 348 WENTSNAERKIIIEKTD--VTVPNLKFLTYCYKARAHYHDEKLKINSVSDAVC 400
Db 384 WKNSDNEEEVAMKETKOTIATVSDSLAPSTLYCYKVAQ--FSEAYNKSSDFSREEC 437

RESULT 2
ID 061190 PRELIMINARY; PRT; 349 AA.
AC 061190:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE CYTOKINE RECEPTOR FAMILY 2, MEMBER 4 (CLASS II CYTOKINE RECEPTOR 4).
GN IL10RB OR CRFB4 OR CRF2-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 71919375.
RA GIBBS V.C., PENNICA D.;
RT "CRF2-4: Isolation of cDNA clones encoding the human and mouse
RT proteins."
RL Gene 186:97-101(1997).
DR EMBL; U53696; AAC33062.1;
DR MGD; MG:109380; I1107b.
DR PFAM; PF00041; fn3; 1.
SQ SEQUENCE 349 AA; 39774 MW; 4AC1802A CRC32;

Query Match 10.1%; Score 216.5; DB 11; Length 349;
Best Local Similarity 28.4%; Pred. No. 8e-10; 79; Indels 27; Gaps
Matches 60; Conservative 45; Mismatches -----CKRSTACDSES 77
OY 7 POKVEVDIIDNFIILKRNRSDESQVNTSFSDYQ--KTGDMNMIKLSGCONITSTCNFS 64
Db 24 PEKYRNHVSFKNILNIDQVPAFPKNTLTFQAQESYRSFQD-----CKRSTACDSES 77
OY 65 SLKLNYEEIKLRIRAE-KENTSSWTEVDSFTFPKRAQIPEPVHLEAEKAVIHIS-- 122
Db 78 --HLSKGDTYVRRALADEHSWMVW--TFCEVEDTIIIPPEMQIESLAESLHRSAP 134
OY 122 -----PQTKOSVMMALDGL--SFYSLIKKNSGVERIENIYSRHKIKYLSPTETTYCL 174
Db 135 QIENEPEPT-----WTLKNITDSMAYIRQYKKNKNGINEFQVYSPDSEVLNLEPWTTCI 189
OY 175 KYRAALLTSWKIGVYSPVHCIKITVENELPP 205
Db 190 QVQGFLLDNQRTGEMSEPIC-ERTGNDIELP 219

RESULT 3
ID 063953 PRELIMINARY; PRT; 332 AA.
AC 063953:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA RECEPTOR BETA SUBUNIT).
GN IFNGR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE: 94170381.
RA HEMMI S., BONNI R., STARK G., DI MARCO F., AGUET M.;
RT "A novel member of the interferon receptor family complements
RT functionality of the murine interferon gamma receptor in human
RT cells.";
RL Cell 76:803-810(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-128SV/J.
RD MEDLINE: 97128072.
RA EBENSPPRGER C., RHEE S., MUTHUKUMARAN G., LEMBO D., DONNELLY R.,
RS PESTKA S., DEMBIC Z.;
RT "Genomic organization and promoter analysis of the gene Ifngr2
RT encoding the second chain of the mouse interferon-gamma receptor.";
RL Scand. J. Immunol. 44:599-606(1996).
DR EMBL: U69599; AAC52938.1; JOINED.
DR EMBL: U69594; AAC52938.1; JOINED.
DR EMBL: U69595; AAC52938.1; JOINED.
DR EMBL: U69596; AAC52938.1; JOINED.
DR EMBL: U69597; AAC52938.1; JOINED.
DR EMBL: U69598; AAC52938.1; JOINED.
DR EMBL: S69356; AAB30165.1; -.
DR GMD: MG1:107654; Ifng2.
DR PFAM: PF00041; fn3; 1.
SQ SEQUENCE 332 AA; 37471 MW; 0BF24B9E CRC32;

Query Match          9.3%; Score 199; DB 11; Length 332;
Best Local Similarity 30.1%; Pred. No. 1.9e-08;
Matches 65; Conservative 38; Mismatches 81; Indels 32; Gaps 12

QY 4 LN$POKVEVDIIDDNFLIKNRNDE$-----VGNTFSFDOKTGM-D-NWIKL--SGCQ 54
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 29 LAAPLNPRHLIYNDEOLINREPSNDPRVYYQVEYF$-----IDGSMHRLLEPNCT 82
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 55 NITSTCKNFSS---LKUNYE-EIKLRIRAEKEN-TSKTEVDSFTPFKRAQGPPE-VH 108
   ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 83 DIETKCDLLGGGRKLFPHPFTVFPLRVAKRGNLTSKWGLPFGHYENVTGVPPKNIS 142
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 109 LEADKATIVHTIPGRIKDSYMAALDGLSTFYSLILKNSGSVERIENTISRRKIY--KL 166
    : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 143 VPTGKGSLVIHFSPDPD----VFHGATFOYLIVHYEKSETGOOYDGPKSNSIYVLNL 197
    : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 167 SPETTCLAYKAA-LISWKI---GYVSPHCIKTT 198
   | ||| : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 198 KPYRYVLOTETAOLILKNKKIRPHGLLSNVSCHETT 233

RESULT 4
Q9YGC8 PRELIMINARY; PRT; 341 AA.
AC Q9YGC8;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR 2.
GN IL10R2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Archosauaria; Aves;
NC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RA REBOUL J., GARDIRER K., MONNERON D., UZE G., LUTPALIA G.;
RT "Comparative genomic analysis of the Interferon/Interleukin-10
RT Receptor gene cluster.";
RL Genome Res. 0:0-0(1999).
DR EMBL: AF082667; AAD13678.1; -.
DR EMBL: AF082666; AAD13671.1; -.
DR Receptor.
SQ SEQUENCE 341 AA; 39062 MW; 743D3D364 CRC32;
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RESULT 7
P97798 PRELIMINARY: PRT: 1493 AA.
AC P97798;
DT 01-MAY-1997 (TREMELREL. 03, Created)
DT 01-MAY-1997 (TREMELREL. 03, last sequence update)
DT 01-NOV-1999 (TREMELREL. 12, last annotation update)
DE NEOGENIN (NEOGENIN PROTEIN).
GN NEOL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97407661.
RA KEELING S.L., GAD J.M., COOPER H.M.;
RT "Mouse Neogenin, a DCC-like molecule, has four splice variants and is
expressed widely in the adult mouse and during embryogenesis."
RL Oncogene 15:691-700(1997).
DR EMBL: Y09535; CAAT7027.1; -
DR HSSP: P02751; 1TTC.
DR MGD: MGI:1097159; Neol.
DR PFAM: PF00041; fn3; 6.
DR PRINTS: PR00014; FNTYPEI1.
SQ SEQUENCE 1493 AA; 163159 MW; 98F26676 CRC32;

Query Match 5.8%; Score 125; DB 11; Length 1493;
Best Local Similarity 21.3%; Pred. No. 0.12;
Matches 86; Conservative 74; Mismatches 184; Indels 60; Gaps 20;

QY 6 SPOKVEVDIIDNFI-LRNR--SDSEVGNVTFSDYQKGMNMIKLSGCONITSTKCN 59
DB 472 APRVVASLSTFRFKIKLWRTSPASDPDGNLTYSIFTFKEGDR---ERVENISQGE 527
QY 59 --TTCNFSKLNYEEIKLIRAEKENTSSWEVDSTFPRKAOIGPEVHLEADKAI 116
DB 528 QVTIONLMPATVYIF-----KVMQNKHGSC---ESSAPLRVET--QPEVOLGPAPANI 576
QY 117 VIHISPTKDSVMAL---DGLSTYSLLIMKNSGVEERIENTYSHKIKYKSPETTY 172
DB 577 RAYATSPSTIVETWETPLSGNGEIONKLYWEKGTDEKODIDVSSHYTNGLKRYTEY 636
QY 173 CLKAKALITSMKIGVSPVHCITVTENELPPENIEVSQN--ONYVLK---DYTYAN 228
DB 637 SFRVVA--YKNHGPVSTQDVAVRFLSDVPSAAPONLSLEVRKSKSYIHKQPPSSITON 694
QY 229 --MTFOVOMLHAFILKRNPNHLLKMKQIPDCENVKTTCQVFPONVFCIGIYLLRVOASD 285
DB 695 GOITGKRRYKAKRSKSDVETLVTGTOL-----SGLI--BGLDRGTENFRVALT 744
QY 286 GNNT---SFWSEIKFDTETIAFLIPV---FNIRSLDSFHIYIGAPKOSGNPIVDY 339
DB 745 VNGTGPAIDWLSAETFEESDLETRVPEVPSLHVRLVTSI--VVSMTPEPQNI--VVRGY 802
QY 340 PLIYEIIFMENTNAER-KIIEKTDVTPNKLPLTVYCVKARA 382
DB 803 AIGIGI---GSPHAQTIKVDYKQRYTIENTLDPSSHYVITLKA 842

RESULT 8
Q90610 PRELIMINARY: PRT: 1443 AA.
AC Q90610;
DT 01-NOV-1996 (TREMELREL. 01, Created)
DT 01-NOV-1996 (TREMELREL. 01, last sequence update)
DT 01-NOV-1999 (TREMELREL. 12, last annotation update)
DE NEOGENIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LECHORN; TISSUE-BRAIN;
RX MEDLINE: 95105243.
RA VIELMEYER J., ROMAN J.M., DREYER W.J.;
RT "Neogenin, an avian cell surface protein expressed during terminal
neural differentiation, is closely related to the human tumor
suppressor molecule deleted in colorectal cancer."
RL J. Cell Biol. 127:2009-2020(1994).
DR EMBL: U07644; AAC59662.1; -
DR HSSP: P80362; 1WTL.
DR PFAM: PF00041; fn3; 6.
DR PFAM: PF00047; 19; 4.
FT NON_TER
SQ SEQUENCE 1443 AA; 158050 MW; 270B77DC CRC32;

Query Match 5.8%; Score 123.5; DB 13; Length 1443;
Best Local Similarity 22.0%; Pred. No. 0.15;
Matches 89; Conservative 60; Mismatches 194; Indels 61; Gaps 19;

QY 6 SPOKVEVDIIDNFI-LRNR--SDSEVGNVTFSDYQKGMNMIKLSGCONITSTKCN 62
DB 427 APRDVYATLVSTFRFKIKLWRTSPASDPDGNLTYSIFTFKEG---INREVEN-TSPGE 481
QY 63 FSLKLNVEEIKLIRAEKENTSSWEVDSTFPRKAOIGPEVHLEADKAIYIHSP 122
DB 482 TQVMIONLMPETVYVFRVVAQNKHGGE--SSAPLKVAT--QPEVOLGPAPANIRAYAGS 537
QY 123 GPKDSVMAL---DGLSTYSLLIMKNSGVEERIENTYSHKIKYKSPETTYCLKYKA 178
DB 538 PSTVATWETPLSGNGEIONKLYWEKGDSEQDVAGLSITTLGLKRYTEYSFRVVA 597
QY 179 ALLTSKIKVSPVHCITVTENELPPENIEVSQN--ONYVLKMDYTYANTFOVOMLH 237
DB 598 --YKNHGPVSTQDVAVRFLSDVPSAAPONLTLEARNKSIHLHQPPA----- 646
QY 238 AFLKRNPNHNL-----YKNKQIPDCENVKTTCQVFPQNTFO--KGI-----YLLRVOASD 285
DB 646 -----GTHSGQITGKIRYKRSKSDVETSGTOLFOLIEGTERENFRVLAAT 698
QY 286 GNNT---SFWSEIKFDTETIAFLIPV---FNIRSLDSFHIYIGAPKOSGNPIVDY 339
DB 699 VNGTGPAIDWLSAETFEESDLETRVPEVPSLHVRLVTSI--VVSMTPEPQNI--VVRGY 756
QY 340 PLIYEIIFMENTNAER-KIIEKTDVTPNKLPLTVYCVKARA 382
DB 757 AIGIGI---GSPHAQTIKVDYKQRYTIENTLDPSSHYVITLKA 796

RESULT 9
Q94537 PRELIMINARY: PRT: 1375 AA.
AC Q94537;
DT 01-FEB-1997 (TREMELREL. 02, Created)
DT 01-FEB-1997 (TREMELREL. 02, last sequence update)
DT 01-NOV-1999 (TREMELREL. 12, last annotation update)
DE FRAZZLED.
GN FRAZZLED.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97015076.
RA KOTLOZIER P.A., TIMPE L., MITCHELL K.J., GOODMAN C.S., FRIED S.,
VAN L.Y., VAN Y.N.;
RT "Frazzled encodes a Drosophila member of the DCC immunoglobulin
subfamily and is required for CNS and motor axon guidance."
RL Cell 87:197-204(1996).
DR EMBL: U71001; AAC47314.1; -
DR FLYBASE: FBgn0011592; fra.
DR PFAM: PF00041; fn3; 6.

DR PFAM: PF00047; 19; 3.
 DR PRINTS: PR00014; FNTYPE11.
 SQ SEQUENCE 1375 AA; 151692 MW; 43806DBC CRC32;

Query Match 5.7%; Score 123; DB 5; Length 1375;
 Best Local Similarity 16.3%; Pred. No. 0.15;
 Matches 101; Conservative 68; Mismatches 184; Indels 268; Gaps 22;

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QY 1 GKMLKS-----POKEVDIIDDNFI-LRW-----NRSDSVG 31
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 448 GKRLDGLQARLPSPQRLDVAQIVKSRFTLSMVEPLQAGDVVYTYKKNNSEBOK 507
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 32 NTFESFDYOKTGMNWKIKSGCONITSTKCNFS-----LKLNYEEIKLR-----78
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 508 MYTKSHDDQVNIQSILPGRTYQFRVEANTNFGSASAPLEVSTQPEVNIAGPPRNFEG 567
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 78 -IRAENKSSWYE-----VD 92
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 568 YARSHKEIYKKEEPTVTNGEILKRYVYSENDGADLYHDSTALEAVLTLPHTDYI 627
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 93 SEFPKKAQIG-----PREVHLE-AEDKAIYIHISPGTKDSVMALD 133
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 628 SYVPEFRNGMGDSASAEIRKFTSPSEPNNVTLEVTSSSITVHMEPPAEDRNGQIT 687
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 134 GLSFTYSLIMKNSGVEERIENTYSRHKIYKLSPEPTYCLVKKALL-----TSWKIG 187
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 688 GKIRIRYK--FKDAPQVKSTPANI-RYFELSLNDRNAEYQVIAAMTVNGSGPTEMNRA 744
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 188 VSPVHCITTYENELP-----PENIEVSQNONVYK 222
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 745 -----NTLENDLDETQVPGKPIWISHPGANNIALHMGPPQHPKIKI--RNYVLGW 793
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 223 -----DY-----225
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 794 GRGIPDENTIELKETERHYILKNLESMDYVYSLARANYKGGPPHYDNKTRDEPVA 853
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 225 -----TYANMTFOVOMLHAFILKN-----PGNHLTKKQIPD 256
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 854 PPLEVPVGLRAITWSSSIYVYIMIDMLNKHQVTDNRHYTVSYGIGSNRYR-----909
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 257 CENVKTCQVFPQNFQKGIYLLRYQASDGNNTSPMSEIEKFDTELQAFLLPVPVFNIRSL 316
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 909 -HNTDLNCKI-NDLRPNTOYEFPAVKVYKGRSSMSVSLNSTYQNVPTP-----960
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 317 SDSFHYIGAPKOSGNTPIQDYP-----LIYEIIEMENTSNAER-----KIIIEKT 363
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 960 ---REVTVRLDEMNPPYIVQWIPPKHILGOITGINIYTTDTTKRDROMSVFAFGEET 1016
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 364 DVTVPNLKPLTYCVKARAHNT 384
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1017 MLMPLNLKPYTYFFKVOART 1037
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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RESULT 10

094538 PRELIMINARY; PRT; 1526 AA.
 AC 094538;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE FRAZZLED.
 GN
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97015076.
 RA KOLODZIEJ P.A., TIMPE L., MITCHELL K.J., GOODMAN C.S., FRIED S.,
 RA JAN L.Y., JAN Y.N.;
 RT "frazzled encodes a Drosophila member of the DCC immunoglobulin

RT subfamily and is required for CNS and motor axon guidance.";
 DR Cell 87:197-204(1996).
 DR EMBL; U71002; AAC47315.1;
 DR FLYBASE; FBgn0011592; fra.
 DR PFAM: PF00041; fn3; 6.
 DR PFAM: PF00047; 19; 3.
 DR PRINTS: PR00014; FNTYPE11.
 SQ SEQUENCE 1526 AA; 168787 MW; F17B1EC9 CRC32;

Query Match 5.7%; Score 123; DB 5; Length 1526;
 Best Local Similarity 16.3%; Pred. No. 0.18;
 Matches 101; Conservative 68; Mismatches 184; Indels 268; Gaps 22;

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QY 1 GKMLKS-----POKEVDIIDDNFI-LRW-----NRSDSVG 31
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 599 GKRLDGLQARLPSPQRLDVAQIVKSRFTLSMVEPLQAGDVVYTYKKNNSEBOK 658
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 32 NTFESFDYOKTGMNWKIKSGCONITSTKCNFS-----LKLNYEEIKLR-----78
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 659 MYTKSHDDQVNIQSILPGRTYQFRVEANTNFGSASAPLEVSTQPEVNIAGPPRNFEG 718
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 78 -IRAENKSSWYE-----VD 92
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 719 YARSHKEIYKKEEPTVTNGEILKRYVYSENDGADLYHDSTALEAVLTLPHTDYI 778
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 93 SEFPKKAQIG-----PREVHLE-AEDKAIYIHISPGTKDSVMALD 133
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 779 SYVPEFRNGMGDSASAEIRKFTSPSEPNNVTLEVTSSSITVHMEPPAEDRNGQIT 838
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 134 GLSFTYSLIMKNSGVEERIENTYSRHKIYKLSPEPTYCLVKKALL-----TSWKIG 187
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 839 GKIRIRYK--FKDAPQVKSTPANI-RYFELSLNDRNAEYQVIAAMTVNGSGPTEMNRA 895
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 188 VSPVHCITTYENELP-----PENIEVSQNONVYK 222
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 896 -----NTLENDLDETQVPGKPIWISHPGANNIALHMGPPQHPKIKI--RNYVLGW 944
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 223 -----DY-----225
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 945 GRGIPDENTIELKETERHYILKNLESMDYVYSLARANYKGGPPHYDNKTRDEPVA 1004
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 225 -----TYANMTFOVOMLHAFILKN-----PGNHLTKKQIPD 256
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1005 PPLEVPVGLRAITWSSSIYVYIMIDMLNKHQVTDNRHYTVSYGIGSNRYR-----1060
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 257 CENVKTCQVFPQNFQKGIYLLRYQASDGNNTSPMSEIEKFDTELQAFLLPVPVFNIRSL 316
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1060 -HNTDLNCKI-NDLRPNTOYEFPAVKVYKGRSSMSVSLNSTYQNVPTP-----1111
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 317 SDSFHYIGAPKOSGNTPIQDYP-----LIYEIIEMENTSNAER-----KIIIEKT 363
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1111 ---REVTVRLDEMNPPYIVQWIPPKHILGOITGINIYTTDTTKRDROMSVFAFGEET 1167
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 364 DVTVPNLKPLTYCVKARAHNT 384
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1168 MLMPLNLKPYTYFFKVOART 1188
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

```

RESULT 11

092859 PRELIMINARY; PRT; 1461 AA.
 AC 092859;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE NEOGENIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN
 RP SEQUENCE FROM N.A.
 RA MEYERHARDT J.A., LOOK A.T., BIGNER S.H., FEARON E.R.;

RL Oncogene 0:0-0(0).
 DR EMBL: U61262; AAB17263.1; -
 DR HSSP: P02751; 1TTG.
 DR PFAM: PF00041; fn3; 6.
 DR PFAM: PF00047; 19; 4.
 DR PRINTS: PR00014; FNTYPEII.
 SO SEQUENCE 1461 AA; 159958 MW; 0AB7247E CRC32;

Query Match 5.78; Score 121; DB 4; Length 1461;
 Best Local Similarity 20.8%; Pred. No. 0.24;
 Matches 83; Conservative 77; Mismatches 188; Indels 52; Gaps 19;

QY 6 SPOKVEVDIIDDNFI-LRMN--RSDSVGNVTFSPDYQKTM--DNMILKSGCONITSTK 60
 DB 441 APRDVAVSLVSTRFKILMTTPASDPHGDNLTYSVYTKEGIANERENTSHPEGMOYTI 500
 QY 61 CNFSLKLVYEEIKLRIRAEKENTSSWYVDSTPFRKAQIGPPEVHLEADKAIVIH 120
 DB 501 ONLMPATVYIF-----RVMAQNKHGSG-----ESSAPLRVET--QPEVQLPGPAPNLRAYA 549
 QY 121 SPTKSDVMMAL----DGLSTTISLLIMKNSGVEERENIYSHKIIYKLSPTTYCLKV 176
 DB 550 ASPTSTIVTETWPVSGNGEIONKLYMEKGTDEKODVDVSSHSTYINGLKKYTEYSFRV 609
 QY 177 KAALLTSMKIGVSPVHCITKTVENELPPENIEVSQN--ONYLKWMD-----ITYANMT 230
 DB 610 VA--YKNGHGVSTPDVAVRTLSDVPSAAPONLSLEVRANSKSMIMHOPAPATONCOIT 667
 QY 231 -FOVOMLHAFKRNPNHLYKWKQIPDCENVKTQCVFPONVFOKGIYLLRVQASDGNNT 289
 DB 668 GYKIRYRKASRKSVDVETLVSGTQ-----SGLI--EGLDRGTEYNEFRVALTINGT 717
 QY 290 ---SFNSEIKFDTETQAFLLPV---FNIRSLDSFHIIYGAKOSGNTPIYIDYPLIY 343
 DB 718 GPATDMLSAETFEESDLETRVPEVPSLHVRLVTSI--VSWTPPENONI--VVRGVAIGY 775
 QY 344 EIFFMENTSNAER-KIIEKTDVTPVNLKPLTVYCVKARA 382
 DB 776 GI-----GSPHAQTIKVDKORYTIENLDPSSHYITLKA 811

RESULT 12
 ID 000340 PRELIMINARY; PRT: 1461 AA.
 AC 000340;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE NEUGENIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-BRAIN;
 RC MEDLINE: 97312699.
 RA VIELMEIJER J., CHENG X.N., MISKEYICH F., LANE R.P., YAMAKAWA K.,
 RA KOENIGBERG J.R., DREYER W.J.;
 RT "Molecular characterization of human neogenin, a DCC-related protein,
 RT and the mapping of its gene (NEO1) to chromosomal position 15q22.3-
 RT q23."
 RL Genomics 41:414-421(1997).
 DR EMBL: U72391; AAC51287.1; -
 DR HSSP: P02751; 1TTG.
 DR PFAM: PF00041; fn3; 6.
 DR PFAM: PF00047; 19; 4.
 DR PRINTS: PR00014; FNTYPEII.
 SO SEQUENCE 1461 AA; 160015 MW; 9D5AE1C4 CRC32;

Query Match 5.78; Score 121; DB 4; Length 1461;
 Best Local Similarity 20.8%; Pred. No. 0.24;

Matches 83; Conservative 77; Mismatches 188; Indels 52; Gaps 19;

QY 6 SPOKVEVDIIDDNFI-LRMN--RSDSVGNVTFSPDYQKTM--DNMILKSGCONITSTK 60
 DB 441 APRDVAVSLVSTRFKILMTTPASDPHGDNLTYSVYTKEGIANERENTSHPEGMOYTI 500
 QY 61 CNFSLKLVYEEIKLRIRAEKENTSSWYVDSTPFRKAQIGPPEVHLEADKAIVIH 120
 DB 501 ONLMPATVYIF-----RVMAQNKHGSG-----ESSAPLRVET--QPEVQLPGPAPNLRAYA 549
 QY 121 SPTKSDVMMAL----DGLSTTISLLIMKNSGVEERENIYSHKIIYKLSPTTYCLKV 176
 DB 550 ASPTSTIVTETWPVSGNGEIONKLYMEKGTDEKODVDVSSHSTYINGLKKYTEYSFRV 609
 QY 177 KAALLTSMKIGVSPVHCITKTVENELPPENIEVSQN--ONYLKWMD-----ITYANMT 230
 DB 610 VA--YKNGHGVSTPDVAVRTLSDVPSAAPONLSLEVRANSKSMIMHOPAPATONCOIT 667
 QY 231 -FOVOMLHAFKRNPNHLYKWKQIPDCENVKTQCVFPONVFOKGIYLLRVQASDGNNT 289
 DB 668 GYKIRYRKASRKSVDVETLVSGTQ-----SGLI--EGLDRGTEYNEFRVALTINGT 717
 QY 290 ---SFNSEIKFDTETQAFLLPV---FNIRSLDSFHIIYGAKOSGNTPIYIDYPLIY 343
 DB 718 GPATDMLSAETFEESDLETRVPEVPSLHVRLVTSI--VSWTPPENONI--VVRGVAIGY 775
 QY 344 EIFFMENTSNAER-KIIEKTDVTPVNLKPLTVYCVKARA 382
 DB 776 GI-----GSPHAQTIKVDKORYTIENLDPSSHYITLKA 811

RESULT 13
 ID 091562 PRELIMINARY; PRT: 1427 AA.
 AC 091562;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE TUMOR SUPPRESSOR.
 GN XPCCA.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
 CC Batrachia; Anura; Mesobatrachia; Pipridae; Xenopodinae;
 CC Xenopus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95113183.
 RA PIERCEBALI W.E., REALE M.A., CANDIA A.F., WRIGHT C.V., CHO K.R.,
 RA FEARON E.R.;
 RT "Expression of a homologue of the deleted in colorectal cancer (DCC)
 RT gene in the nervous system of developing xenopus embryos."
 RL Dev. Biol. 166:654-665(1994).
 DR EMBL: U10986; AAT0168.1; -
 DR HSSP: P56276; 1TLK.
 DR PFAM: PF00041; fn3; 6.
 DR PFAM: PF00047; 19; 4.
 DR PRINTS: PR00014; FNTYPEII.
 SO SEQUENCE 1427 AA; 156533 MW; E50B7475 CRC32;

Query Match 5.58; Score 117.5; DB 13; Length 1427;
 Best Local Similarity 22.2%; Pred. No. 0.44;
 Matches 93; Conservative 70; Mismatches 163; Indels 93; Gaps 22;

QY 6 SPOKVEVDIIDDNFI-LRMN--RSDSVGNVTFSPDYQKTM--DNMILKSGCONITSTKCNF 63
 DB 431 APRDVAVSLVSTRFKILMTTPASDPHGDNLTYSVYTKEGIANERENTSHPEGMOYTI 484
 QY 64 SSKLVN-----YEEIKLRIRAEKENTSSWYVDSTPFR-----KAQIGPPEVHLEAD 113
 DB 484 -SLQITVGNLTPETVYFRVAYANE-----WGPBSSQEVKVVYQPELVQGVPEVNILO--- 536
 QY 114 KATVTHISPTKSDVMMALDGLSTF-----YSLIMKNSGVEERENIYSHKIIYKLS 167

Db 536 ---VSTAP---TSVLISMDPPAYANGPVOCYILFCAETFSGREQINTEVDGIYRLGLR 589
Qy 168 PETTYCLKYKALLTSMKIVSPVHCIKTTVENELPPENIEVSQONONYLKNDYTA 227
Db 590 KFEYSIRVLA--YNRGCGVSESEHTVTLSPVSAMQONVLEVAN----- 636
Qy 228 NMTFOVOMLHAFKRNPNHNL-----YKMKQIPDCENVKT-----OCVFPONVF----- 273
Db 636 SRSIKVSW---LPPEPGTONGFITGYK-----IRHRTKTRGELETLEPNLWLYFTG 685
Qy 273 -OKGI-YLLRYOASDGNNTSFMSEIKFDT-----EIQAFLLPPVFNRLSDSHIYI 324
Db 686 LEKGSQISQVAAATVNGGSPSSDWTATFEPENDLDESQVDPQPSLHVRPLTTSI-INS 744
Qy 325 GAPKOSGNTPVIODYPLIYEIIFMENTSNAER-KIIEKTDVTPVNLKPLTYCVKARA 382
Db 745 WPPPLNPNL-VVRGVIIGIV-----GSPYAEYVRVDSKORYSIENLEPSSHIVISLKA 798

RESULT 14
ID 017859 PRELIMINARY: PRT: 1585 AA.
AC 017859: Q20137:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE C09D8.1 PROTEIN.
GN C09D8.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabdilita; Rhabdilitida;
OC Rhabdilita; Rhabdilitidae; Rhabdilitidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA COLES L.
RL Submitted (NOV-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: Z46811; CA86842.1; -
DR EMBL: Z49938; CA86842.1; JOINED.
DR EMBL: Z49938; CA86842.1; JOINED.
DR EMBL: Z46811; CA90189.1; JOINED.
DR HSP: P28827; 1RP.
DR PFM: PF00041; fn3; 3.
SQ SEQUENCE 1585 AA; 178386 MW; E403A8DD CRC32;

Query Match 5.5%; Score 117.5; DB 5; Length 1585;
Best Local Similarity 19.7%; Pred. No. 0.51;
Matches 86; Conservative 74; Mismatches 171; Indels 105; Gaps 24;

Qy 7 POKVEVDIIDNFIKMNRSDES- GNVTFSEYOKTGMWIKLSCGONITSTKCNFS 64
Db 263 PIDVGEVAKKIVSWRPSEKRNIT-SYKALISMD-ATADRYEQVPAPSTSS 319
Qy 65 SIKLVYEEIKLRIR-----EKNTSSYEV---D 92
Db 320 TEEVNRAYLFKVAATKKGIPSPVLINPDADLIDNNEIEENQDGEKTMEE 379
Qy 93 SFTPFKAQIGPEVLEAEKAIYHISPGTKDSYVMAALDGLSFYSLILKNSGVEE 152
Db 380 NNNPKKSIKSTADY-----SALIHANP-----LTHISALAKAKATTGA 423
Qy 153 RIENIYSRKIKYKSPETTYCLKVKAALLTSMKIVSPVHCIKTTVENELPPENIEV- 212
Db 424 PVPAPYTTTS---TPSTLFFQVTLFPMTTAMN-----RYTKLETLVGPPTVAYE 470
Qy 212 SYQONONYVKKMDYTYANM-TFOVOMLHAFKRNPNHNL---YKMKQIP-----DCENKTKQ 264
Db 471 AISNSNAVVOQMPDESOKADSFVVKIWH-----EPGNRMDEKMKQPLVVSIDENKRA 525
Qy 265 CVFPONVFOKGIYLLRVQASDGNNTSFMSEIEIKFDEIOAFLLPVPFNIRSL-----SD 318
Db 526 VVSDLNANRP--YAFCVLAVKNNRQPCSDP---PTVLES--VTPIYMQNLRLMKTSN 578

Qy 319 SFHI---YIGAKQSG---NPEVIODYPLIYEIIFMENTSNAE---KIIEKTDVTPVN 369
Db 579 SVQLTWEYNG-PRNFGFYNNHTRGRDY-VNHEL--QEKTMSTPGQGVDEKHEVLTN 634
Qy 370 LKPLTYCVKARAHNM 385
Db 635 LRPHMYTILHVGRTIL 650

RESULT 15
ID 092673 PRELIMINARY: PRT: 2214 AA.
AC 092673: Q92856;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN LR11 PRECURSOR (LR11).
GN LR11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA MOERWALD S., YAMAZAKI H., BUJO H., KUSUNOKI J., KANANI T., SEIMIYA K.,
RA MORISAKI N., NIMPE J., SCHNEIDER W.J., SAITO Y.;
RL Arterioscler. Thromb. Vasc. Biol. 17:996-1002(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 97094912.
RA JACOBSEN L., MADSEN P., MOESTRUP S.K., LUND A.H., TOMMERUP N.,
RA NYKJAER A., SOTTRUP-JENSEN L., GLEIMANN J., PETERSEN C.M.;
RT "Molecular characterization of a novel human hybrid-type receptor that
RL binds the alpha2-macroglobulin receptor-associated protein.";
RL J. Biol. Chem. 271:31379-31383(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA JACOBSEN L., MADSEN P., LUND A.H., TOMMERUP N., GLEIMANN J.,
RA PETERSEN C.M.;
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: LIKELY TO BE A MULTIFUNCTIONAL RECEPTOR. BINDS LDL, THE
CC MAJOR CHOLESTEROL-CARRYING LIPOPROTEIN OF PLASMA, AND TRANSPORTS
CC IT INTO CELLS BY ENDOCYTOSIS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN BRAIN, LIVER, KIDNEY AND PANCREAS
CC WITH DETECTABLE LEVELS IN PLACENTA, LONG AND HEART.
CC -1- SIMILARITY: CONTAINS 11 LDL-RECEPTOR CLASS A DOMAINS.
CC EMBL: Y08110; CA69325.1; -
DR EMBL: U60975; AAC50891.2; -
DR HSP: P01130; 1A0J.
DR PROSITE: PS01209; LDLRA_1; 10.
DR PFM: PF00057; ldl_recept_a; 11.
DR PFM: PF00058; ldl_recept_b; 4.
DR PFM: PF00041; fn3; 5.
DR PRINTS: PR00261; LDLRECEPTOR.
DR PRINTS: PR00014; FNTYPEPIT1.
KM Receptor; Transmembrane; Signal; Repeat; Glycoprotein; LDL;
KW Cholesterol metabolism; Lipid transport.
FT SIGNAL 1 28
FT CHAIN 29 2214
FT DOMAIN 29 2135
FT DOMAIN 1076 1114 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 1115 1155 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 1156 1194 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 1197 1226 LDL-RECEPTOR CLASS A 4.
FT DOMAIN 1233 1285 LDL-RECEPTOR CLASS A 5.
FT DOMAIN 1287 1317 LDL-RECEPTOR CLASS A 6.
FT DOMAIN 1323 1361 LDL-RECEPTOR CLASS A 7.
FT DOMAIN 1366 1405 LDL-RECEPTOR CLASS A 8.

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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:17:57 ; Search time 12.38 seconds
(without alignments)
834,180 Million cell updates/sec

Title: US-09-240-675-2
Perfect score: 2313
Sequence: 1 MMVVLGATTLVAVGPWV.....KSVFSDAVCEKTPGNTSK 436

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues
Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2313	100.0	R14487	Soluble Interferon
2	2313	100.0	R28495	Sequence of a soul
3	2313	100.0	R11958	Human alpha-interf
4	2313	100.0	R14488	Complete Interfero
5	2313	100.0	R28496	Sequence of a soul
6	2313	100.0	R42635	Human Interferon r
7	2309	99.8	R75356	Human IFN receptor
8	2308	99.8	R21804	Transmembranal int
9	2304	99.6	R11723	IFN receptor extra
10	2260	97.7	R21805	Spliced-deleted in
11	2208	95.5	R21806	Spliced-deleted in
12	228.5	9.9	R52296	CRFB4 protein. New
13	203	8.8	R75282	IFN-gamma receptor
14	198	8.6	R79155	cytor7 cytokine r
15	155.5	6.7	R71035	Human IFN-gamma ac
16	153.5	6.6	R75783	IFN-gamma receptor
17	151	6.5	R97861	Human cytokine rec
18	131.5	5.7	R7864	Human cytokine rec
19	118.5	5.1	R70113	Gamma-IFN-R-GBP 13
20	118	5.1	R16442	Gamma interferon r
21	118	5.1	R14641	Gamma interferon r
22	118	5.1	R55749	Extracellular doma
23	118	5.1	R07469	Plasmod pABLU hu
24	118	5.1	R83147	Rat receptor tyros
25	117.5	5.1	R57139	Interleukin-10 rec
26	117.5	5.1	R57139	Mouse IL-10 recept
27	117.5	5.1	R41803	Human LDL receptor
28	115.5	5.0	R26357	Gamma Interferon r
29	114.5	5.0	R14643	Soluble human inte
30	113.5	4.9	R62023	Deleted in Colorec
31	111.5	4.8	R13144	Human Down syndrom
32	111.5	4.8	R43087	Human Down syndrom
33	110	4.8	R43086	Rabbit LDL receptor
34	108	4.7	R85090	EPH-like receptor

35	107	4.6	426	1	W09822	Human Interleukin-
36	107	4.6	427	1	W24973	Human Interleukin-
37	107	4.6	753	1	W83927	Human r85 protein.
38	107	4.6	1370	1	P60005	Sequence encoded b
39	106.5	4.6	928	1	R97853	Rat RKR7 eph-relat
40	105.5	4.6	400	1	R75203	Tyrosine phosphata
41	105.5	4.6	878	1	R78608	Murine IL-3 recept
42	104.5	4.5	596	1	R78616	Expression vector
43	104.5	4.5	600	1	R78610	Expression vector
44	104.5	4.5	600	1	R25226	Fas antigen #1. Im
45	104.5	4.5	660	1	R69633	Human Interleukin-

ALIGNMENTS

RESULT 1	R14487	R14487 standard; Protein: 436 AA.
ID	R14487	
AC	R14487	
DE	16-JAN-1992 (first entry)	
KW	Soluble Interferon-alpha/beta receptor.	
OS	IFN; autoimmune disease; graft rejection; histocompatibility.	
KM	Homo sapiens.	
PN	FR2657881-A.	
PD	09-AUG-1991.	
PF	05-FEB-1990; 001298.	
PR	05-FEB-1990; FR-001298.	
PA	(EUBI-) LAB EURO BIOTECHNO.	
PI	Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;	
PI	Tovey MG. Use G;	
DR	WPI, 91-31978/44.	
DR	N-PSDB: Q14239.	
PT	New water-soluble polypeptide(s) with affinity for IFN-alpha and	
PT	beta - used to treat e.g. lupus erythematosus, Behcet's disease,	
PT	aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.	
PS	Claim 2; Page 45; 52pp; French.	
CC	The transmembrane and cytoplasmic domains of the native IFN receptor	
CC	have been deleted to obtain a soluble, circulating form of the	
CC	receptor. Potentially immunogenic epitopes have thus been eliminated.	
CC	Derivatives obtained by substitution or deletion of this sequence	
CC	are also claimed as are hybrid molecules comprising the soluble	
CC	receptor (or deriv.) and an immunoglobulin such as IgG1.	
CC	See also Q14240.	
CC	Sequence 436 AA:	
SO		

Query Match 100.0%; Score 2313; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.3e-203;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MMVVLGATTLVAVGPWVLSAAGGKLNKSPKVEVDIIDDNFLLRMNSDESVCNVT	60
DB	1	MMVVLGATTLVAVGPWVLSAAGGKLNKSPKVEVDIIDDNFLLRMNSDESVCNVT	60
QY	61	FSPDYQKGMNWKLSGCONITSTKCNFSLKNVVEIKLRRAEKENTSSVYEYDSF	120
DB	61	FSPDYQKGMNWKLSGCONITSTKCNFSLKNVVEIKLRRAEKENTSSVYEYDSF	120
QY	121	TPFRKAQIGPEVHLEADKAIVIHISPGTDSVMALDGSFTYSLLIMKNSGVEERI	180
DB	121	TPFRKAQIGPEVHLEADKAIVIHISPGTDSVMALDGSFTYSLLIMKNSGVEERI	180
QY	181	ENIYSRHKIYKLSPEPTYCLAVKAAALTSKIGIVSPVHCIKTYVENLPPENIEVSQ	240
DB	181	ENIYSRHKIYKLSPEPTYCLAVKAAALTSKIGIVSPVHCIKTYVENLPPENIEVSQ	240
QY	241	NONVYLKMDYTAANNTPQVOMHAFLKRNPGNHLKKMOIPDCEVNTQCFPQNVOK	300
DB	241	NONVYLKMDYTAANNTPQVOMHAFLKRNPGNHLKKMOIPDCEVNTQCFPQNVOK	300
QY	301	GYLLRVQASDGNNTSFWESEIKFDEIOAFLPPVFNIRLSDSFHIYIGAPKOSGNT	360
DB	301	GYLLRVQASDGNNTSFWESEIKFDEIOAFLPPVFNIRLSDSFHIYIGAPKOSGNT	360

Db 301 GYLLRVOASDGNNTSFWSSEIKFDTEIOAFLLPVPFNIRSLSDSFHIIYGAPKQSGNTP 360
QY 361 VIODYPLIYEIIIFWENTSNAERKIIKKTDVTPVNLKPLTVYCVKARAHMDEKLKSSV 420
Db 361 VIODYPLIYEIIIFWENTSNAERKIIKKTDVTPVNLKPLTVYCVKARAHMDEKLKSSV 420
QY 421 FSDAVCEKTPGNTSK 436
Db 421 FSDAVCEKTPGNTSK 436

RESULT 2

R28495
ID R28495 standard; Protein; 436 AA.
AC R28495;
DT 31-MAR-1993 (first entry) 1
DE Sequence of a soluble form of the interferon (IFN) receptor
KW With a high affinity for IFN-alpha and -beta.
OS Interferon receptor; alpha-interferon; beta-interferon.
PN Synthetic.
PM WO9218626-A.
PD 29-OCT-1992.
PF 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE.
PI Toyey M, Uze G;
DR WPI: 92-382110/46.
DR N-PSDB: Q30532.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
PT diseases and transplant rejection
PS Claim 2; Fig 1; 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
CC IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template. For example,
CC bacteriophage lambda ZAP, containing the entire coding sequence of
CC the IFN-alpha and -beta receptor (Q30533), was incubated with Oligos
CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
CC lacks the transmembrane and cytoplasmic domains. Both forms bind
CC IFN in the same way as antibodies so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SO Sequence 436 AA;

Query Match 100.0%; Score 2313; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.3e-203;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVVLGATTLLVAVGPVWLSAAGGNLKSPOKVEVDIIDNFIILRNRSDESIGNVT 60
Db 1 MMVVLGATTLLVAVGPVWLSAAGGNLKSPOKVEVDIIDNFIILRNRSDESIGNVT 60
QY 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSKLNVYEIKLRIRAEKENTSSWYEVDSF 120
Db 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSKLNVYEIKLRIRAEKENTSSWYEVDSF 120
QY 121 TPFRAQOIGPPEVHLEADKAIVIHISPGTDSVMALDGLSFYISLLIMKSSGVEERI 180
Db 121 TPFRAQOIGPPEVHLEADKAIVIHISPGTDSVMALDGLSFYISLLIMKSSGVEERI 180
QY 181 ENIYSRHKIYKLSPEYTCCLKVKAALLTSWKIGYSPVHCITTYENELPPENIEVSQ 240
Db 181 ENIYSRHKIYKLSPEYTCCLKVKAALLTSWKIGYSPVHCITTYENELPPENIEVSQ 240
QY 241 NONVYLKMDTYAANTFOVOMLHAFLKRNPNHLYKKKQIPDCENVTTCQCFPQNTFOK 300
Db 241 NONVYLKMDTYAANTFOVOMLHAFLKRNPNHLYKKKQIPDCENVTTCQCFPQNTFOK 300
QY 301 GYLLRVOASDGNNTSFWSSEIKFDTEIOAFLLPVPFNIRSLSDSFHIIYGAPKQSGNTP 360
Db 301 GYLLRVOASDGNNTSFWSSEIKFDTEIOAFLLPVPFNIRSLSDSFHIIYGAPKQSGNTP 360

QY 361 VIODYPLIYEIIIFWENTSNAERKIIKKTDVTPVNLKPLTVYCVKARAHMDEKLKSSV 420
Db 361 VIODYPLIYEIIIFWENTSNAERKIIKKTDVTPVNLKPLTVYCVKARAHMDEKLKSSV 420
QY 421 FSDAVCEKTPGNTSK 436
Db 421 FSDAVCEKTPGNTSK 436

RESULT 3

R11958
ID R11958 standard; Protein; 557 AA.
AC R11958;
DT 18-JUL-1991 (first entry)
DE Human alpha-interferon receptor protein.
KW Human alpha IFN; IFN agonists; antiviral; anti tumour agent;
OS Homo sapiens.
PN Key
PM WO9105862-A.
PD 02-MAY-1991.
PF 19-OCT-1990; F00758.
PR 20-OCT-1989; FR-013770.
PA (CNRS) CNRS CENT NAT RECH SCI.
PI Mogensen KE, Uze G, Lutfalla G, Gresser I;
PI WPI: 91-148740/20.
DR N-PSDB: Q11701.
PT New human alpha-interferon receptor protein - useful for testing
PT Interferon agonists and in treatment or diagnosis
PS Disclosure: fig 4; 30pp; French.
CC This recombinant human alpha interferon (IFN) receptor protein is
CC useful for the testing of IFN agonists and for treatment and diag-
CC nosis of viral diseases and tumours. Antibodies raised against
CC this protein can be used for blocking the receptor when required,
CC eg where overexpression of alpha-IFN is harmful. The Abs are
CC also useful for eg drug targeting. Variants of the protein,
CC having residue 164 (Thr) replaced by Arg and an Asp inserted
CC between residues 479 and 480, are also useful.
SO Sequence 557 AA;

Query Match 100.0%; Score 2313; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.3e-203;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVVLGATTLLVAVGPVWLSAAGGNLKSPOKVEVDIIDNFIILRNRSDESIGNVT 60
Db 1 MMVVLGATTLLVAVGPVWLSAAGGNLKSPOKVEVDIIDNFIILRNRSDESIGNVT 60
QY 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSKLNVYEIKLRIRAEKENTSSWYEVDSF 120
Db 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSKLNVYEIKLRIRAEKENTSSWYEVDSF 120
QY 121 TPFRAQOIGPPEVHLEADKAIVIHISPGTDSVMALDGLSFYISLLIMKSSGVEERI 180
Db 121 TPFRAQOIGPPEVHLEADKAIVIHISPGTDSVMALDGLSFYISLLIMKSSGVEERI 180
QY 181 ENIYSRHKIYKLSPEYTCCLKVKAALLTSWKIGYSPVHCITTYENELPPENIEVSQ 240
Db 181 ENIYSRHKIYKLSPEYTCCLKVKAALLTSWKIGYSPVHCITTYENELPPENIEVSQ 240
QY 241 NONVYLKMDTYAANTFOVOMLHAFLKRNPNHLYKKKQIPDCENVTTCQCFPQNTFOK 300
Db 241 NONVYLKMDTYAANTFOVOMLHAFLKRNPNHLYKKKQIPDCENVTTCQCFPQNTFOK 300
QY 301 GYLLRVOASDGNNTSFWSSEIKFDTEIOAFLLPVPFNIRSLSDSFHIIYGAPKQSGNTP 360
Db 301 GYLLRVOASDGNNTSFWSSEIKFDTEIOAFLLPVPFNIRSLSDSFHIIYGAPKQSGNTP 360
QY 361 VIODYPLIYEIIIFWENTSNAERKIIKKTDVTPVNLKPLTVYCVKARAHMDEKLKSSV 420

Db 361 VIQDPLIYEITFEIIFMENTSNAERKIIIEKTDVTPNKLPLTYCVKARAHITMDEKLKSSV 420
QY 421 FSDAVCEKTRPGNTSK 436
Db 421 FSDAVCEKTRPGNTSK 436

RESULT 4
R14488
ID R14488 standard; Protein: 557 AA.
AC R14488:
DT 16-JAN-1992 (first entry)
DE Complete interferon-alpha/beta receptor.
KW IFN; autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 437..457
FT /label= transmembrane
FT 458..557
FT /label= cytoplasmic
FN FR2657881-A.
PN 09-AUG-1991.
PD 05-FEB-1990; 001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Toyey MG, Uze G;
PI MPI: 91-319778/44.
DR N-PSDB: Q14240.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Disclousure: Page 47; 52pp; French.
CC The invention covers derivatives of the interferon-alpha and/or beta
CC receptor obtained by deleting the transmembrane and cytoplasmic domains
CC of the native receptor or by substitution. Potentially immunogenic
CC epitopes are eliminated and the deriv. can be secreted from
CC transformed cells. Soluble deriv.s block the activity of IFN alpha/beta
CC and can be used to treat autoimmune diseases or to inhibit graft
CC rejection. See also Q14239.
SQ Sequence 557 AA:

Query Match 100.0%; Score 2313; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.3e-203;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMYVLLGATTLVAVAGPVLVLSAAGGNLKSPOKVEVDIIDNFIILRNRSDESIGNVT 60
Db 1 MMYVLLGATTLVAVAGPVLVLSAAGGNLKSPOKVEVDIIDNFIILRNRSDESIGNVT 60
QY 61 FSDYOKTGMNDWIKLSGCONITSTKCNFSSLKLVYEIEIKIRIAEKENTSSWEYVDSF 120
Db 61 FSDYOKTGMNDWIKLSGCONITSTKCNFSSLKLVYEIEIKIRIAEKENTSSWEYVDSF 120
QY 121 TPFRAQOIGPPEVHLAEEDKAIYIHISPTKDSVMALDGLSFTYSLILMKNSSGVEERI 180
Db 121 TPFRAQOIGPPEVHLAEEDKAIYIHISPTKDSVMALDGLSFTYSLILMKNSSGVEERI 180
QY 181 ENIYSHRKIIYKLSPEPTYCLKVAALITSWKIGVSPVHCITTYENELPPENIEVSQ 240
Db 181 ENIYSHRKIIYKLSPEPTYCLKVAALITSWKIGVSPVHCITTYENELPPENIEVSQ 240
QY 241 NONYVLKMDYTYANMTFOVOMLHAFILKRNPNHLYKWKQIIPCCENVKTTQCVFPQVNF 300
Db 241 NONYVLKMDYTYANMTFOVOMLHAFILKRNPNHLYKWKQIIPCCENVKTTQCVFPQVNF 300
QY 301 GIYLLRVOASDGNNTSFWSEELKFDTEIOAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
Db 301 GIYLLRVOASDGNNTSFWSEELKFDTEIOAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
QY 361 VIQDPLIYEITFEIIFMENTSNAERKIIIEKTDVTPNKLPLTYCVKARAHITMDEKLKSSV 420

Db 361 VIQDPLIYEITFEIIFMENTSNAERKIIIEKTDVTPNKLPLTYCVKARAHITMDEKLKSSV 420
QY 421 FSDAVCEKTRPGNTSK 436
Db 421 FSDAVCEKTRPGNTSK 436

RESULT 5
R28496
ID R28496 standard; Protein: 557 AA.
AC R28496:
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the interferon (IFN) receptor
DE with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-interferon; beta-interferon.
OS Synthetic.
PN MO9218626-A.
PD 29-OCT-1992.
PR 17-APR-1991; WO-F00318.
PR 17-APR-1991; WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PI Toyey M, Uze G;
PI MPI: 92-382110/46.
DR N-PSDB: Q30533.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
PT and beta - useful as immunosuppressants, for treating auto-immune
PT diseases and transplant rejection
PS Claim 3; Fig 2; 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
CC IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template. For example,
CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
CC Q30334 and Q30535. R28496 represents the complete receptor. R28495
CC lacks the transmembrane and cytoplasmic domains. Both forms bind
CC IFN in the same way as antibodies so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 557 AA:

Query Match 100.0%; Score 2313; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.3e-203;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMYVLLGATTLVAVAGPVLVLSAAGGNLKSPOKVEVDIIDNFIILRNRSDESIGNVT 60
Db 1 MMYVLLGATTLVAVAGPVLVLSAAGGNLKSPOKVEVDIIDNFIILRNRSDESIGNVT 60
QY 61 FSDYOKTGMNDWIKLSGCONITSTKCNFSSLKLVYEIEIKIRIAEKENTSSWEYVDSF 120
Db 61 FSDYOKTGMNDWIKLSGCONITSTKCNFSSLKLVYEIEIKIRIAEKENTSSWEYVDSF 120
QY 121 TPFRAQOIGPPEVHLAEEDKAIYIHISPTKDSVMALDGLSFTYSLILMKNSSGVEERI 180
Db 121 TPFRAQOIGPPEVHLAEEDKAIYIHISPTKDSVMALDGLSFTYSLILMKNSSGVEERI 180
QY 181 ENIYSHRKIIYKLSPEPTYCLKVAALITSWKIGVSPVHCITTYENELPPENIEVSQ 240
Db 181 ENIYSHRKIIYKLSPEPTYCLKVAALITSWKIGVSPVHCITTYENELPPENIEVSQ 240
QY 241 NONYVLKMDYTYANMTFOVOMLHAFILKRNPNHLYKWKQIIPCCENVKTTQCVFPQVNF 300
Db 241 NONYVLKMDYTYANMTFOVOMLHAFILKRNPNHLYKWKQIIPCCENVKTTQCVFPQVNF 300
QY 301 GIYLLRVOASDGNNTSFWSEELKFDTEIOAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
Db 301 GIYLLRVOASDGNNTSFWSEELKFDTEIOAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
QY 361 VIQDPLIYEITFEIIFMENTSNAERKIIIEKTDVTPNKLPLTYCVKARAHITMDEKLKSSV 420

Db 361 VIQDYPLIYEIIFFWENTSAERKIIIEKKTDTVPNLKPLTYVCVKAHAHTDEKLNKSSV 420
QY 421 FSDAVCEKTRPGNTSK 436
Db 421 FSDAVCEKTRPGNTSK 436

RESULT 6
ID R42635 standard; Protein; 557 AA.
AC R42635;
DT 20-APR-1994 (first entry)
DE Human interferon receptor.
KW IFR-R; extracellular domain; monoclonal antibody; viral infection;
cell proliferation; allograft rejection; systemic lupus erythematosus;
KM psoriasis; multiple sclerosis; Behcet's disease; aplastic anaemia;
OS immunodeficiency; measles virus; interferon-alpha-beta.
FH Homo sapiens.
FT Key
FT domain
FT 1. 436
FT /label= extracellular_domain
FT /note= "soluble, immunogenic form of IFR-R"
EP-563487-A.
PD 06-OCT-1993.
PF 31-MAR-1992; EP-400902.
PR 31-MAR-1992; EP-400902.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG;
DR MPI; 93-312951/40.
DR P-PSDB: R42635.
PT Monoclonal antibody to human interferon type-I receptor - having
PT neutralising activity against human type I interferon, used for
PT therapy and diagnosis
PS Disclosure; Fig 3; 21pp; English.
CC Monoclonal antibodies produced against soluble forms of the human
CC interferon alpha-beta receptor based on the full-length human IFR-R
CC sequence are claimed. The antibodies are useful for treatment and
CC prophylaxis of disorders involving cell proliferation and/or viral
CC infection.
SQ Sequence 557 AA:

Query Match 100.0%; Score 2313; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.3e-203;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMVVLGATTLVAVGPWVLSAAGKNTKSPQKVEVDIIDNFIILRNRSDESVGNT 60
Db 1 MMVVLGATTLVAVGPWVLSAAGKNTKSPQKVEVDIIDNFIILRNRSDESVGNT 60
QY 61 FSDYOKTGMDNWKILSGCONITSTKCNFSSKLNTVEEIKIRIRAEKENTSSWYEVDSF 120
Db 61 FSDYOKTGMDNWKILSGCONITSTKCNFSSKLNTVEEIKIRIRAEKENTSSWYEVDSF 120
QY 121 TFFRKAQIGPPEVHLEADKAIYIHISPGTDSVMALDGLSFTYSLLIMKSSGVEERI 180
Db 121 TFFRKAQIGPPEVHLEADKAIYIHISPGTDSVMALDGLSFTYSLLIMKSSGVEERI 180
QY 121 TFFRKAQIGPPEVHLEADKAIYIHISPGTDSVMALDGLSFTYSLLIMKSSGVEERI 180
Db 121 TFFRKAQIGPPEVHLEADKAIYIHISPGTDSVMALDGLSFTYSLLIMKSSGVEERI 180
QY 181 ENIYSRHKIYKLSPEITCYLKYKAAALLTSWKIGVSPVHCIKITVENELPPENIEVSQ 240
Db 181 ENIYSRHKIYKLSPEITCYLKYKAAALLTSWKIGVSPVHCIKITVENELPPENIEVSQ 240
QY 241 NONVYLKMDYTYANNMFQVOMLHAFKLRNPGNHLKMKOIPDCENKTTQCVFQVNFQK 300
Db 241 NONVYLKMDYTYANNMFQVOMLHAFKLRNPGNHLKMKOIPDCENKTTQCVFQVNFQK 300
QY 301 GIYLLRVOASGNNSTFSESEIKFDEIQAFLLPPVFNRSLSDSFHIIIGAPKOSGNT 360
Db 301 GIYLLRVOASGNNSTFSESEIKFDEIQAFLLPPVFNRSLSDSFHIIIGAPKOSGNT 360
QY 361 VIQDYPLIYEIIFFWENTSAERKIIIEKKTDTVPNLKPLTYVCVKAHAHTDEKLNKSSV 420
Db 361 VIQDYPLIYEIIFFWENTSAERKIIIEKKTDTVPNLKPLTYVCVKAHAHTDEKLNKSSV 420

QY 421 FSDAVCEKTRPGNTSK 436
Db 421 FSDAVCEKTRPGNTSK 436

RESULT 7
ID R75356 standard; Protein; 557 AA.
AC R75356;
DT 16-OCT-1995 (first entry)
DE Human IFN receptor.
KW IFN receptor; interferon receptor; interferon-alpha;
interferon-beta; monoclonal antibody; immunomodulator; AIDS.
OS Homo sapiens.
FH Key
FT domain
FT 1. 436
FT /label= Extracellular_domain
MO9507716-A.
PD 23-MAR-1995.
PF 16-SEP-1994; E03114.
PR 17-SEP-1993; EP-402279.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benlzeri EJ, Tovey MG;
DR MPI; 95-131187/17.
DR N-PSDB: 086458.
PT Compn. of monoclonal antibodies against interferon receptor -
PT useful as immunomodulator, eg. for treating AIDS
PS Disclosure; Fig. 3A-2B; 105pp; English.
CC The amino acid sequence of human interferon class I receptor is
CC given in R75356. A recombinant soluble form of the extracellular
CC domain of this receptor (R71723) has been used to raise
CC immunomodulatory monoclonal antibodies.
SQ Sequence 557 AA:

Query Match 99.8%; Score 2309; DB 1; Length 557;
Best Local Similarity 99.8%; Pred. No. 7.7e-203;
Matches 435; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MMVVLGATTLVAVGPWVLSAAGKNTKSPQKVEVDIIDNFIILRNRSDESVGNT 60
Db 1 MMVVLGATTLVAVGPWVLSAAGKNTKSPQKVEVDIIDNFIILRNRSDESVGNT 60
QY 61 FSDYOKTGMDNWKILSGCONITSTKCNFSSKLNTVEEIKIRIRAEKENTSSWYEVDSF 120
Db 61 FSDYOKTGMDNWKILSGCONITSTKCNFSSKLNTVEEIKIRIRAEKENTSSWYEVDSF 120
QY 121 TFFRKAQIGPPEVHLEADKAIYIHISPGTDSVMALDGLSFTYSLLIMKSSGVEERI 180
Db 121 TFFRKAQIGPPEVHLEADKAIYIHISPGTDSVMALDGLSFTYSLLIMKSSGVEERI 180
QY 181 ENIYSRHKIYKLSPEITCYLKYKAAALLTSWKIGVSPVHCIKITVENELPPENIEVSQ 240
Db 181 ENIYSRHKIYKLSPEITCYLKYKAAALLTSWKIGVSPVHCIKITVENELPPENIEVSQ 240
QY 241 NONVYLKMDYTYANNMFQVOMLHAFKLRNPGNHLKMKOIPDCENKTTQCVFQVNFQK 300
Db 241 NONVYLKMDYTYANNMFQVOMLHAFKLRNPGNHLKMKOIPDCENKTTQCVFQVNFQK 300
QY 301 GIYLLRVOASGNNSTFSESEIKFDEIQAFLLPPVFNRSLSDSFHIIIGAPKOSGNT 360
Db 301 GIYLLRVOASGNNSTFSESEIKFDEIQAFLLPPVFNRSLSDSFHIIIGAPKOSGNT 360
QY 361 VIQDYPLIYEIIFFWENTSAERKIIIEKKTDTVPNLKPLTYVCVKAHAHTDEKLNKSSV 420
Db 361 VIQDYPLIYEIIFFWENTSAERKIIIEKKTDTVPNLKPLTYVCVKAHAHTDEKLNKSSV 420

Key Location/Qualifiers
FT domain 1..427
FT /label= Extracellular domain
FT /note= "Comprises amino acids 1-427 of the
FT transmembrane IFNAR.
FT 428..434
FT domain /label= S-domain
PN A09475977-A.
PD 11-MAY-1995.
PE 20-OCT-1994; 075977.
PR 24-OCT-1993; IL-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PI (ABRA/) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M;
PI WPI: 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Example 2; Fig 7; 46pp: English.
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 1
CC (W21805) is characterised by a new domain (S) which follows an
CC end-deleted extracellular domain when compared to transmembrane
CC IFNAR (W21804). There is no transmembrane domain. The amino acid
CC sequence is predicted from a cDNA clone (see also T73520) cdt.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 and 2 (see also W21806) probably regulate
CC the response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating the activity of the multiple IFN
CC subtypes. They can be expressed in host cells and used to inhibit,
CC modulate or modify the activities of IFNs alpha and beta in cells,
CC tissues and organisms, or for diagnostic purposes.
SQ Sequence 434 AA:

Query Match 97.7%; Score 2260; DB 1; Length 434;
Best Local Similarity 99.8%; Pred. No. 1.6e-198;
Matches 426; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMVLLGATTLVAVGPMVLSAAGGKRLKSPQVEVDIIDNFI LRNRSDSEVGNT 60
DB 1 MMVLLGATTLVAVGPMVLSAAGGKRLKSPQVEVDIIDNFI LRNRSDSEVGNT 60
QY 61 FSPDYOKTGMNWKILSGCONITSTKCNFSSKLNVYEELKIRAEKENTSSWEYDSF 120
DB 61 FSPDYOKTGMNWKILSGCONITSTKCNFSSKLNVYEELKIRAEKENTSSWEYDSF 120
QY 121 TPFKAQIGPEVHLAEADKAIVIHISPGTKDSVMALDGLSTYSLLIKNNSGVEERI 180
DB 121 TPFKAQIGPEVHLAEADKAIVIHISPGTKDSVMALDGLSTYSLLIKNNSGVEERI 180
QY 181 ENISYRHKIYKLSPEPTYCLKVAKALLTSWKIGVSPVHCIKTVEENELPPENIEVSQ 240
DB 181 ENISYRHKIYKLSPEPTYCLKVAKALLTSWKIGVSPVHCIKTVEENELPPENIEVSQ 240
QY 241 NONVYLKMDTYTANMTFOVOMLHAFKLRNPGNHLKWKQIPDCENKTTQCVFPONVFQK 300
DB 241 NONVYLKMDTYTANMTFOVOMLHAFKLRNPGNHLKWKQIPDCENKTTQCVFPONVFQK 300
QY 301 GIYLLRVOASDGNNTSFSESEIKFDEIQAFLLPVPFNIRSLSDSFHIYIGAPKQSGNTP 360
DB 301 GIYLLRVOASDGNNTSFSESEIKFDEIQAFLLPVPFNIRSLSDSFHIYIGAPKQSGNTP 360
QY 361 VIQDYPLIYEIIIFWENTSNAEKRIIEKKTDTVPNLKPLTYVCVKAARAHMDEKLKSSV 420
DB 361 VIQDYPLIYEIIIFWENTSNAEKRIIEKKTDTVPNLKPLTYVCVKAARAHMDEKLKSSV 420
QY 421 FSDAVCE 427
DB 421 FSDAVCE 427

RESULT 11
W21806
ID W21806 standard; Protein; 496 AA.

AC W21806;
DE 23-SEP-1997 (first entry)
DE Spliced-deleted interferon alpha-receptor form 2.
KW Interferon alpha-receptor: IFNAR.
OS Homo sapiens.
FT Key Location/Qualifiers
FT domain 1..419
FT /label= Extracellular domain
FT /note= "Comprises amino acid residues 1-413 and
FT 422-427 of transmembrane IFNAR"
FT 420..496
FT domain /label= Intracellular domain
FT /note= "Comprises amino acids 481-557 of
FT transmembrane IFNAR"
PN A09475977-A.
PD 11-MAY-1995.
PE 20-OCT-1994; 075977.
PR 24-OCT-1993; IL-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PI (ABRA/) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M;
PI WPI: 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Example 3; Fig 7; 46pp: English.
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2
CC (W21806) is characterised by a double deletion when compared to
CC transmembrane IFNAR (W21804). The extracellular domain is
CC shortened by 6 amino acid residues and is followed by a truncated
CC intracellular domain. There is no transmembrane region. The amino
CC acid sequence is predicted from a cDNA clone (see also T73521) cdt.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 (see also W21805) and 2 may regulate the
CC response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating IFN activities. They can be expressed
CC in host cells and used to inhibit, modulate or modify the
CC activities of IFNs alpha and beta in cells, tissues and organisms,
CC or for diagnostic purposes.
SQ Sequence 496 AA:

Query Match 95.5%; Score 2208; DB 1; Length 496;
Best Local Similarity 97.9%; Pred. No. 1.1e-193;
Matches 418; Conservative 0; Mismatches 1; Indels 8; Gaps 1;

QY 1 MMVLLGATTLVAVGPMVLSAAGGKRLKSPQVEVDIIDNFI LRNRSDSEVGNT 60
DB 1 MMVLLGATTLVAVGPMVLSAAGGKRLKSPQVEVDIIDNFI LRNRSDSEVGNT 60
QY 61 FSPDYOKTGMNWKILSGCONITSTKCNFSSKLNVYEELKIRAEKENTSSWEYDSF 120
DB 61 FSPDYOKTGMNWKILSGCONITSTKCNFSSKLNVYEELKIRAEKENTSSWEYDSF 120
QY 121 TPFKAQIGPEVHLAEADKAIVIHISPGTKDSVMALDGLSTYSLLIKNNSGVEERI 180
DB 121 TPFKAQIGPEVHLAEADKAIVIHISPGTKDSVMALDGLSTYSLLIKNNSGVEERI 180
QY 181 ENISYRHKIYKLSPEPTYCLKVAKALLTSWKIGVSPVHCIKTVEENELPPENIEVSQ 240
DB 181 ENISYRHKIYKLSPEPTYCLKVAKALLTSWKIGVSPVHCIKTVEENELPPENIEVSQ 240
QY 241 NONVYLKMDTYTANMTFOVOMLHAFKLRNPGNHLKWKQIPDCENKTTQCVFPONVFQK 300
DB 241 NONVYLKMDTYTANMTFOVOMLHAFKLRNPGNHLKWKQIPDCENKTTQCVFPONVFQK 300
QY 301 GIYLLRVOASDGNNTSFSESEIKFDEIQAFLLPVPFNIRSLSDSFHIYIGAPKQSGNTP 360
DB 301 GIYLLRVOASDGNNTSFSESEIKFDEIQAFLLPVPFNIRSLSDSFHIYIGAPKQSGNTP 360
QY 361 VIQDYPLIYEIIIFWENTSNAEKRIIEKKTDTVPNLKPLTYVCVKAARAHMDEKLKSSV 420
DB 361 VIQDYPLIYEIIIFWENTSNAEKRIIEKKTDTVPNLKPLTYVCVKAARAHMDEKLKSSV 420

FT Domain 275..553 sequence claimed in claim 1"
FT /note="intracellular domain"
PD WO9837193-A1.
PF 27-AUG-1998.
PR 18-FEB-1998; 003029.
PR 20-OCT-1997; US-943087.
PR 20-FEB-1997; US-803305.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Farrah TM, Jelmberg AC, Kho CJ, Lok S,
PI Whitmore TE:
DR WPI: 98-480798/41.
DR N-PDDB: V57515.
PT Novel human zcytor7 DNA encodes a type 2 cytokine receptor - useful
PT for treating renal, neural, pancreatic and prostatic diseases
PS Claim 1; Pages 55-59; 72pp; English.
CC This represents the zcytor7 cytokine receptor. zcytor7 is a ligand-
CC binding receptor polypeptide and is a novel member of the type 2 cytokine
CC receptor family (CRF2). An expression vector containing the zcytor
CC polynucleotide, operably linked to transcription promoter, a sequence
CC encoding a transmembrane and intracellular domain, or both, and a
CC transcriptional terminator can be used to transform host cells for the
CC recombinant production of the polypeptide. The sequences can be used to
CC study the zcytor7 gene and to isolate ligands binding to it. zcytor7 is
CC preferentially expressed in the kidney, pancreas, prostate or nervous
CC tissue. Agonists of zcytor7 can be used to stimulate proliferation and
CC differentiation of cell in these organs. The antagonists and agonists can
CC also be used in the treatment of renal, neural, pancreatic and prostate
CC diseases.
SQ Sequence 553 AA:

Query Match 8.6%; Score 198; DB 1; Length 553;
Best Local Similarity 21.0%; Pred. No. 7e-10;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPR--VLSAAGGKLNKSPQKVEVDIIDNFILRNRSDESVG--NTFSEFDYOK 67
DB 18 LLLLLAAMPGRAPVCSG--LPKPANITFLSINMKNVLPQPEGLQGVKTYTQYPI 75
QY 66 TQMDMKIKSGCONITSTGKCNFSSSLKLNVEEIKLRIR--EKENTSSWTEVDSETPPKRA 126
DB 76 YQCKMKNKSEKRNINRYCDLSAETSDYEHQYAKVKAIWGTCKSKMAESGRFPFLET 135
QY 127 QIGPEVHLAEADKAIHISPGTK-----DSVMALDGLSTVSLIMKSSGVE 177
DB 136 QIGPEVALTTDEKTSIVLTAPKPKRNPEDLPVSMQIYNLNKYNVSVLTKSNRTWS 195
QY 178 ERIENIYSRHKIYK--LSPETTYCLKVKAALLTSMKIGVSPHCIKTTVENE----- 229
DB 196 QCVTN---HTLVLTWLEBNTLYCVHESFVGPBRAPQPSKQCARLTKDQSSFEKAKI 251
QY 229 -----LPPPENIEVSQNONVYLNKMDITYANTFOY--QMLAFLLKRNQGNHLYKKQJPD 282
DB 252 IFWYVLP-----ISITV-----FLFSVGYSIIRYIHGKKEKHPANLI----- 290
QY 283 CENVKTCQVFPONFQKGIYLLRVQASDGNNTSPMSEIKPDEI---QAFLLPVPNI 339
DB 290 -----LIYGNFEDKRFV---PAKTIYINFTILNISDSKISHQMSLLKSSDV 336
QY 340 RSLSDSFHIYIGAPKQSGNTPIYDIPLYEI-----IFWENTNAEKRIIEKKTDV 391
DB 337 SSLND-----POPSGNLRPQDEEYKHLGYASHLMEIFCDSEENTEGTSFTQESL 388
QY 392 --TVPNLKPLVY 402
DB 389 SRTIPDPKTVLEY 401

RESULT 15
ID R71035
AC R71035 standard; protein; 337 AA.
R71035;
R71035;

DR 11-OCT-1995 (first entry)
DE Human IFN-gamma accessory factor-1.
KM Interferon-gamma; Af-1; tumour.
OS Homo sapiens.
PN WO9505847-A.
PD 02-MAR-1995.
PF 22-AUG-1994; U09438.
PR 20-AUG-1993; US-110119.
PA (UNIV-) UNIV NEW JERSEY.
PI Cook JR, Donnelly RJ, Emanuel S, Kotenko S, Mariano TM,
PI Pestka S, Schwartz B, Soh J;
DR WPI: 95-106679/14.
DR N-PDDB: 084697.
PT Suppressing tumours in mammals with accessory factor 1 (Af-1) -
PT for interferon gamma, specifically induction of class I HLA
PT antigens, including use of Af-1 DNA in gene therapy
PS Disclosure: Fig 21A; 114pp; English.
CC The sequence is that of human interferon-gamma accessory factor-1.
CC Incorporation of Af-1 into immune and tumour cells re-establishes
CC normal function with elimination of malignant cells.
SQ Sequence 337 AA;

Query Match 6.7%; Score 155.5; DB 1; Length 337;
Best Local Similarity 22.3%; Pred. No. 2.6e-06;
Matches 67; Conservative 54; Mismatches 112; Indels 67; Gaps 14;

QY 12 VLVAVGPRVLSAAGG--KNLSPQKVEVDIIDNFILRN-----NRSDESVGNWTF 62
DB 9 LLLLLGVFAAALAAAPPDPLSQLPAPQHPKIRLYNAEGLSWEPVALSNSTPVPYVOFK 68
QY 63 FDYQKTMKMDNFKLS-----GCONITSTKCNFSS-----LKNVEEIKLRIRAEK 108
DB 69 ITDSK-----WFTADINSIGVNCQTITATEDFTAAFSAGFPMDFNV---TLRLRAEL 119
QY 109 ENT--SMTEVDSFTPFKRAQIGPEVHLE---AEDKAIHISPGTKDSVMALDGLSFT 164
DB 120 GALSAMWTMTMFOHRYRNVTVGPPE--NIEVTPGEGSLIIRSSFPDLADISTAF-----FC 174
QY 165 YSLIMKNSGVEERENIYSRHKIY--KSPETTYCLKVKAALLTS---WKIGVSPV 218
DB 175 YVHYWE--KGIQOVKGPFRSNSISLDNLEKPSRYCLOVOAQLMKNKSNIFRGHLSNI 232
QY 219 HCITTYENELPPPENIEVS-----QONVYLNKMDITYANTFOYQ 260
DB 233 SCYETMADASTELQOVILISVGTFSLSVLGACFVLVLYKRYGLIKYWFHTPPSPIDQIE 292

Search completed: June 1, 2000, 04:40:21
Job time: 1344 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:35:21 ; Search time 12.75 Seconds
(without alignments)
493.702 Million cell updates/sec

Title: US-09-240-675-2

Perfect score: 2313
Sequence: 1 MMVVLGATTLVAVGPV.....KSSVSDAVCEKTKPGNTSK 436Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 145308 seqs, 14437401 residues

Total number of hits satisfying chosen parameters: 145308

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/p/odata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/p/odata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/p/odata/1/1aa/6.COMB.pep.*
4: /cgn2_6/p/odata/1/1aa/PCrus.COMB.pep.*
5: /cgn2_6/p/odata/1/1aa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2313	100.0	436	2	US-08-307-588-2
2	2313	100.0	557	1	US-08-328-256-10
3	2313	100.0	557	1	US-08-471-454-2
4	2313	100.0	557	2	US-08-466-974-2
5	2313	100.0	557	2	US-08-471-453-2
6	2313	100.0	557	2	US-08-307-588-4
7	2265	97.9	434	1	US-08-328-256-11
8	2213	95.7	496	1	US-08-328-256-12
9	490.5	21.2	202	4	PCT-US94-14277-3
10	466.5	20.2	200	4	PCT-US94-14277-4
11	228.5	9.9	325	2	US-08-683-743-4
12	203	8.8	332	4	PCT-US94-14277-2
13	198	8.6	553	2	US-08-943-087-2
14	198	8.6	553	2	US-08-943-087-14
15	198	8.6	553	2	US-08-943-087-16
16	198	8.6	553	2	US-08-943-087-18
17	198	8.6	553	2	US-08-943-087-20
18	198	8.6	553	2	US-08-943-087-22
19	198	8.6	553	2	US-08-943-087-24
20	198	8.6	553	2	US-08-943-087-26
21	198	8.6	553	2	US-08-943-087-28
22	198	8.6	553	2	US-08-943-087-30
23	198	8.6	553	2	US-08-943-087-32
24	198	8.6	553	2	US-08-943-087-34
25	198	8.6	553	2	US-08-943-087-36
26	198	8.6	553	2	US-08-943-087-38
27	198	8.6	553	2	US-08-943-087-40
28	198	8.6	553	2	US-08-943-087-42
29	198	8.6	553	2	US-08-943-087-44

30	198	8.6	553	2	US-08-943-087-46	Sequence 46, Appl
31	198	8.6	553	2	US-08-943-087-48	Sequence 48, Appl
32	192	8.3	223	4	PCT-US94-14277-6	Sequence 6, Appl
33	174.5	7.5	221	2	US-08-943-087-56	Sequence 56, Appl
34	169.5	7.3	221	2	US-08-943-087-54	Sequence 54, Appl
35	168.5	7.3	221	2	US-08-943-087-50	Sequence 50, Appl
36	167.5	7.2	221	2	US-08-943-087-52	Sequence 52, Appl
37	165.5	7.2	221	2	US-08-943-087-60	Sequence 60, Appl
38	162.5	7.0	221	2	US-08-943-087-58	Sequence 58, Appl
39	153.5	6.6	337	4	PCT-US94-14277-8	Sequence 8, Appl
40	151	6.5	574	4	US-08-906-713-2	Sequence 2, Appl
41	118	5.1	489	4	PCT-US93-11110-1	Sequence 1, Appl
42	118	5.1	489	5	5221789-1	Patent No. 5221789
43	118	5.1	1005	2	US-08-469-537A-103	Sequence 103, App
44	117.5	5.1	575	1	US-08-424-788-2	Sequence 2, Appl
45	117.5	5.1	575	1	US-08-110-683-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-307-588-2
Sequence 2, Application US/08307588
Patent No. 5919453
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
TITLE OF INVENTION: INTERFERON
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/CUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-588-2
Query Match 100.0%; Score 2313; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 1.8e-230;

Matches 436: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYVLLGATTLVLAAGPWWLSAAGKLNKSPQKVEVDIIDNFIIRNRSDSEVGNVT 60
 DB 1 MMYVLLGATTLVLAAGPWWLSAAGKLNKSPQKVEVDIIDNFIIRNRSDSEVGNVT 60
 QY 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSKLNYEEIKLRIRAKENTSSWYEVDSF 120
 DB 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSKLNYEEIKLRIRAKENTSSWYEVDSF 120
 QY 121 TPFKRAQIGPPEVHLEADKAIYIHISPTKDSYMMALDGLSFTYSLLIWKNSGYEERI 180
 DB 121 TPFKRAQIGPPEVHLEADKAIYIHISPTKDSYMMALDGLSFTYSLLIWKNSGYEERI 180
 QY 181 ENIYSRHKIKYKLSPEPTYCKLVKAAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240
 DB 181 ENIYSRHKIKYKLSPEPTYCKLVKAAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240
 QY 241 NONVYLKMDYTYANMTFOVOMLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPOVNFQK 300
 DB 241 NONVYLKMDYTYANMTFOVOMLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPOVNFQK 300
 QY 301 GIYLLRVOASDGNNTSFWSEIEIKFDEIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
 DB 301 GIYLLRVOASDGNNTSFWSEIEIKFDEIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
 QY 361 VIQDYPLIYEIIFWENTSNAERKIIKKTDTVPNLKPLTYCVKARAHATMDEKLKSSV 420
 DB 361 VIQDYPLIYEIIFWENTSNAERKIIKKTDTVPNLKPLTYCVKARAHATMDEKLKSSV 420
 QY 421 FSDAVCEKTRPGNTSK 436
 DB 421 FSDAVCEKTRPGNTSK 436

RESULT 2
 US-08-328-256-10
 ; Sequence 10, Application US/08328256
 ; Patent No. 5643749
 ; GENERAL INFORMATION:
 ; APPLICANT: REVEL, Michel
 ; APPLICANT: ABRAMOVICH, Carolina
 ; APPLICANT: RATOVITSKI, Edward
 ; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
 ; TITLE OF INVENTION: PREPARATION AND USE
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/328,256
 ; FILING DATE: 24-OCT-1994
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: IL 107378
 ; FILING DATE: 24-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROWDY, Roger L.
 ; REGISTRATION NUMBER: REVEL-13
 ; REFERENCE/DOCKET NUMBER: 25,618
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633
 ; INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
 LENGTH: 557 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-328-256-10

Query Match 100.0%; Score 2313; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 2,7e-230;
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYVLLGATTLVLAAGPWWLSAAGKLNKSPQKVEVDIIDNFIIRNRSDSEVGNVT 60
 DB 1 MMYVLLGATTLVLAAGPWWLSAAGKLNKSPQKVEVDIIDNFIIRNRSDSEVGNVT 60
 QY 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSKLNYEEIKLRIRAKENTSSWYEVDSF 120
 DB 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSKLNYEEIKLRIRAKENTSSWYEVDSF 120
 QY 121 TPFKRAQIGPPEVHLEADKAIYIHISPTKDSYMMALDGLSFTYSLLIWKNSGYEERI 180
 DB 121 TPFKRAQIGPPEVHLEADKAIYIHISPTKDSYMMALDGLSFTYSLLIWKNSGYEERI 180
 QY 181 ENIYSRHKIKYKLSPEPTYCKLVKAAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240
 DB 181 ENIYSRHKIKYKLSPEPTYCKLVKAAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240
 QY 241 NONVYLKMDYTYANMTFOVOMLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPOVNFQK 300
 DB 241 NONVYLKMDYTYANMTFOVOMLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPOVNFQK 300
 QY 301 GIYLLRVOASDGNNTSFWSEIEIKFDEIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
 DB 301 GIYLLRVOASDGNNTSFWSEIEIKFDEIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
 QY 361 VIQDYPLIYEIIFWENTSNAERKIIKKTDTVPNLKPLTYCVKARAHATMDEKLKSSV 420
 DB 361 VIQDYPLIYEIIFWENTSNAERKIIKKTDTVPNLKPLTYCVKARAHATMDEKLKSSV 420
 QY 421 FSDAVCEKTRPGNTSK 436
 DB 421 FSDAVCEKTRPGNTSK 436

RESULT 3
 US-08-471-454-2
 ; Sequence 2, Application US/08471454
 ; Patent No. 5731169
 ; GENERAL INFORMATION:
 ; APPLICANT: MOGENSEN, Knud E.
 ; APPLICANT: UZE, Gilles
 ; APPLICANT: LUTFALLA, Georges
 ; APPLICANT: GRESSER, Ion
 ; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
 ; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHAYE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: U.S.A.
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/471,454

FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-454-2

Query Match 100.0%; Score 2313; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 2.7e-230;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYVLLGATTLVAVGPMVLSAAGGNLKSPOKVEVDIIDNFIILRMNSDESVCNT 60
DB 1 MMYVLLGATTLVAVGPMVLSAAGGNLKSPOKVEVDIIDNFIILRMNSDESVCNT 60
QY 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSLSKLVYEELKRIAREKENTSSMYEVSF 120
DB 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSLSKLVYEELKRIAREKENTSSMYEVSF 120
QY 121 TPFRAOIGPPEVHLEADKALIVHISPTKDSVMALDGLSFTYSLIMKNSGVEERI 180
DB 121 TPFRAOIGPPEVHLEADKALIVHISPTKDSVMALDGLSFTYSLIMKNSGVEERI 180
QY 181 ENIYSRHKIYKLSPEPTTCLAKKAAALLTSWKIGVSPVHCITTYENELPPENIEVSQ 240
DB 181 ENIYSRHKIYKLSPEPTTCLAKKAAALLTSWKIGVSPVHCITTYENELPPENIEVSQ 240
QY 241 NONVYLKMDYTYANNTFOVQWLHAFLEKRNPGNHLKWKQIPDCENVKTTQCVFPQNVOK 300
DB 241 NONVYLKMDYTYANNTFOVQWLHAFLEKRNPGNHLKWKQIPDCENVKTTQCVFPQNVOK 300
QY 301 GYLLRVQASDGNNTSFSEELKFDTELOAFLLPVEFNIRSLDSFHIYIGAPKOSGNT 360
DB 301 GYLLRVQASDGNNTSFSEELKFDTELOAFLLPVEFNIRSLDSFHIYIGAPKOSGNT 360
QY 361 VIQDPLIYEITFWENTSNAERKIIIEKTDVTPNKLPLTYCYKARAHNTDEKLNKSSV 420
DB 361 VIQDPLIYEITFWENTSNAERKIIIEKTDVTPNKLPLTYCYKARAHNTDEKLNKSSV 420
QY 421 FSDAVCEKTPGNTSK 436
DB 421 FSDAVCEKTPGNTSK 436

RESULT 4
US-08-466-974-2
Sequence 2, Application US/08466974
Patent No. 5861258

GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,974
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-974-2

Query Match 100.0%; Score 2313; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 2.7e-230;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYVLLGATTLVAVGPMVLSAAGGNLKSPOKVEVDIIDNFIILRMNSDESVCNT 60
DB 1 MMYVLLGATTLVAVGPMVLSAAGGNLKSPOKVEVDIIDNFIILRMNSDESVCNT 60
QY 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSLSKLVYEELKRIAREKENTSSMYEVSF 120
DB 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSLSKLVYEELKRIAREKENTSSMYEVSF 120
QY 121 TPFRAOIGPPEVHLEADKALIVHISPTKDSVMALDGLSFTYSLIMKNSGVEERI 180
DB 121 TPFRAOIGPPEVHLEADKALIVHISPTKDSVMALDGLSFTYSLIMKNSGVEERI 180
QY 181 ENIYSRHKIYKLSPEPTTCLAKKAAALLTSWKIGVSPVHCITTYENELPPENIEVSQ 240
DB 181 ENIYSRHKIYKLSPEPTTCLAKKAAALLTSWKIGVSPVHCITTYENELPPENIEVSQ 240
QY 241 NONVYLKMDYTYANNTFOVQWLHAFLEKRNPGNHLKWKQIPDCENVKTTQCVFPQNVOK 300
DB 241 NONVYLKMDYTYANNTFOVQWLHAFLEKRNPGNHLKWKQIPDCENVKTTQCVFPQNVOK 300
QY 301 GYLLRVQASDGNNTSFSEELKFDTELOAFLLPVEFNIRSLDSFHIYIGAPKOSGNT 360
DB 301 GYLLRVQASDGNNTSFSEELKFDTELOAFLLPVEFNIRSLDSFHIYIGAPKOSGNT 360
QY 361 VIQDPLIYEITFWENTSNAERKIIIEKTDVTPNKLPLTYCYKARAHNTDEKLNKSSV 420
DB 361 VIQDPLIYEITFWENTSNAERKIIIEKTDVTPNKLPLTYCYKARAHNTDEKLNKSSV 420

OY 421 FSDAVCEKTPGNTSK 436
DB 421 FSDAVCEKTPGNTSK 436

RESULT 5

US-08-471-453-2
; Sequence 2, Application US/08471453
; Patent No. 5886153
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LUTFALLA, Georges
; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYTE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,453
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELE: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-471-453-2

Query Match 100.0%; Score 2313; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 2.7e-230;

Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMVVLGATTVLVAVGVVLSAAGGNKLSPOKVEVDIIDNFIILMNSDESQVNT 60
DB 1 MMVVLGATTVLVAVGVVLSAAGGNKLSPOKVEVDIIDNFIILMNSDESQVNT 60
OY 61 FSDYQKTMGNWIKLSQONTSTKCNFSSLSKLVVEEIKLRIRAEKENTSSWYEVDSF 120
DB 61 FSDYQKTMGNWIKLSQONTSTKCNFSSLSKLVVEEIKLRIRAEKENTSSWYEVDSF 120
OY 121 TPFRAQIGPEPVHLEADKAIVIHISPTKDSVMMALDGLSFTYSLIMKNSGVEERI 180
DB 121 TPFRAQIGPEPVHLEADKAIVIHISPTKDSVMMALDGLSFTYSLIMKNSGVEERI 180

OY 181 ENIYSRHKIYKSPETTYCLKVKAAALITSMKIGVSPVACIKTYVENELPPENIEVSQ 240
DB 181 ENIYSRHKIYKSPETTYCLKVKAAALITSMKIGVSPVACIKTYVENELPPENIEVSQ 240
OY 241 NONVYKMDYTYANMTFOVQWLAFLKRNPNHLYKWKQIPDCENVKTTQCVFQNVFQK 300
DB 241 NONVYKMDYTYANMTFOVQWLAFLKRNPNHLYKWKQIPDCENVKTTQCVFQNVFQK 300
OY 301 GYLLRVQASDGNNTSFMSEEEKFTDEIQAFLPPVFNIRSLDSFHIYIGAPKOSGNTP 360
DB 301 GYLLRVQASDGNNTSFMSEEEKFTDEIQAFLPPVFNIRSLDSFHIYIGAPKOSGNTP 360
OY 361 VIQDPLVIEIIFMENTSNAERKIEKTDVVPNLKPLTVYCVARAHATMDEKLNKSSV 420
DB 361 VIQDPLVIEIIFMENTSNAERKIEKTDVVPNLKPLTVYCVARAHATMDEKLNKSSV 420
OY 421 FSDAVCEKTPGNTSK 436
DB 421 FSDAVCEKTPGNTSK 436

RESULT 6

US-08-307-588-4
; Sequence 4, Application US/08307588
; Patent No. 5919453
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MAGUIRE, Deborah
; APPLICANT: PLAVEC, Ivan
; APPLICANT: TOVEY, Michael G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; TITLE OF INVENTION: RECEPTOR WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992

ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/GUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-588-4

Query Match 100.0%; Score 2313; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 2.7e-230;

Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 436: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
OY 1 MMVLLGATTLVAVGPWVLSAAGGNLKSPOKVEVDIIDNFIIRNRSDSEYGNVT 60
   |||||
Db 1 MMVLLGATTLVAVGPWVLSAAGGNLKSPOKVEVDIIDNFIIRNRSDSEYGNVT 60
OY 61 FSPDYOKTGDMNLIKSGCONITSTKCNFSSSLKNVYEEIKLIRAKENTSMYEVDSF 120
   |||||
Db 61 FSPDYOKTGDMNLIKSGCONITSTKCNFSSSLKNVYEEIKLIRAKENTSMYEVDSF 120
OY 121 TPRKAOIGPPEVHLEAEDKAIVIHISPGTKDSVMALDGLSTYSLLIKNSSGYEERI 180
   |||||
Db 121 TPRKAOIGPPEVHLEAEDKAIVIHISPGTKDSVMALDGLSTYSLLIKNSSGYEERI 180
OY 181 ENIYSRRIKIKLSPETTYCLKVAALLTSKIGVSPVHCIKTVENELPPENIEYSVQ 240
   |||||
Db 181 ENIYSRRIKIKLSPETTYCLKVAALLTSKIGVSPVHCIKTVENELPPENIEYSVQ 240
OY 241 NONVYLKMDTYANMTFOVOMLHAFKRNPNLHLYKKKOIPDCENVTTCQVFPQNYFQK 300
   |||||
Db 241 NONVYLKMDTYANMTFOVOMLHAFKRNPNLHLYKKKOIPDCENVTTCQVFPQNYFQK 300
OY 301 GIYLLRVOASDGNNTSFWESEIKFDEIQAFLLPVPFNINSLSDSFHITYGAPKQSGNTP 360
   |||||
Db 301 GIYLLRVOASDGNNTSFWESEIKFDEIQAFLLPVPFNINSLSDSFHITYGAPKQSGNTP 360
OY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTPNKLPLVYCVKARAHMDEKLKNSV 420
   |||||
Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTPNKLPLVYCVKARAHMDEKLKNSV 420
OY 421 FSDAVCEKTKPGNTSK 436
   |||||
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 7
US-08-328-256-11
: Sequence 11, Application US/08328256
: Patent No. 5643749
: GENERAL INFORMATION:
: APPLICANT: REVEL, Michel
: APPLICANT: ABRAMOVICH, Carolina
: APPLICANT: RATOVIITSKI, Edward
: TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
: TITLE OF INVENTION: PREPARATION AND USE
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROMDY AND NEIMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/328.256
: FILING DATE: 24-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 107378
: FILING DATE: 24-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: BROMDY, Roger L.
: REGISTRATION NUMBER: REVEL-13
: REFERENCE/DOCKET NUMBER: 25,618
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: TELEX: 248633
: INFORMATION FOR SEQ ID NO: 11:
```

```
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-256-11

Query Match          97.9%; Score 2265; DB 1; Length 434;
Best Local Similarity 100.0%; Pred. No. 1,6e-225;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMVLLGATTLVAVGPWVLSAAGGNLKSPOKVEVDIIDNFIIRNRSDSEYGNVT 60
   |||||
Db 1 MMVLLGATTLVAVGPWVLSAAGGNLKSPOKVEVDIIDNFIIRNRSDSEYGNVT 60
OY 61 FSPDYOKTGDMNLIKSGCONITSTKCNFSSSLKNVYEEIKLIRAKENTSMYEVDSF 120
   |||||
Db 61 FSPDYOKTGDMNLIKSGCONITSTKCNFSSSLKNVYEEIKLIRAKENTSMYEVDSF 120
OY 121 TPRKAOIGPPEVHLEAEDKAIVIHISPGTKDSVMALDGLSTYSLLIKNSSGYEERI 180
   |||||
Db 121 TPRKAOIGPPEVHLEAEDKAIVIHISPGTKDSVMALDGLSTYSLLIKNSSGYEERI 180
OY 181 ENIYSRRIKIKLSPETTYCLKVAALLTSKIGVSPVHCIKTVENELPPENIEYSVQ 240
   |||||
Db 181 ENIYSRRIKIKLSPETTYCLKVAALLTSKIGVSPVHCIKTVENELPPENIEYSVQ 240
OY 241 NONVYLKMDTYANMTFOVOMLHAFKRNPNLHLYKKKOIPDCENVTTCQVFPQNYFQK 300
   |||||
Db 241 NONVYLKMDTYANMTFOVOMLHAFKRNPNLHLYKKKOIPDCENVTTCQVFPQNYFQK 300
OY 301 GIYLLRVOASDGNNTSFWESEIKFDEIQAFLLPVPFNINSLSDSFHITYGAPKQSGNTP 360
   |||||
Db 301 GIYLLRVOASDGNNTSFWESEIKFDEIQAFLLPVPFNINSLSDSFHITYGAPKQSGNTP 360
OY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTPNKLPLVYCVKARAHMDEKLKNSV 420
   |||||
Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTPNKLPLVYCVKARAHMDEKLKNSV 420
OY 421 FSDAVCE 427
   |||||
Db 421 FSDAVCE 427

RESULT 8
US-08-328-256-12
: Sequence 12, Application US/08328256
: Patent No. 5643749
: GENERAL INFORMATION:
: APPLICANT: REVEL, Michel
: APPLICANT: ABRAMOVICH, Carolina
: APPLICANT: RATOVIITSKI, Edward
: TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
: TITLE OF INVENTION: PREPARATION AND USE
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROMDY AND NEIMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/328.256
: FILING DATE: 24-OCT-1994
: PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: IL 107378
 FILING DATE: 24-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: REVEL-13
 REFERENCE/DOCKET NUMBER: 25,618
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEFAX: 248633
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 496 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-328-256-12

Query Match 95.7%; Score 2213; DB 1; Length 496;
 Best Local Similarity 98.1%; Pred. No. 4,7e-220;
 Matches 419; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

OY 1 MMVVLGATTLVAVGPPVLSAAGGKRLKSPQVEVDIIDNFI LRNRSDESGVNT 60
 DB 1 MMVVLGATTLVAVGPPVLSAAGGKRLKSPQVEVDIIDNFI LRNRSDESGVNT 60
 OY 61 FSEFDYQKTMNMKILSGCONITSTKCNFSSKLNVYEIKRIRAEKENTSSWYEVDSF 120
 DB 61 FSEFDYQKTMNMKILSGCONITSTKCNFSSKLNVYEIKRIRAEKENTSSWYEVDSF 120
 OY 121 TPFKAQIGPEPEVHLEADKAIVIHISPGKDSVMALDGLSTFSLIMKNSGVEERI 180
 DB 121 TPFKAQIGPEPEVHLEADKAIVIHISPGKDSVMALDGLSTFSLIMKNSGVEERI 180
 OY 181 ENISRHKIYKLSPEPTCYKALKALTSWKIGVSPVHCITTYENELPPENIEVSQ 240
 DB 181 ENISRHKIYKLSPEPTCYKALKALTSWKIGVSPVHCITTYENELPPENIEVSQ 240
 OY 241 NQNTVLMKDYTYANTFQVQWHLAFKRNPNHLYKRAQIDCEVKTQCVFQNTVQK 300
 DB 241 NQNTVLMKDYTYANTFQVQWHLAFKRNPNHLYKRAQIDCEVKTQCVFQNTVQK 300
 OY 301 GIVLLRQASDGNNTSFSEIKFDTETQAFLLPVENIRSLDSFHIYIGAPKQSGNTP 360
 DB 301 GIVLLRQASDGNNTSFSEIKFDTETQAFLLPVENIRSLDSFHIYIGAPKQSGNTP 360
 OY 361 VIQDYPLIYEITFEMNTSNAERKIIETKTDVTYVNLKPLTYVCYKARAHMTDE----- 414
 DB 361 VIQDYPLIYEITFEMNTSNAERKIIETKTDVTYVNLKPLTYVCYKARAHMTDE----- 414
 OY 421 FSDAYCE 427
 DB 414 -SDAYCE 419

RESULT 9
 PCT-US94-14277-3
 Sequence 3, Application PC/TUS9414277
 GENERAL INFORMATION:
 APPLICANT: Agnet, Michel
 APPLICANT: Bohnl, Ruth
 APPLICANT: Hemml, Silvio
 TITLE OF INVENTION: Receptor Subunit Polypeptides
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/14277
 FILING DATE: 07-DEC-1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/164596
 FILING DATE: 09-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: 866PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5530
 TELEFAX: 415/952-9881
 TELEFAX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 202 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 PCT-US94-14277-3

Query Match 21.2%; Score 490.5; DB 4; Length 202;
 Best Local Similarity 48.5%; Pred. No. 7,4e-43;
 Matches 98; Conservative 34; Mismatches 69; Indels 1; Gaps 1;

OY 28 KNLKSPQVEVDIIDNFI LRNRSDESGVNTFSEFDYQKTMNMKILSGCONITSTK 87
 DB 1 ENLSPKINIXIYIIDNYLTLMKSHGSGSVFSAVIRKDERKMLKXQCHITTKC 60
 OY 88 NFSKLNVYEIKRIRAEKEN-TSSWYEVDSFTPFKAQIGPEPEVHLEADKAIVIH 146
 DB 61 EFSLIDTNYIKTQFRRAEENSGSTSMNEVDPIFYTAHMSPPVEVLEREDKALVHI 120
 OY 147 SPGKDSVMALDGLSTFSLIMKNSGVEERIENYSHKIKYKLSPEPTCYKALKAL 206
 DB 121 SPGKDSVMALDGLSTFSLIMKNSGVEERIENYSHKIKYKLSPEPTCYKALKAL 206
 OY 207 LTSWKIGVSPVHCITTYENE 228
 DB 181 PSLKHSNYSXOCISTVANK 202

RESULT 10
 PCT-US94-14277-4
 Sequence 4, Application PC/TUS9414277
 GENERAL INFORMATION:
 APPLICANT: Agnet, Michel
 APPLICANT: Bohnl, Ruth
 APPLICANT: Hemml, Silvio
 TITLE OF INVENTION: Receptor Subunit Polypeptides
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/14277
 FILING DATE: 07-DEC-1994

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-4

Query Match 20.2%; Score 466.5; DB 4; Length 200;
Best Local Similarity 44.7%; Pred. No. 2.2e-40;
Matches 93; Conservative 37; Mismatches 69; Indels 9; Gaps 3;

QY 229 LPPENIVSVQNONVYLKMDY-ITYANTFOYQMLHAFKRNPNHLYKKQIPCCENVK 287
DB 1 MPVGNLQVDAQGSYVLKMDYASADYLFRAQWLPYKSSSGSHSDKWPDPICANVQ 60
QY 288 TTCQCFPNVFOKGIYILRVASDGNNTSFNSEELKPDTEIQAFLLPPVFNIRSLDSF 347
DB 61 TTHCFSDQTYTGTFFLHVQASGNHTSFNSEKFTDSQKHILPPPVITVTASDILL 120
QY 348 IYIGAPKSGNTPIYIDYPIYEIFMENTSNAERKIIKKTVDYVPLKPLTYCVKAR 407
DB 121 VYXNQDSTCD-----GLNVEIIFMENTSSTKISMKEDGEFTLKNLQPLTYCVQAR 173
QY 408 AHTMDEKLNKSVSDAVCEKTPGNTS 435
DB 174 V-LFRALNKTSNFSEKLCETKTPGNTS 200

RESULT 11
US-08-683-743-4
Sequence 4, Application US/08683743
Patent No. 5843697
GENERAL INFORMATION:
APPLICANT: Pestka, Sidney
APPLICANT: Kolenko, Serguei
TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
TITLE OF INVENTION: CHAIN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,743
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-050
TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
US-08-683-743-4

Query Match 9.9%; Score 228.5; DB 2; Length 325;
Best Local Similarity 29.9%; Pred. No. 1.8e-15;
Matches 67; Conservative 42; Mismatches 96; Indels 19; Gaps 8;

QY 19 WYLSAAGCKNLS-----POKEVDIIDNFIILRNRSDESGVNTSFQYQKGM 71
DB 3 WSLGSLWGLGLVSLAMVPPENVNRNVSFNKNILOWESPAPKGLTITAOY---LS 58
QY 72 NWIKSGCQNTSTKCNFSSSLKLNVEIKLRIRAE-KENTSSVYEVDSFTPERKAOIGP 130
DB 59 YRIQDCKMNTTLECPSS--LSKYGDTLVRVAEFADSHDQVNI-TCPVDITLIGP 115
QY 131 PEVHLEA-EDKAIYHISPGTKDSV-NWALDGL--STYSLILWKNSSGVBERIENTYSR 186
DB 116 PGMQVEVLADSLHFRFLAPKRIENEYETWMKNVYNSWTYNVQYKKNCTDEKFOITPOYDF 175
QY 187 HKIKLSPETTYCCKYKAAALLTSKIGVYSVPHKIKTTVENELP 230
DB 176 EVLNLEPWTYTCVVRGFLPDRNKAGEWSEPCVETTHDETVP 219

RESULT 12
PCT-US94-14277-2
Sequence 2, Application PC/TUS9414277
GENERAL INFORMATION:
APPLICANT: Aguet, Michel
APPLICANT: Bohnl, Ruth
APPLICANT: Hemml, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 332 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-2

Query Match 8.8%; Score 203; DB 4; Length 332;
Best Local Similarity 30.1%; Pred. No. 8e-13;
Matches 69; Conservative 38; Mismatches 86; Indels 36; Gaps 13;

OY 21 LSAAGG-----KNLKSPOKVEVDIIDNFI LRNRSDSE-----VGNTFSPFDOKTOM.70
DB 16 LCAASSPSFSCOLAPLPRLHLYNDEQILTWBSPSSNDPRVYQVEYSF-----I.69
OY 71 D-NWIKL--SGCONITSTKCNFS--LKLNTYE-EIKLRIRAKEN-TSSVYEDSFTF.122
DB 70 DCSWRLLEPNCTDITETCDLTGGGRLLKLPFTVFLRAKAGNLSKRWGLPEFPOH.129
OY 123 FKAQIGPPE-VHLEAEDNAIYIHISPGTKDSVMALDGLSFTYSLLIWRKSSGVEERIE.181
DB 130 YENVTGPPKRNISVTPGKSLVHFSPPD-----VFHGATFOYLHVHYEKSETQOEQVE.184
OY 182 NYSRHKIY--KLSPETTYCLVKAAAL-LTSMKI---GVYSPVHCITKT.224
DB 185 GPFKNSIYLGKLPKRYVCIQTEAQLIKKKIRPHGLLSNVSCHETT.233

RESULT 13

US-08-943-087-2

; Sequence 2, Application US/08943087
; Patent No. 5945511

; GENERAL INFORMATION:
; APPLICANT: Lok, Si

; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.

; APPLICANT: Whitmore, Robyn L.
; APPLICANT: Fairah, Theodore E.

; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.

; STREET: 1201 Eastlake Avenue East
; CITY: Seattle

; STATE: WA
; COUNTRY: USA

; ZIP: 98102

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087

; FILING DATE:
; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305

; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:

; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743

; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678

; TELEX:
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids

; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Protein
; FRAGMENT TYPE: Internal
US-08-943-087-2

Query Match 8.6%; Score 198; DB 2; Length 553;
Best Local Similarity 21.0%; Pred. No. 6e-12;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

OY 11 LVLVAVGW--VLSAAGGNLKSPOKVEVDIIDNFI LRNRSDSEVG--NVTSPDYOK.67
DB 18 LLLILAPEGWRAVPCVSGG--LPRPANITFLSINNNKVLQWTPREGIQQVKTVOYFI.75
OY 68 TGMNWKLSGCONITSTKCNFS--LKLNTYE-EIKLRIRAKEN-TSSVYEDSFTF.126
DB 76 YGOKRWLKSSCRNNINRTCDLSAETSDEYEHQYAKAKAIGTKCSKWAESGREYPLET.135
OY 127 QIGPEVHLEAEDNAIYIHISPGTKDSVMALDGLSFTYSLLIWRKSSGVE.177
DB 136 QIGPEVALTTDEKISVVLAPKMKRNPEDDLPSMOQIYSNLKYNVSLNLTNSNTWS.195
OY 178 ERIENYSRHKIY--KLSPETTYCLVKAAAL-LTSMKI---GVYSPVHCITVENE-----229
DB 196 QCVTN---HTLVLTWLEPMTLYCVHYESFVCPGPPRAOPSEKQACARTLKDQSEFRAKI.251
OY 229 -----LPPENIEVSQNONVLMKDYTYANMTFOV-QMLHAPLKRNPGRHLYMKRQIPD.282
DB 252 IFWYVLP---ISITV-----FLFSVMGISITRYIHVGKKHPAULI-----290
OY 283 CENVKTTQCVFPOVFOKGIYLLRVQASDCNNTSFMSEEEKIPDEI---QAFLLPVENI.339
DB 290 -----LIGNEPFRKREFV---PAEKIVIFILNISDSKISHQMSLIGKSSDV.336
OY 340 RSLDSFHHIYGAPKQGNTPVIQDPLIYEI-----IFWENTSMAERKIIIEKTDV.391
DB 337 SSLND-----FQPSGNLRPQEEHEVKKHLYASHLMEIFCDSEBNTGTSFTQOEST.388
OY 392 --TVPNLKLTVY.402
DB 389 SRTIPDKTIVLEY.401

RESULT 14

US-08-943-087-14

; Sequence 14, Application US/08943087
; Patent No. 5945511

; GENERAL INFORMATION:
; APPLICANT: Lok, Si

; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.

; APPLICANT: Whitmore, Robyn L.
; APPLICANT: Fairah, Theodore E.

; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.

; STREET: 1201 Eastlake Avenue East
; CITY: Seattle

; STATE: WA
; COUNTRY: USA

; ZIP: 98102

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087

; FILING DATE:
; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305

FILING DATE: 20-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Lunn, Paul G
 REGISTRATION NUMBER: 32,743
 REFERENCE/DOCKET NUMBER: 96-24CL1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678
 TELEX:
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 553 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 OS-08-943-087-14

Query Match	8.6%	Score 198;	DB 2;	Length 553;
Best Local Similarity	21.0%;	Pred. No. 6e-12;		
Matches 91;	Conservative 79;	Mismatches 173;	Indels 90;	Gaps 17;

```

0Y 11 LVAAGPW--VLSAAGKTKLSPKVEVDIIDDNFILMNNSSDESVC--NYFESPDYOK 67
Db 18 LLLLLAAPGAVNAYCVSGG--LPKPANITELSTIMKKVNLDTMPPEGLQGKYYITVOYFI 75
0Y 68 TGDMDWIKLSCQONITSTKCNFSSLLKNVEELKIRIRA-EKENTSSWEYVDSFTPEFRKA 126
Db 76 YGOKMLTKKSECRNINRYCDSLAEtSDYEHQYAKVAKLMTGTRCKSMABSGHFPDELE 135
0Y 127 QIGPPEVHLEMDAIAIYHISPGRK-----DSYMALDGLSFTYSLILKKNSSGVE 177
Db 136 QIGPEVALTDEKISIVYLAPAEKMRNPEDLPVSQOQIYSNLKYNVSVLNTKRNPTWS 195
0Y 178 ERIENIYSRHKIYK--LSPETTYCLKVAALLTSMKIGVSPVCHICTYENE----- 229
Db 196 QCVYN---HILVLTWLEPNILYCVHNESFPGPBPRAQPSERKOCATILNDQSSFPKAI 251
0Y 229 -----LPPENIEVSVONQNTVLKMDTYANMTQV--QMLHAFIKRNPQHLLYKWKQIPD 262
Db 252 IFWVYLP--ISITV-----FLFSYMGISIRYIHVGEKHPANLI----- 290
0Y 283 CENYKTTQCVPONVFOKGIYLLRVOASDGNNTSFSEEEKITFDEI---QAFLLPVEYNI 339
Db 290 -----LIYGBEDFKRFY---PAEKIYVIFITLINSDDSKISHQMSLLGKSSDV 336
0Y 340 RSLDSFHIYIGABROSGNTPVODYPLIYEI-----IEMWTSNAERKIIIEKKTQV 391
Db 337 SSLND-----PQPSGNLRPQDEEVBKHLGYASHLMLEIFCDSEENTGTSPTQOESL 388
0Y 392 ---TPVNLKPLTVY 402
Db 389 SRTIPPKDTVLEY 401

```

RESULT 15
 US-08-943-087-16
 Sequence 16, Application US/08943087
 Patent No. 5945511
 GENERAL INFORMATION:
 APPLICANT: lok, si
 APPLICANT: kho, Choon J.
 APPLICANT: Jeimberg, Anna C.
 APPLICANT: Adams, Robyn L.
 APPLICANT: Whitmore, Theodore E.
 APPLICANT: Farrah, Theresa M.
 TITLE OF INVENTION: CYTOKINE RECEPTOR
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Zymogenetics, Inc.
 STREET: 1201 Eastlake Avenue East

```

1      City: Seattle
2      STATE: WA
3      COUNTRY: USA
4      ZIP: 98102
5
6      COMPUTER READABLE FORM:
7      MEDIUM TYPE: Diskette
8      COMPUTER: IBM Compatible
9      OPERATING SYSTEM: DOS
10     SOFTWARE: FASTSEQ for Windows Version 1.0
11     CURRENT APPLICATION DATA:
12     APPLICATION NUMBER: US/08/943,087
13     FILING DATE:
14     CLASSIFICATION: 536
15     PRIOR APPLICATION NUMBER:
16     APPLICATION NUMBER: 08/803,305
17     FILING DATE: 20-FEB-1997
18     ATTORNEY/AGENT INFORMATION:
19     NAME: Lunn, Paul G
20     REGISTRATION NUMBER: 32,743
21     REFERENCE/DOCKET NUMBER: 96-24C1
22     TELECOMMUNICATION INFORMATION:
23     TELEPHONE: 206-442-6627
24     TELEFAX: 206-442-6678
25     TELEX:
26
27     INFORMATION FOR SEQ ID NO: 16:
28
29     SEQUENCE CHARACTERISTICS:
30     LENGTH: 553 amino acids
31     TYPE: amino acid
32     STRANDEDNESS: single
33     TOPOLOGY: linear
34
35     MOLECULE TYPE: protein
36     FRAGMENT TYPE: internal
37
38     US-08-943-087-16

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Query Match	8.6%;	Score 198;	DB 2;	Length 553;
Best Local Similarity	21.0%;	Pred. No. 6e-12;		
Matches	91;	Conservative	79;	Mismatches 173;
			Indels	90;
			Gaps	17;

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0Y 11 LVAIVGFW--VLSAAGGNKULSPKQVEVDIIDDNFILMNRNSDESVG--NTFSPDYOK 67
0Y 18 LLLLLAAAGAAVPCVSGG--LKPANITFSLIMKNVLOMTPEGLQGVITYOYFI 75
0Y 68 TGMDMWIKLSCGCONITSTKCNFSSLKINYEEIKLIRA--EKENTSSWYEVDSFTPRKA 126
0Y 76 YGOKMKLTKSCBSCRNIINTRYCDLSAETSDYEHQYAKKALMGTKCSMAESGREFPLET 135
0Y 127 QIGPPEVHLEADKAIVHISPGK-----DSYMAIDGSLFTSYLLIMKNSGVE 177
0Y 136 QIGPEVALITDEKISIVLTLAPBKRMRNPEDLPVSMQOIIYSLNKYVAVSLNKTNSPTWS 195
0Y 178 ERIEITYSRHKIYK--LSPETTYCLNKAALLTSMKIGVYSPVHCITRYENE----- 229
0Y 196 QCVYN-----HLVLTWLEPNLPCVHNESFPGPRPRAQOSEKCATLNDQSEFPKXI 251
0Y 229 -----LPPENIEVSQONQNTVLMWDYTNMFOV--QWLHAFIKRNPCHLKYMKOIPD 282
0Y 251 IFWYLP-----ISTY-----FLFSWGSISIRYIHVGKEXHPANLI----- 290
0Y 283 GENVATTCQVPPONVFOKGIYLLRVAQSDGNTSFWSBEIKFDEI--QAFLLPVPFNI 339
0Y 290 -----LTYGNEEDKRFV---PAEKIVITFITLNSDSKISHODMSLLGKSDV 336
0Y 340 RSLDSFHIYIGAPROSGNTFVIDYPLIYEI-----IFWNTSNAERKILIEKTDV 391
0Y 337 SLSLND-----PQPSNLNLPQDEEVBKHLGVAASHLMEIFCDSSENTGTSFTQOESL 388
0Y 392 --TVPNLKPLVY 402
0Y 389 SRTIIPDKTVLEY 401

```

Mon Jun 5 12:54:26 2000

us-09-240-675-2.modif.ra1

Page 10

Search completed: June 1, 2000, 05:52:41
Job time: 4640 sec

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: June 1, 2000, 04:36:46 ; Search time 16.46 Seconds
(Without alignments)
1553.011 Million cell updates/sec

Title: US-09-240-675-2

Perfect score: 2313

Sequence: 1 MMVLLGATTLLVAVGPNV.....KSSVSDAVCEKTRKPGNTSK 436

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Database :

1: PIR.63:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2313	100.0	557	2	A32694	Interferon alpha/b
2	1507	65.2	560	2	S27387	Interferon alpha r
3	1069	46.2	590	2	A45283	Interferon alpha/b
4	233.5	10.1	273	2	G01418	Cytokine receptor
5	228.5	9.9	325	2	A47003	Cytokine receptor
6	221.5	9.6	349	2	JC6311	Interferon recepto
7	203	8.8	332	2	A49447	Interferon gamma r
8	155.5	6.7	337	2	I38500	Interferon gamma r
9	129	5.6	1375	2	T13822	frizzled gene prot
10	129	5.6	1375	2	T13822	frizzled gene prot
11	127.5	5.5	1443	2	I50600	neogenin - chicken
12	123.5	5.3	1451	2	S42167	190K protein - hum
13	119	5.1	1383	2	A36080	insulin receptor p
14	118	5.1	489	2	A31555	interferon gamma r
15	118	5.1	981	2	S51604	receptor-like tyro
16	118	5.1	1005	2	S49015	receptor tyrosine
17	117.5	5.1	575	2	A49667	interleukin-10 rec
18	117.5	5.1	1427	2	I51669	tumor suppressor -
19	117.5	5.1	1585	2	T19121	probable protein-t
20	117	5.1	817	2	A48721	titin, muscle - ch
21	116	5.0	1912	2	A56178	protein-tyrosine-p
22	115.5	5.0	658	2	T16040	hypothetical prote
23	115	5.0	1450	2	A44027	165K myofibrillar
24	115	5.0	26826	1	I38344	titin, cardiac mus
25	113.5	4.9	880	1	JC4166	protein-tyrosine k
26	113	4.9	1615	2	B49502	protein-tyrosine-p
27	113	4.9	1767	2	A49502	protein-tyrosine-p
28	113	4.9	1898	2	S46216	leukocyte antigen-
29	113	4.9	6831	2	T27934	hypothetical prote
30	113	4.9	6839	2	S57242	twilchin - Caenorh

31	113	4.9	7160	2	T27935	hypothetical prote
32	111.5	4.8	1896	2	T08851	Down syndrome cell
33	109	4.7	416	2	T25036	hypothetical prote
34	109	4.7	1372	2	A34157	insulin receptor p
35	108.5	4.7	1028	2	I58164	IG-1 protein - ra
36	108.5	4.7	2033	2	T09123	hybrid receptor So
37	108.5	4.7	2215	2	T00348	LtR1 protein - mou
38	108	4.7	991	2	I78843	receptor protein-t
39	106.5	4.6	878	1	S47489	receptor tyrosine
40	105.5	4.6	898	1	A44091	interleukin-3 rece
41	105.5	4.6	893	2	S51603	receptor-like tyro
42	105.5	4.6	1825	2	T32828	hypothetical prote
43	105	4.5	36	2	S41602	interferon alpha r
44	105	4.5	13055	2	T16580	hypothetical prote
45	104.5	4.5	662	2	I37892	IL12 receptor comp

ALIGNMENTS

RESULT 1

A32694

Interferon alpha/beta receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 22-Oct-1999

C:Accession: A32694; S17112

R:Uze, G.; Lutfalla, G.; Gresser, I.

Cell 60, 225-234, 1990

A:Title: Genetic transfer of a functional human interferon alpha receptor into mo

A:Reference number: A32694; MUID:90124632

A:Accession: A32694

A:Molecule type: mRNA

A:Residues: 1-557 <UZE>

A:Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1; PID:g306914

R:Lutfalla, G.

submitted to the EMBL Data Library, July 1991

A:Description: The structure of the human interferon alpha/beta receptor gene.

A:Reference number: S17112

A:Accession: S17112

A:Molecule type: DNA

A:Residues: 1-16, 'A', '18-329, 'V', '343-557 <LUT>

A:Cross-references: EMBL:X60459; NID:g32671

C:Genetics:

A:Gene: GDB:IFNAR1; IFNAR; IFRC

A:Cross-references: GDB:120078; OMIM:107450

A:Map position: 21q22.1-21q22.1

A:introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3

C:Keywords: cytokine receptor; glycoprotein; transmembrane protein

F1-21/Domain: transmembrane #status predicted <TRN1>

F1-437-455/Domain: transmembrane #status predicted <TRN2>

F150,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydr.

Query Match

Best Local Similarity 100.0%; Score 2313; DB 2; Length 557;

Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	MMVLLGATTLLVAVGPNVLSAAAGKRLSPKVEVDIIDNFIIRNNSDESGVNT	60
DB	1	MMVLLGATTLLVAVGPNVLSAAAGKRLSPKVEVDIIDNFIIRNNSDESGVNT	60
OY	61	FSFDYQTKGMNWKLSGCONITSTKCNFSSILKLVYEIKLRIRAEKENTSSWEVDSE	120
DB	61	FSFDYQTKGMNWKLSGCONITSTKCNFSSILKLVYEIKLRIRAEKENTSSWEVDSE	120
OY	121	TPFRQAQGPPEVHLAEADKAIVHISPGTDSVYMAIDGSLFTYSLILNNSGVEERI	180
DB	121	TPFRQAQGPPEVHLAEADKAIVHISPGTDSVYMAIDGSLFTYSLILNNSGVEERI	180
OY	181	ENIYRHRHIIYKLSPEPTTCLAVKAAALLTSMKIGVSPVHCITVTENELPPENIEVSQ	240
DB	181	ENIYRHRHIIYKLSPEPTTCLAVKAAALLTSMKIGVSPVHCITVTENELPPENIEVSQ	240

QY	241	NONVLA	KDYI	YV	YANN	FE	VO	WL	HL	FL	KRN	PN	NH	L	KK	KK	IP	DC	EN	VT	TO	CV	P	Q	AN	FO	K	300	
Db	241	NONVLA	KDYI	YV	YANN	FE	VO	WL	HL	FL	KRN	PN	NH	L	KK	KK	IP	DC	EN	VT	TO	CV	P	Q	AN	FO	K	300	
QY	301	GIYLLR	VO	AS	GD	NN	TS	EF	SE	EI	KD	TE	IO	AE	LP	PN	IN	SL	SS	PH	IY	GA	P	Q	OS	GN	TP	360	
Db	301	GIYLLR	VO	AS	GD	NN	TS	EF	SE	EI	KD	TE	IO	AE	LP	PN	IN	SL	SS	PH	IY	GA	P	Q	OS	GN	TP	360	
QY	361	VIODY	PL	YE	IF	EF	EN	TS	NA	ER	KI	IE	KT	DV	YV	NL	KP	LV	YV	CY	KA	RA	H	M	D	E	K	LN	SSV 420
Db	361	VIODY	PL	YE	IF	EF	EN	TS	NA	ER	KI	IE	KT	DV	YV	NL	KP	LV	YV	CY	KA	RA	H	M	D	E	K	LN	SSV 420

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QY      421 FSDAVCEKTKPGNTSK 436  
        |||||  
Db      421 FSDAVCEKTKPGNTSK 436
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RESULT      2
S27387
Interferon alpha receptor type 1 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jan-1995 #sequence_revison 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S27387; S33770
R:Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
A>Title: Specific antiviral activities of the human alpha interferons are determined at
A:Reference number: S27387; MUID:93076908
A:Accession: S27387
A:Status: Preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-560 <MOU>
A:Cross-references: EMBL:X68443; NID:9431; PIDN:CAA48484.1; PID:9432
A:Experimental source: MDBK cells
R:Lim, J.K.; Langer, J.A.
Biochim. Biophys. Acta 1173, 314-319, 1993
A>Title: Cloning and characterization of a bovine alpha interferon receptor.
A:Reference number: S33770; MUID:93305725
A:Accession: S33770
A:Status: Preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-421, 'V', 423-560 <LIM>
A:Cross-references: EMBL:L066290; NID:g163187; PIDN:AAA02571.1; PID:g163188
A:Experimental source: lung
C:Keywords: antiviral; cytokine receptor; transmembrane protein
F:1-34/Domain: signal sequence #status predicted <SIG>
F:235-560/Product: Interferon alpha receptor type 1 #status predicted <MAT>

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[illegible]

Db 299 SRGIIYAVVRASNGSGISFMSEEEENFEMTKTIIFFPIVIAKSTIDSDLSHVSGASESE 358
OY 358 NTPVIQDYPILYIEIIFEMTSSNAERKIIETKTDVTENLPLFYVCYKAAHTEDELNK 417
Db 359 NMSVQQLPFLYIEVIFEMTSSNAERKYLEKRTNIFDLKPLFYVCYKABALLIENDRNK 418
OY 418 SSVFSDAYCEKTKPGNTSK 436
Db 419 GSSFSQDYCEKTKPGNTSK 437

Db 419 GSSFSDTVCEKTKPGNTSK 437

RESULT 3
A45283

C.Date: 25-May-1993 #sequence_revision 18-Nov-1994 #ext_change 05-Nov-1999
C.Accession: A45283; I48422; I48424; I48426; I48428; I48422252
R.Uzu, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogenssen, K.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
A.Title: Behavior of a cloned murine interferon alpha/beta receptor expressed
A.Reference number: A45283; MIMD:92262522

A:Residues: 1-590 <UZE>
A:Cross-references: GB:889641; NID:g194111; PIDN:AAA37890.1; PID:g194112
A:Note: sequence extracted from NCBI backbone (NCBIN:102354, NCBIIP:102357)
R:Rutfalla, G.: Use, G
Gene 148, 343-346, 1994
A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: h1g4
A:Reference number: 148423; M01D:95047447

A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 118-125 <RES>
A:Cross-references: EMBL:U06237; NID:g497103; PIDs:AAA65003.1; PID:g755810
A:Accession: I48424
A:Status: preliminary; translated from GB/EMBL/DBD

A:Cross-references: EMBL:U066238; NID:g497104; PIND:AMC01749.1; PID:g755811
A:Accession: I48425
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 243-264 <RE3>
A:Cross-references: EMBL:U066239; NID:g497106; PIND:AAA65004.1; PID:g510261

A:Accession: 148426
A:Status: preliminary; translated from GB/EMBL/DDJ
A:Molecule type: DNA
A:Residues: 265-375 <RFA>
A:Cross-References: EMBL:U06240; NID:g497108; PIDN:AAA65005.1; PID:g510262

A:Accession: 14842/
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 397-424 <RES>
A:Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.1; PID:g755812

A:Accession: 148428
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 126-445 <REG>
A:Cross-references: EMBL:U06242; NID:g487112; PIDN:AAA65007.1; PID:g755813

A:Accession: 148429
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 473-590 <RET>
A:Cross-References: EMBL:U06244; NID:g497114; PIDN:AAA65008.1; PID:g510265

C:Genetics:
A:Gene: IFNAR
A:Introns: 177/3; 331/1
C:Keywords: cytokine receptor; transmembrane protein

[illegible]

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Oy 187 HKIYELSPETTYCLVKYKALLTSWKIGVSPHICIKTIVENELP 230
      : : | | | | | : : : : : : : : : : : : : : : : :
Db 176 EYLRNLEPWTITCYOVRGFLPDRNKAAGESEPCQETHTDEIVP 219

RESULT 5
A47003
Cytokine receptor family class II protein CRF2-4 precursor - human
C:Species: Homo sapiens (man)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1997
A:Accession: A47003
R:Rutafalla, G.; Gardiner, K.; Uze, G.
Genomes 16, 366-373, 1993
A:Title: A new member of the cytokine receptor gene family maps on chromosome 21
A:Reference number: A47003; MUID:93300510
A:Accession: A47003
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-325 <LUN>
A:Cross-references: GB:217227; NID:9393378; PID:9393379
C:Keywords: transmembrane protein

Query Match 9.9%; Score 228.5; DB 2; Length 325;
Best Local Similarity 29.9%; Pred. No. 7.8e-10;
Matches 67; Conservative 42; Mismatches 96; Indels 19; Gaps 8;

Oy 19 WVLSSAAGGKNLKS-----POKYEVDIIDNFIILRNRSDESQGNVTFSPDYQRTGMD 71
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 WSLGSMLGCLLVSLGWPPEENVRMNSVFNKRNILQWESPAFAKNLFTAGY----LS 58

Oy 72 WKIKISGCONITSTYCNFSSSLKLVNVEIKLIRAE-KENTSMYVVDSETPPKRAQIGP 130
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 YRIFQDKMNTLTTECDFFSS--LSKYGDHTLVRARFADEHSDWVNI-TFCPPDDITIGP 115

Oy 131 PEVHLEA-EDKRIYVHIHSQTKDSV-MMALDGL--SFYSLLIKRSGVEEIEINYSR 186
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 116 PMQVEVLADSLHMRFLAKIENSETWTKKYNYSMTINVOYWKNGIDKEFOITQYDF 175

Oy 187 HKIYELSPETTYCLVKYKALLTSWKIGVSPHICIKTIVENELP 230
      : : | | | | | : : : : : : : : : : : : : : : : :
Db 176 EYLRNLEPWTITCYOVRGFLPDRNKAAGESEPCQETHTDEIVP 219

RESULT 6
JC6311
Interferon receptor class II cytokine receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
A:Accession: JC6311
R:Gibbs, V.C.; Pennica, D.
Gene 186, 97-101, 1997
A:Title: CRF2-4: isolation of cDNA clones encoding the human and mouse proteins.
A:Reference number: JC6311
A:Accession: JC6311
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-349 <GIB>
A:Cross-references: GB:U53696

Query Match 9.6%; Score 221.5; DB 2; Length 349;
Best Local Similarity 28.1%; Pred. No. 2.9e-09;
Matches 64; Conservative 49; Mismatches 86; Indels 29; Gaps 10;

Oy 16 VGPWTLSAAGGKNLKSPOKYEVDIIDNFIILRNNSDESQGNVTFSPDYQ--KTGQDNW 73
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 9 LGGFLLVPLRG--MIPPEPKVRMNSVFNKRNILQWEPAPRPNKTLFTAGYESYRSQDH- 66

Oy 74 IILSGCONITSTYCNFSSSLKLVNVEIKLIRAE-KENTSMYVVDSETPPKRAQIGPPE 132

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Db      66  -----CKRTASTOCDFE--HLKSKYGDYTVRAELADEHESEWNV--TFCEVEDTITGPPE 117
OY      133  VHEADEKAIYIHIS-----PGTKDSVMALDGL--SFTYSLLTKNKGVEERENT 183
Db      118  MQIESLAESLELRSAPQIENEPET-----WTAKNIYSMAVYRQVKNKGTNEKFEQVYSP 172
OY      184  YSRHKIKYKLPETTYCLKVAALTSWKIGVSPVHCIRKTVENELPP 231
Db      173  YDSEVLNLEPMTTTCYQVGGFLLDONRGESEPIC-ERTGDEITP 219

RESULT  7
Interferon gamma receptor beta subunit - mouse
N:Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor; type
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
R:Hemml, S.; Bohml, R.; Stark, G.; Di Marco, F.; Aguet, M.
A:Title: A novel member of the interferon receptor family complements functionality of
A:Accession number: A49947; MID:94170381
A:Accession: A49947
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-332 <HEM>
A:Cross-references: GB:S69336; NID:9545841; PIDN:AA830165.1; PID:9545842
A:Experimental source: early B-cell line Y16
A:Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIPI:145656)
C:Keywords: cytokine receptor

```

```

Query Match      8.8%; Score 203; DB 2; Length 332;
Best Local Similarity 30.1%; Pred. No. 6.5e-08;
Matches 69; Conservative 38; Mismatches 86; Indels 36; Gaps 13;

OY      21  LSAAGC-----KNLSPQKVEVDIIDNFIIRNRSDES-----VGNVTFSEFDYQKGM 70
Db      16  LGAASPSDFSQLAAPLNRLHYNDEQILTWEPSSSNDPRVYQVEYSF-----I 69
OY      71  D-NWIKI--SGCONITSTKCNFSS---LKNVTE-EIKLRIRAKEN-TSSWEVDSFTP 122
Db      70  DGSNHRLEPNCTDITETCKDGLTGCGRLKLPHPFTVFLVRAKRGNTLSKMGGLPEFOH 129
OY      123  FRKAQIGPPE-VHLEADEKAIYHISPGTKDSVMALDGLSFTYSLLTKNKGVEERIE 181
Db      130  YENVTYGPKNISVTPEKGSVLTHFSPFD-----VFHGATFQYLVHYWKSSETQOEQVE 184
OY      182  NISYRHKIY--KLSPEYTYCLKVAAL-LTSWKI---GVSPVHCIRKT 224
Db      185  GPKRSNIVAGNLKPYRVYCLQTEAQILNKKIRPHGLLSNVSCHETT 233

```

```

RESULT  8
Interferon gamma receptor accessory factor-1 precursor - human
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 05-Nov-1999
R:Soth, J.; Donnelly, R.J.; Kolenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S.
A:Title: Identification and sequence of an accessory factor required for activation of
A:Reference number: A49946; MID:94170380
A:Accession: I38500
A:Molecule type: mRNA
A:Residues: 1-337 <RES>
A:Cross-references: EMBL:U05875; NID:9463549; PIDN:AAA16955.1; PID:9463550
A:Experimental source: clone PSK1
A:Accession: I38501
A:Molecule type: mRNA
A:Residues: 1-63; 'Q', 65-337 <RE2>
A:Cross-references: EMBL:U05877; NID:9463551; PIDN:AAA16956.1; PID:9463552

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```

A:Experimental source: clone pJS3
C:Genetics:
A:Map position: 21
C:Keywords: cytokine receptor

```

```

Query Match      6.7%; Score 155.5; DB 2; Length 337;
Best Local Similarity 22.3%; Pred. No. 0.00023;
Matches 67; Conservative 54; Mismatches 112; Indels 67; Gaps 14;

OY      12  VLVAVGPVYLSAAGC-----KNLSPQKVEVDIIDNFIIRW-----NRSDESQVNTFS 62
Db      9  LILLGVFAAAAPDPDLSQLPAPQHPKIRLYRNEQVLSMEPVALSSTRPVYRVQFK 68
OY      63  FVYQKGMNWKLS-----GCONITSTKCNFSS-----LKNVTEEIKLRIRAK 108
Db      69  YDTSK-----WFTADINSIGNCTQITATEDFTAASAGFPMDFN---TLRLREL 119
OY      109  ENT-SSWEVDSFTPFKRAQIGPPEVHLE---AEDKAIYHISPGTKDSVMALDGLSFT 164
Db      120  GALHSAWYTMFQHYRNVTVGPPE-NIEVTPGESSLIIRSSPDIDTSTAF----FC 174
OY      165  YSLILWKNSSGVEERIEINYSRHKIY--KLSPEYTYCLKVAALTS---WKIGVSPV 218
Db      175  YVHYWME--KGGIQQVKGPFRRNSISLDNLKPSRYCLOVQAOLLMKNSNIFRVGHLN 232
OY      219  HGKIKTVENELPPENIEVSV-----QNONVYLKMDITYANNTFOVO 260
Db      233  SCYETMAADSTELQOVILISVGTFSLSVLGACFVLKRYGLIKYFHTPPSIPLOIE 292

```

```

RESULT  9
Frazzled gene protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
R:Kolodziej, P.A.; Tluppe, L.; Mitchell, K.J.; Goodman, C.S.; Fried, S.; Jan, L.Y.;
Cell 87, 197-204, 1996
A:Title: Frazzled encodes a Drosophila member of the DCC immunoglobulin subfamily &
A:Accession number: Z17780
A:Accession: T13822
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1375 <ROL>
A:Cross-references: EMBL:U71001; NID:91621114; PID:91621115; PIDN:AA047314.1
C:Genetics:
A:Gene: frazzled
A:Map position: 2
C:Function:
A:Description: may function in vivo as a receptor or component of a receptor mediat

```

```

Query Match      5.6%; Score 129; DB 2; Length 1375;
Best Local Similarity 16.4%; Pred. No. 0.15;
Matches 102; Conservative 68; Mismatches 184; Indels 268; Gaps 22;

OY      26  GGNLKS-----PKRVEVDIIDNFI-LRW-----NRSDESQV 56
Db      447  GKKPLDSGLQARLPSPQPDVAQIVKSRFTVLSWEPQLONAGDVYVYVYKMNNSEREQ 506
OY      57  GNVTFSEFDYQKGMNWKLSGCONITSTKCNFSS-----LKNVTEEIKLR----- 104
Db      507  KMYTSHDDQOVNIOSLPLGRYQORVAVANNFSGASASAPLEVSTQPEVAINIAGPRRNF 566
OY      104  --IRAENTSSWYE-----V 117
Db      567  GYARSHKEIYVWEPEVTNGEILTKRVYSESDSGADLYHDSALAEVLTAPHTDYV 626
OY      118  DSFTPFKRAQIG-----PPEVHLE-AEDKAIYHISPGTKDSVMAL 158
Db      627  ISVVPFNRNGMDSSAEIRVKTFSSTPSEPPNNVTLEVTSSSITVHWEPAEDDRNGOI 686

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QY 159 DGLSTVSYLLIMKNSSGVGEERIENTYSRHKIKXLSPEYYCCKYAAALL-----TSKRI 212
Db 687 TGYKIRYRK--FKDAPQVKSTPRANI-RYFELSNLDRAEAYOKYIAAMTVNGSGPTEENR 743
QY 213 GYVSPVHCIKTTVENEL-----PENIEVSGVQNONYVLK 247
Db 744 A-----NTLENDLDETQVPRKPIWISIHGANNIALHMGPPQHPEIKI--RNYVLG 792
QY 248 W-----DY-----251
Db 793 WGRGIPDENTIELKETERYHIKLNESNMDYVSLRARNVKGDPPIYDNIKTRDEBPVD 852
QY 251-----TYAMTFQVOMLHAFKRN-----PGNHLYKMKQIP 281
Db 853 APTPLEVEVGRALIMSSSIPIVYWMIDMLKNKNOHTDNRHYTVSYGIGTSNRVRY--- 909
QY 282 DCEENVKTCQVCPQVPOVFKGIIYLLRVOASDGNNTSFWSESEIKFDEIDQAFLLPVPFNIRS 341
Db 909 --HNTTDLNCMI-NDLRNTOYEFPAVKYVKGRRSSWSMSVLSNITYQVNPVTPP----- 960
QY 342 LSDSFHIYIGAPKOSGNTPVIODYP-----LIYEIIFMENTSNAER-----KIEKK 388
Db 960 ----REVTVRLDENMNPVYIQWIMPKHTLIGQITGYNITYTTDTLTKRDRDMSVEAFAGEE 1015
QY 389 TDVYVFNKLPFLVYCVKRAHRT 410
Db 1016 TMLMLPNLKPYTTYFKVQART 1037

```

RESULT 10
T13823
frazzled gene protein, log isoform - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T13823
R:Kjodalej, P.A.; Timpe, L.; Mitchell, K.J.; Goodman, C.S.; Fried, S.; Jan, L.Y.; Jan, Y.
Cell 87, 197-204, 1996
A>Title: Frazzled encodes a Drosophila member of the DCC immunoglobulin subfamily and is
A:Reference number: 217780
A:Accession: T13823
A>Status: preliminary: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1526 <KOL>
A:Cross-references: EMBL:U071002; NID:g1621116; PID:g1621117; PIDN:AAC47315.1
C:Genetics:
A:Gene: frazzled
A:Map position: 2

[illegible]

```

QY 213 GYSPVHCITTYENLPP-----PPENLEVSQONQNYLK 247
      : : : : :
Db 895 A-----NLENDLDETVOGPKRWISHPGANNIALHWPQPHBEIKI--RNYVLG 943
      : : : : :
QY 248 W-----DY-----251
      : : :
Db 944 WGRGIPDENTIELKETERHILKNLESNDIYVSLRARNKGDGPPIYDNIKTDEEPPVD 1003
      : : :
QY 251 -----TYANNTPYOYOMLHAFLEKN-----PGNHLYKWKQIP 281
      : : : : :
Db 1004 APTPLEYVPGRLAITWSSSSIVYWMYDMLKNNQHYTDNRHNTYSYGTIGSNRRRY----- 1060
      : : : : :
QY 282 DCENVKTTQCVFPQNVYFQKGIYLLRYVOASDGNNTSFWESEIKFDTEIOAFLLPYVENIRS 341
      : : : : :
Db 1060 ---NHTTDLCMI--NDLRPTQYEFAYKVVYKGRRESMSVSLNSTYQWVPTP----- 1111
      : : : : :
QY 342 LQSDFHLYTAPKQSGNTPYIODP-----LIYEIIFWNTSINAER-----KIIKK 388
      : : : : :
Db 1111 ---REYTVRLDEMNPPYTVQWIPKHTLGOITGYNITYTDTTKRDRDMSVEAFAGE 1166
      : : : : :
QY 389 TDYTVPLKRLPYVCVKARAHT 410
      : : : : :
Db 1167 TMLLPLNLRKPYTYTYFRVQART 1188
      : : : : :

```

```

RESULT 11
150600
neogenin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
C:Accession: 150600
R:Vielmetter, J.; Kayem, J.F.; Roman, J.M.; Dreyer, W.J.
J. Cell Biol. 127, 2009-2020, 1994
A:Title: Neogenin, an avian cell surface protein expressed during terminal neuron
A:Reference number: A51193; MUID:95105243
A:Accession: 150600
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1443 <VIEW>
A:Cross-references: EMBL:U07644; NID:G641965; PID:G641966

```

[illegible]

RESULT 12

S42167

190K protein - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_rev13on 13-Jan-1995 #text_change 24-Sep-1999

C:Accession: S42167

R:Linkmeter: U.: Obermann, W.; Weber, K.; Fuerst, D.O.

J. Cell Sci. 106, 319-330, 1993

A:Title: The globular head domain of tltin extends into the center of the sarcomeric M

A:Reference number: S42166; MOID:94095665

A:Accession: S42167

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1451 <VIN>

A:Cross-references: EMBL:X69090; NID:g407098; PIDN:CAA4883.1; PID:g407099

C:Superfamily: skelamin

Query Match

Best Local Similarity 5.3%; Score 123.5; DB 2; Length 1451;

Matches 91; Conservative 67; Mismatches 181; Indels 121; Gaps 21;

QY 43 DNFILRNRSDESVDN--VFSEFDYOKTGMNMIKSGCONITSTKCNFSLKLNVEEI 100
 DB 388 DYIISMKOPAVDGGSPILGIFDKCEVGTDSM-----SQCNDTPVAFARPVT 436
 QY 101 KL-----RIRAEKENTSSW-----YEVDSFTPFKRAQIGPEVHLAEADKAIYIHS 147
 DB 437 GLIEGRSYIFRVAVNKMGIGFSPRSEAVAAALDPAEKARLKP--LSTLDWTVIYTEE 493
 QY 148 PGKIDSVMAALDLSFT-----YSLIWK-----NSGVEERENIYS----- 186
 DB 494 EPEEGVPGPPTDLSVTEATRSYVLSMKPPGORGHEGIMYFEKCEAGTEMQORNTL 553
 QY 186 -----RHKIKYKSPETTYCLKRAALTSWIKIGYSPVHCIXKTV-----ENELP 230
 DB 554 PVKSPRALFDLAEKSGYCRVRC-----SNSAGGSESEATEVTYVGDKIDIRAKPKII 609
 QY 231 PENIEYVONONYVLKMD-----YTYANMTFOVOMLHAFLEKRNPGNHLKKWK 278
 DB 610 PSRNTDTSV-----VVSMEESKDAKELVGYIEANVAGSGKWEPC--NNNPVKTHRP-- 660
 QY 279 QIDCEVAVKTCQVFPNPNVOKGIYLLRVQASDGNNTSFSEIEKFTDIOAFLP-- 336
 DB 660 ---TCGGLVTGQS-----YIFRVAVNMAAGLSEYSQDSE-AIEVKAALAPSPSP 704
 QY 336 --VFNIKSLSDSFHIYIGAPKQSGNTPVIDYPLIYEII-----FWENTSNAERKIIERK 388
 DB 705 CDITCLESPRDSWVLGKQKQDKGAGAITIGTYVNYNREVIDGVPQKMR---EAVVKAVREE 761
 QY 389 TDVTVPNLKPLTYCYVKARAHITDEKINKSSVFSDAVCEK 428
 DB 762 A-YKISNLKENMYOFOVAAAMNAGLGPASVSECFCEE 800

RESULT 13

A36080

Insulin receptor precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 14-Dec-1990 #sequence_rev13on 14-Dec-1990 #text_change 18-Jun-1999

C:Accession: A36080

R:Goldstein, B.J.; Dudley, A.L.

Mol. Endocrinol. 4, 235-244, 1990

A:Title: The rat insulin receptor: primary structure and conservation of tissue-specific

A:Reference number: A36080; MOID:90231337

A:Accession: A36080

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1183 <GOL>

A:Cross-references: GB:M29014; NID:g204953; PIDN:AAA1441.1; PID:g204954

C:Superfamily: Insulin receptor; protein kinase homology

C:Keywords: ATP; autophosphorylation; hormone receptor; phosphoprotein; transmembr
 F:1023-1298/Domain: protein kinase homology <KIN>
 F:1030-1038/Region: protein kinase ATP-binding motif

Query Match

Best Local Similarity 5.1%; Score 119; DB 2; Length 1383;

Matches 89; Conservative 52; Mismatches 151; Indels 172; Gaps 20;

QY 43 DNFILRNNSDSVGNVTFSEFDYOKTGMN-----WIKSGCON 81
 DB 481 NMIALKTNDQASCENELKFSIRTSFDKILLRPEYPPDFRDLGLMFLYKAPYON 540
 QY 82 IT-----STKCNFSKLKLNVEIKLIRAEKENTSSWYEVDSFTPFKRAQIGPEVHLA 137
 DB 541 VTEFDGQDNC-----GNSWYVD-----IDPPQ---RS 566
 QY 138 EDKAIYIHSPTGKDSVMAALDLSFTYSLIWKNSGVEERENIYSRHKIKYKSPETT 197
 DB 567 NDPKSOTPSHPG-----WLMRG-----LKPWTQ 589
 QY 198 YCLKVAALITSMK--IGVSPVHCITTVENELPPENIEYVONONYVLK--DYT 251
 DB 590 YAIFFVKTLYTFSDERTYGAKSIIYVOTDANPSYPLDPISSVSSSOIILKMRPPSDP 649
 QY 252 YANMTFOVOMLHAFLEKRNPNHLKKW-KOIPCEVAVKTCQVFPQVFPQGIYL----- 305
 DB 650 NGNIT-----HYLVYTERQAEDELFDLYCL-----KGKLKLSRTWS 687
 QY 305 --LRVQASDGNNTSFSEIEI-----KEDTIOAFLPPVNIKSLSDSFHIYIGAPKO 355
 DB 688 PPEESDSQKHNQSEYDSDASCCGPKTDSOILKELESSPR-KTFEDYLNINVFVPRK 746
 QY 356 --SGN-----TPVIQDPLIYEIIFWENTSNAERKIIERK--- 388
 DB 747 TSSGNAEDTRPSRRKRSLEEVGNATATPTLPDPFNISSTI--APTSHHEHRPREKVVN 804
 QY 388 KTDVTVPNLKPLTYCYVKARAHITDEKINKSSVFSDAVCEKRP 431
 DB 805 KESLVISGLRHFTGYRIELQACNODSPERSGV-AAIYSARIMP 847

RESULT 14

A31555

Interferon gamma receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 28-Feb-1990 #sequence_rev13on 28-Feb-1990 #text_change 23-Jul-1999

C:Accession: A31555

R:Agnet, M.; Dembic, Z.; Meriin, G.

Cell 55, 273-280, 1988

A:Title: Molecular cloning and expression of the human interferon-gamma receptor.

A:Reference number: A31555; MOID:89003065

A:Accession: A31555

A:Molecule type: mRNA

A:Residues: 1-489 <AGQ>

A:Cross-references: GB:J03143; NID:g184650; PIDN:AAA52731.1; PID:g306915

C:Genetics: GDB:IFNGR1; IFNGR

A:Cross-references: GDB:120688; OMIM:107470

A:Map position: 6q23-q24

C:Superfamily: Interferon gamma receptor

C:Keywords: cytokine receptor; transmembrane protein

Query Match

Best Local Similarity 5.1%; Score 118; DB 2; Length 489;

Matches 50; Conservative 39; Mismatches 102; Indels 34; Gaps 10;

QY 227 NELPPENIEYVONONYVLKMDIYVYANM--TFQVOMLHAFLEKRNPNHLKKMOIPDCE 284
 DB 27 SSVPPTNTIITSYNNPPLVYWEYQIMQVPPFTYE-----YKNYGVKNSDM--IDACI 78
 QY 285 NVTTCQVFPQVNFQKGIYL-LRVQASDGNNTSFSEIEKFTDIOAFLPPVNIKRS-- 342

Job time: 4582 sec

```
Db 79 NISHHCNIDSHDGPNSLWVRKAVGKESAVAKSEFAVCRDGGKIGPPLDIRKEE 138
OY 342 ---LSDSFH--IYIGAPKOSGN--TPYIDPPLYEIIIFMENTSNARKIIEKKT----- 391
Db 139 KQIMIDIFHPSPVFNDEQEDVDYDPTTCIRYNNYVRMNGSEIYKILITOKEDDCDEI 198
OY 391 ---VTVPNLKPPLTVYCVKARA--HTNDEKLKNS----SVFSDAV 425
Db 199 OCOLAIPVSSINSQYCSAGVLRHWGVTEKSEKVCITIFNSSI 243
```

RESULT 15

```
SS1604
receptor-like tyrosine kinase Eph-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 29-May-1998
C:Accession: S51604
R:Malsonpierre, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A:Title: Eph-1 and Eph-2: two novel members of the Eph receptor-like tyrosine kinase fam
A:Reference number: S49015; MUID:94067777
A:Accession: S51604
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-981 <MAIL>
A:Cross-references: EMBL:568029
A>Note: the authors translated the codon GAC for residue 170 as Glu
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
F:651-917/Domain: protein kinase ATP-binding motif
F:659-667/Region: protein kinase ATP-binding motif
```

Query Match

5.1%; Score 118; DB 2; Length 981;

Best Local Similarity 20.1%; Pred. No. 0.64; Mismatches 165; Indels 150; Gaps 21;

```
Matches 92; Conservative 51;
OY 27 GKNLKSPQYVEDII--DQNF-----ILRNRSDESYGNT---FSFDYQKQGMNW 73
Db 165 GRNINKNOYIKIDTIADESEFTELDGDRVMKLNTEVRDYGPLSKGFYLAQDVG---- 221
OY 74 IKLSGCONITST-----KCNFSSIKLNVYEILRLIRAENKNTSSWTEVDSTPRKKAQI 128
Db 221 ----ACIALVSVRVYKKCPSVVRHLAVFPD-----TITGADSSQLLEVSGCVNHSVTD 271
OY 129 GPPEVHLEADKAIVHISGTDKDSVMALDGLSTYSLLINKNSSGVEERIENI--YSRH 187
Db 272 DPPRMHCSAGEWLV---PIGKMC-----KAGYEKNGTCQVCRP 309
OY 188 KIKLSPETTYCLKVKAALLTSWKIGVSPVH-----CIKTVENELPP----- 232
Db 310 GFFKASHSOTCSKCP-----HSTHEASTSCVCEKDYFRRESDPPTMACTRP 359
OY 232 ---PENIEVSQONQNTVLYKM-----DYTYANTFOVQWLHAFKRNPGNHLKWK 278
Db 360 PSAPRNALISVNVETSVLEWIPPADTGGKDVSYIILCKKN--SHAGVCEECGHVR--- 416
OY 279 QIPDCEVNTKTCVFPQNVQKGIYILRVASGNNNTSFWSEIKFTDEIOAFLLPVEN 338
Db 416 -----YLPQOIGLKNTSVMMADPLAHTNTTF-----ELEA-----VNG 448
OY 339 IRSLSDSFHIYIG---APKOSGNTPVIO-----DYP-----LIVEIIF 373
Db 449 VSDLSPEGTROYVSNVTNTQAAPSPVNVKKGKIAKNSISLSMQEPDRPNCIILEYIKY 508
OY 374 WENTSNARKIIE-KTQDVTPNKLPLTVYCVKARAHT 410
Db 509 FEKDOETSYTIKSKETITAEGLKPAVYVFOIRART 546
```

Search completed: June 1, 2000, 05:53:08

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:40:22 ; Search time 28.35 Seconds

(without alignments)
468.373 Million cell updates/sec

Title: us-09-240-675-2

Perfect score: 2313
Sequence: 1 MMVVLGATTLVAVGPWV.....KSYVSDVCEKTPGNTSK 436

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 08
Listing first 45 summaries

Database : SWISSProt_38.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2313	100.0	557	1 INR1_HUMAN	P17181 homo sapien
2	1507	65.2	560	1 INR1_BOVIN	Q04790 bos taurus
3	1503	65.0	560	1 INR1_SHEEP	Q28589 ovis aries
4	1069	46.2	590	1 INR1_MOUSE	P33896 mus musculu
5	228.5	9.9	325	1 CRP2_HUMAN	Q08334 homo sapien
6	155.5	6.7	337	1 INGS_HUMAN	P38484 homo sapien
7	123.5	5.3	1451	1 MYM1_HUMAN	P52179 homo sapien
8	119	5.1	1383	1 INSR_RAT	P15127 rattus norv
9	118	5.1	489	1 INGR_HUMAN	P15260 homo sapien
10	118	5.1	1005	1 EPAS_RAT	P54757 rattus norv
11	117.5	5.1	575	1 I10R_MOUSE	Q61727 mus musculu
12	116	5.0	1912	1 PTPD_HUMAN	P23468 homo sapien
13	115	5.0	1450	1 MPSP_CHICK	Q02173 gallus gall
14	113.5	4.9	880	1 TYO3_RAT	P55146 rattus norv
15	111.5	4.8	1447	1 DCC_MOUSE	P70211 mus musculu
16	109	4.7	1372	1 INSR_MOUSE	P15208 mus musculu
17	108	4.7	1037	1 EPAS_HUMAN	P54756 homo sapien
18	107	4.6	427	1 I131_HUMAN	P78152 homo sapien
19	105.5	4.6	878	1 IL3B_MOUSE	P26954 mus musculu
20	104.5	4.5	662	1 I12R_HUMAN	P42701 homo sapien
21	104.5	4.5	1447	1 DCC_HUMAN	P31416 homo sapien
22	104	4.5	866	1 CYR2_MOUSE	P26855 mus musculu
23	104	4.5	1239	1 NRG_DROME	P20241 drosophila
24	104	4.5	1897	1 PTPD_HUMAN	P10586 homo sapien
25	103.5	4.5	2280	1 YCF2_TOBAC	P00976 nicotiana t
26	103.5	4.5	918	1 IL6R_HUMAN	P40189 homo sapien
27	102.5	4.4	477	1 INGR_MOUSE	P15261 mus musculu
28	101	4.4	1304	1 CDA5_HUMAN	P08575 homo sapien
29	101	4.4	2131	1 YCF2_SPTOL	P08573 spiracula ol
30	100.5	4.3	2294	1 YCF2_ARATH	P43816 arabidopsis
31	99.5	4.3	677	1 SPOT_HAEIN	P43811 haemophilus
32	99.5	4.3	897	1 CYR2_HUMAN	P32927 homo sapien
33	99.5	4.3	3135	1 S230_PLAFO	Q08372 plasmodium
34	99	4.3	1091	1 C1C2_RAT	P54290 rattus norv

35	99	4.3	1382	1 INSR_HUMAN	P06213 homo sapien
36	98.5	4.3	1345	1 YH00_YEAST	P38800 saccharomyc
37	98.5	4.3	1615	1 RRPO_TMV	P03586 tobacco mos
38	98	4.2	578	1 I10R_HUMAN	Q13651 homo sapien
39	97.5	4.2	306	1 K128_YEAST	P06242 saccharomyc
40	97.5	4.2	1091	1 C1C2_HUMAN	P54289 homo sapien
41	97.5	4.2	1162	1 LEPR_MOUSE	P48356 mus musculu
42	97.5	4.2	1256	1 FINC_CHICK	P11722 gallus gall
43	97.5	4.2	3124	1 CA1C_CHICK	P13944 gallus gall
44	97	4.2	517	1 KTR7_YEAST	P40504 saccharomyc
45	96.5	4.2	515	1 INR2_HUMAN	P48551 homo sapien

ALIGNMENTS

RESULT 1
INR1_HUMAN STANDARD: PRT: 557 AA.
ID INR1_HUMAN
AC P17181;
DT 01-AUG-1990 (Rel. 15, Created)
DR 01-AUG-1990 (Rel. 15, Last sequence update)
DE 15-FEB-2000 (Rel. 39, Last annotation update)
GN INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
NC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP MEDLINE: 90124632.
RX Uze G., Lutfalla G., Gresser I.;
RT "Genetic transfer of a functional human interferon alpha receptor
into mouse cells: cloning and expression of its cDNA."
RL Cell 60:225-234(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92129376.
RA Lutfalla G., Gardiner K., Proudman D., Vleth E., Uze G.;
RT "The structure of the human interferon alpha/beta receptor gene."
RL J. Biol. Chem. 267:2802-2809(1992).
RN [3]
RP PHOSPHORYLATION BY TYK2.
RX MEDLINE: 95059042.
RA Colomonic O., Yan H., Domanski P., Handa R., Smalley D.,
RA Mullerman J., Witte M., Krishnan K., Krolewski J.;
RT "Direct binding to and tyrosine phosphorylation of the alpha subunit
of the type I interferon receptor by p135tyk2 tyrosine kinase."
RL Mol. Cell. Biol. 14:8133-8142(1994).
CC -I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
SUBUNITS THEMSELVES.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND
EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.
CC -I- PTM: PHOSPHORYLATED 2 TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.
CC -I- SIMILARITY: CONTAINS 2 FIBRINONCTIN TYPE II-LIKE DOMAINS.
CC -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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or send an email to license@isb-slb.ch).
CC
CC EMBL: J03171; AAA52730.1; -
DR EMBL: X60459; AAA42992.1; -
DR PIR: A32694; A32694.
DR PIR: S17112; S17112.
DR MM: 107450; -

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KM Receptor: Transmembrane; Glycoprotein; Signal: Polymorphism;
KM Phosphorylation:
FT SIGNAL 1 27
FT CHAIN 28 557
FT DOMAIN 28 436
FT TRANSMEM 437 457
FT DOMAIN 458 557
FT DISULFID 79 87
FT DISULFID 199 220
FT MOD_RES 466 466
FT CARBOHYD 481 481
FT CARBOHYD 50 50
FT CARBOHYD 58 58
FT CARBOHYD 81 81
FT CARBOHYD 88 88
FT CARBOHYD 110 110
FT CARBOHYD 172 172
FT CARBOHYD 254 254
FT CARBOHYD 313 313
FT CARBOHYD 314 314
FT CARBOHYD 376 376
FT CARBOHYD 416 416
FT CARBOHYD 433 433
FT VARIANT 168 168
FT CONFLICT 17 17
FT SEQUENCE 557 AA: 63525 MW: 0F6744C81ADB273 CRC64;

Query Match 100.0%; Score 2313; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 4,4e-166;
Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGVLLGATTLVLAAGVPMWLSAAGGKNIKSPQKVEVDIIDNFILRMNSDESVCNVT 60
DB 1 MGVLLGATTLVLAAGVPMWLSAAGGKNIKSPQKVEVDIIDNFILRMNSDESVCNVT 60
QY 61 FSPDYORTGMDNMWIKLSGCONITSTKCNFSLKNVEIKLRIRAKENTSSWYEDSF 120
DB 61 FSPDYORTGMDNMWIKLSGCONITSTKCNFSLKNVEIKLRIRAKENTSSWYEDSF 120
QY 121 TPFRAKQIGPPEVLEAEKAIYIHISPGTKDSYMAALDGLSFYSLLIMKNSGVEERI 180
DB 121 TPFRAKQIGPPEVLEAEKAIYIHISPGTKDSYMAALDGLSFYSLLIMKNSGVEERI 180
QY 181 ENISRHKIYKLSPEITCYLKVKAALLTSWKIGVSPVHCIKTTVENELPPENIEVSQ 240
DB 181 ENISRHKIYKLSPEITCYLKVKAALLTSWKIGVSPVHCIKTTVENELPPENIEVSQ 240
QY 241 NONVVLKMDYVYANMTFOYOMLHAFILKRNPGNHLTKKQIPDCENVKTTQCVFQNVFQK 300
DB 241 NONVVLKMDYVYANMTFOYOMLHAFILKRNPGNHLTKKQIPDCENVKTTQCVFQNVFQK 300
QY 301 GIVLLRVAQSDGNTTSEFSEIKEDTEIOALFLPPVFNIRSLDSFHIYIGAPKQSGNTP 360
DB 301 GIVLLRVAQSDGNTTSEFSEIKEDTEIOALFLPPVFNIRSLDSFHIYIGAPKQSGNTP 360
QY 361 VIOQYPLLEYELIFWENTSNARKIIEKKTDTVTPNKLPLYYCYKARAHMDELKNSV 420
DB 361 VIOQYPLLEYELIFWENTSNARKIIEKKTDTVTPNKLPLYYCYKARAHMDELKNSV 420
QY 421 FSDAVCETKPGNTSK 436
DB 421 FSDAVCETKPGNTSK 436

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RESULT 2
INRL_BOVIN STANDARD: PRT: 560 AA.
AC 004790:
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)

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DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
GN IFNARI OR IFNAR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RX MEDLINE: 9305725.
RA Mouchel-Viehl E., Lutfalla G., Mogensen K.E., Uge G.;
RT "Specific antiviral activities of the human alpha interferons are
determined at the level of receptor (IFNAR) structure.";
RL FEBS Lett. 313:255-259(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93305725.
RA Lim J.-K., Langer J.A.;
RT "Cloning and characterization of a bovine alpha interferon receptor.";
RL Blohm. Biophys. Acta 1173:314-319(1993).
CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTRAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC or send an email to license@isb-sib.ch).
DR EMBL: X68443; CAA48484.1; -
DR EMBL: L06320; AAA02571.1; -
DR PIR: S33770; S33770.
DR PIR: S27387; S27387.
DR PFAM: PF00041; fn3; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 560
FT DOMAIN 25 437
FT TRANSMEM 438 458
FT DOMAIN 459 560
FT DISULFID 76 84
FT DISULFID 199 220
FT CARBOHYD 47 47
FT CARBOHYD 55 55
FT CARBOHYD 85 85
FT CARBOHYD 109 109
FT CARBOHYD 172 172
FT CARBOHYD 254 254
FT CARBOHYD 313 313
FT CARBOHYD 377 377
FT CARBOHYD 434 434
FT CONFLICT 422 422
FT SEQUENCE 560 AA: 63818 MW: 66D76B72861E1D11 CRC64;

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Query Match 65.2%; Score 1507; DB 1; Length 560;
Best Local Similarity 64.9%; Pred. No. 1,1e-105;
Matches 285; Conservative 65; Mismatches 83; Indels 6; Gaps 6;

QY 2 MGVLLGATTLVLAAGVPMWLSAAGGKNIKSPQKVEVDIIDNFILRMNSDESVCNVT 61
DB 1 MGVLLGATTLVLAAGVPMWLSAAGGKNIKSPQKVEVDIIDNFILRMNSDESVCNVT 61
QY 62 FSPDYORTGMDNMWIKLSGCONITSTKCNFSLKNVEIKLRIRAKENTSSWYEDSF 119

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Db 59 SADYQLGTDNMKLLSGCHITSTKCNFSSVELKNTFELIRAEENNSTWYEVP 118
Qy 120 FPFRAKQIGPEVHLAEADKAIVIHIS-PGKDSYMAALDGLSFTYSLILKNSGVEE 178
Db 119 FVPFLKQIGPPDVHLEADKAIIISISPGTSDSIMAMDSSFRIVYIKNSSSLEE 178
Qy 179 RIENIYSRRKIYKLSPEITTCYCKVKAALLTSKIGVSPVHCITVENELPPENIEVS 238
Db 179 RRETYVPEDKIYKLSPEITTCYCKVKAALLTSKIGVSPVHCITVENELPPENIEVS 238
Qy 239 VONONVYLVKMDYTYANMFOVOMLHAFKRNPNGNHLYKKOIPDCENVTTCQVPPONF 298
Db 239 ADQIYVLKMDYTYANMFOVOMLHAFKRNPNGNHLYKKOIPDCENVTTCQVPPONF 298
Qy 299 OQGIYLLRQVADGNNTSFWSEIEKPDTEIOAFLLPPVNIISLS-DSFHIYIGAPKQSG 357
Db 299 SNGIYVVRASNGNTSFWSEIEKPDTEIOAFLLPPVNIISLS-DSFHIYIGAPKQSG 358
Qy 358 NTPVVDYDPLIYEIIFWENTSNAERKIEKTDVTPNKLPLTVYCVKARAHTMDEKLNK 417
Db 359 NNSVQNLVPLIYEIIFWENTSNAERKIEKTDVTPNKLPLTVYCVKARAHTMDEKLNK 418
Qy 418 SSFSDAVCEKTRPGNTSK 436
Db 419 GSSFSDTVCCKTRPGNTSK 437

RESULT 3
INRL_SHEEP STANDARD: PRT: 560 AA.
AC Q28389; Q95206;
AD 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
DE (INTERFERON ALPHA/BETA RECEPTOR-1).
GN IFNARI OR IFNAR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Caprinae; Ovis.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM.
RX MEDLINE: 97135690.
RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
RT "Structure of an ovine interferon receptor and its expression in
RT endometrium."
RL J. Mol. Endocrinol. 17:207-215(1996).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM.
RX MEDLINE: 98006426.
RA Han C.-S., Matulalagan N., Klemann S.W., Roberts R.M.;
RT "Molecular cloning of ovine and bovine type I interferon receptor
RT subunits from uteri, and endometrial expression of messenger
RT ribonucleic acid for ovine receptors during the estrous cycle and
RT pregnancy."
RL Endocrinology 138:4757-4767(1997).
RN (3)
RP FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I INS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
CC CONCEPTUS AT DAY 15 OF PREGNANCY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC or send an email to license@isb-sib.ch).
DR EMBL: X95939; CA65183.1; -
DR EMBL: U65978; AAB84231.1; -
DR PIR: P00041; fn3; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 560
FT DOMAIN 25 437
FT TRANSMEM 438 458
FT DOMAIN 459 560
FT DISULFID 76 84
FT DISULFID 199 220
FT CARBOHYD 47 47
FT CARBOHYD 55 55
FT CARBOHYD 85 85
FT CARBOHYD 108 108
FT CARBOHYD 109 109
FT CARBOHYD 172 172
FT CARBOHYD 222 222
FT CARBOHYD 285 285
FT CARBOHYD 313 313
FT CARBOHYD 359 359
FT CARBOHYD 377 377
FT CARBOHYD 434 434
FT CARBOHYD 434 352
FT CONFLICT 522 522
SQ SEQUENCE 560 AA; 63918 MW; E7198A1905D48036 CRC64;

Query Match 65.0%; Score 1503; DB 1; Length 560;
Best Local Similarity 64.5%; Pred. No. 2,2e-105;
Matches 283; Conservative 68; Mismatches 82; Indels 6; Gaps 6;

Qy 2 MYVLGATTLVAVGPMWLSAAGGKNLSPQKVEVDIIDNFIILRNNSDESVCNATF 61
Db 1 MSLLGATTLMLVA-GRWVLPASGEANLKS-ENVEIHIIIDNFIILRNNSSESVRNATF 58
Qy 62 SFDYQKTDNMKLLSGCHITSTKCNFSSVELKNTFELIRAEENNSTWYEVP 118
Db 59 SADYQLGTDNMKLLSGCHITSTKCNFSSVELKNTFELIRAEENNSTWYEVP 118
Qy 120 FPFRAKQIGPEVHLAEADKAIVIHIS-PGKDSYMAALDGLSFTYSLILKNSGVEE 178
Db 119 FVPFLKQIGPPDVHLEADKAIIISISPGTSDSIMAMDSSFRIVYIKNSSSLEE 178
Qy 179 RIENIYSRRKIYKLSPEITTCYCKVKAALLTSKIGVSPVHCITVENELPPENIEVS 238
Db 179 RRETYVPEDKIYKLSPEITTCYCKVKAALLTSKIGVSPVHCITVENELPPENIEVS 238
Qy 239 VONONVYLVKMDYTYANMFOVOMLHAFKRNPNGNHLYKKOIPDCENVTTCQVPPONF 298
Db 239 ADQIYVLKMDYTYANMFOVOMLHAFKRNPNGNHLYKKOIPDCENVTTCQVPPONF 298
Qy 299 OQGIYLLRQVADGNNTSFWSEIEKPDTEIOAFLLPPVNIISLS-DSFHIYIGAPKQSG 357
Db 299 SNGIYVVRASNGNTSFWSEIEKPDTEIOAFLLPPVNIISLS-DSFHIYIGAPKQSG 358
Qy 358 NTPVVDYDPLIYEIIFWENTSNAERKIEKTDVTPNKLPLTVYCVKARAHTMDEKLNK 417
Db 359 NNSVQNLVPLIYEIIFWENTSNAERKIEKTDVTPNKLPLTVYCVKARAHTMDEKLNK 418
Qy 418 SSFSDAVCEKTRPGNTSK 436
Db 419 GSSFSDTVCCKTRPGNTSK 437

RESULT 4
INRL_MOUSE
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Db	161	NSTYVEKTEIPELLEETTYCLETVKAKIAPSLKKNHMYSTVOICSTYIVANKMPVPGNLQYDAQ	240
OY	241	NONVYKWDY-TYANMTFOVOMLAFLKRNPGNLVYMKOIPDCENKTKTCQVFPQVFO	299
Db	241	GKSYVLKWDYIASADVYLFRAOMLGYKSSSGSHSDKWKPIPTCANOTHCVSOOTVY	300
OY	300	KGIYLLRVOAQSDGANTSPWSEIEIKFDEIOIAFLPPVFNIRSLDSFHYIIGAPKOSGNT	359
Db	301	TGTFPLHVQASEGHNTHSPWSEKRIIDBQKHILPPRPVITYTAMSDTLLVYVNOQDSICD-	360
OY	360	PVIDDYPLIYIITMENTSNABRIIEKKDVTYPLNKLPLTYVCVAKARHTMDKLUKS	419
Db	360	-----GLNYIITMENTSNKTIEMKODGPEFTLKNLOPLTYVCQAKV-LFRALLNKTS	4122
OY	420	VESDAVCEKTKPGNTS	435
Db	413	NFSEKLEKTRPGSFS	428

RESULT	5
ID	CRF4_HUMAN
AC	Q08334.1
DT	01-FEB-1995 (Rel. 31, Created)
DT	01-FEB-1995 (Rel. 31, Last sequence update)
DT	01-OCT-1996 (Rel. 34, Last annotation update)
DE	CYOKINE RECEPTOR CLASS-II CR2-4 PRECURSOR.
GN	CRFB4.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC	Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=FETAL BRAIN;
RX	MEDLINE; 93300510.
RA	Lutifalla G., Gardiner K., Uze G.;
RT	"A new member of the cytokine receptor gene family maps on chromosome
RT	21 at less than 35 kb from IFNAR.";
RL	Genomics 16:366-373(1993).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 96054036.
RA	Lutifalla G., McInnis M.G., Antonarakis S.E., Uze G.;
RT	"Structure of the human CRFB4 gene: comparison with its IFNAR
RT	neighbor.";
RL	J. Mol. Evol. 41:338-344(1995).
CC	-1- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC	-1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	tent use by non-profit institutions as long as its content is in no way
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CC	or send an email to license@lsb-sib.ch).
CC	-----
DR	EMBL; Z11227; CAA78933.1; -
DR	EMBL; U08988; AAA86872.1; -
DR	PIR; A47003; AA47003.
DR	HSSP; P13726; IDAN:
DR	MTM; 123869; -
KM	Receptor; Transmembrane; Glycoprotein; Signal.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	TRANSSEM
FT	DOMAIN
FT	DISULFID
FT	DISSIMILARITY
FT	BY SIMILARITY.
FT	BY SIMILARITY.

FT CARBOHYD 49 49 POTENTIAL.
 FT CARBOHYD 68 68 POTENTIAL.
 FT CHAIN 102 102 POTENTIAL.
 FT CARBOHYD 161 161 POTENTIAL.
 FT CONFLICT 124 124 A -> D (IN REF. 2).
 FT CONFLICT 269 273 FLGHP -> VGRME (IN REF. 2).
 FT CONFLICT 274 325 MISSING (IN REF. 2).
 SQ SEQUENCE 325 AA; 37011 MW; 66706C79F8514B23 CRC64;

Query Match 9.9%; Score 228.5; DB 1; Length 325;
 Best Local Similarity 29.9%; Pred. No. 3.5e-10;
 Matches 67; Conservative 42; Mismatches 96; Indels 19; Gaps 8;

QY 19 WLSAAGCKMLKS-----POKVEVDIIDNFIKNNRSDSEVGNVTFSPFYOKTGM 71
 D 3 WLSGSLGGLLYSALGNVPPENRVNMSVKNILQWESPFAAGNLFTQY----LS 58
 QY 72 NWIKLSGCONITSTKCNFSSSLKLVNYEIKLRPAE-KENSSWYEVDSFPRKAOIGP 130
 D 59 YRIFODKCMNTLTRECDSS--LSKYGDHTLRVRAEFADHSDMVNI-TFCVDDTIIGP 115
 QY 131 PEVHLEA-EDKAIVIHISPGTKDSV-MMALDGL--STFYSLIMKNSGVEERIENTYS 186
 D 116 PEMQVEVLADSLHMFELPARKIENEYETWTKNVSMTYNQVYKNGTDEKFOITPQIDF 175
 QY 187 HKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITVENELP 230
 D 176 EYLRLEPWTTCVCGVRGLPDRNKAGESEVPCQTHDETVP 219

RESULT 6
 INGS_HUMAN STANDARD: PRT: 337 AA.
 AC P38484:
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSUCER-1).
 GN IFNGR2 OR IFNGT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP TISSUE-LUNG FIBROBLAST;
 RC MEDLINE: 94170380.
 RA Son J., Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R., Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.;
 RT "Identification and sequence of an accessory factor required for activation of the human interferon gamma receptor.";
 RL Cell 76:793-802(1994).
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO INTERACT WITH GAF, JAK1, AND/OR JAK2.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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 CC EMBL: U05875; AAA16955.1;
 CC EMBL: U05877; AAA16956.1;
 DR MIM: 147569;
 DR PFM: PF00041; fn3; 1.

KM Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 337 INTERFERON-GAMMA RECEPTOR BETA CHAIN.
 FT DOMAIN 28 247 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 248 268 POTENTIAL.
 FT DOMAIN 269 337 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 56 56 POTENTIAL.
 FT CARBOHYD 85 85 POTENTIAL.
 FT CARBOHYD 110 110 POTENTIAL.
 FT CARBOHYD 137 137 POTENTIAL.
 FT CARBOHYD 219 219 POTENTIAL.
 FT CARBOHYD 231 231 POTENTIAL.
 FT VARIANT 64 64 R -> Q.
 SQ SEQUENCE 337 AA; 37834 MW; 18C61B10AD9DE509 CRC64;

Query Match 6.7%; Score 155.5; DB 1; Length 337;
 Best Local Similarity 22.3%; Pred. No. 0.00011;
 Matches 67; Conservative 54; Mismatches 112; Indels 67; Gaps 14;

QY 12 VLVAVGPMVLSAAG--KNLSPKVEVDIIDNFIKRV-----NRSDESVGNVTF 62
 D 9 LLLILGYPFAAAAAAPPDPLSQLPAPQPKITLYNAEOVLSMEPVALSSTPRVYRQFK 68
 QY 63 FDYOKTGMNWKLS-----GCONITSTKCNFSS-----LKVNYEIKLRPAEK 108
 D 69 YTDK-----WTDADISIGVNCQTATATEDCFAPASDFPMDVNV---TLRLAEL 119
 QY 109 ENT-SSWTEVDSFPRKAOIGPREVHLE--AEDKAIVIHISPGTKDSVMMALDGLSFT 164
 D 120 GALHSAWMTMPFQHYRVTVGPPE-NIEVTPGSGSLIRPSPDIADISTAR---FC 174
 QY 165 YSLIMKNSGVEERIENTYSRHKTY-KLSPEPTYCLKVKAAALLTS--WKIGVSPV 218
 D 175 YVYHWE--KGIQVQKPFPSNSISLDNLKPSRYVCLQVQAOILMKNSNIFRCHLSNI 232
 QY 219 HCITVENELPPENIEVSV-----QONVYLVKWDYTYANMFOVO 260
 D 223 SCYETMADASTELQOVLISVGFSLSLVLAGCFVLVKYRGLIKYVHFHPSPISPIQIE 292

RESULT 7
 MYM1_HUMAN STANDARD: PRT: 1451 AA.
 AC P52179:
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE MYOMESIN 1 (190 KD TITIN-ASSOCIATED PROTEIN) (190 KD CONNECTIN-ASSOCIATED PROTEIN).
 GN MYO1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP TISSUE-SKELETAL MUSCLE;
 RC MEDLINE: 94095665.
 RA Vinkemeier U., Obermann W., Weber K., Fuerst D.O.;
 RT "The globular head domain of titin extends into the center of the sarcomeric M band. cDNA cloning, epitope mapping and immunoelection RT microscopy of two titin-associated proteins.";
 RL J. Cell Sci. 106:319-330(1993).
 CC -1- FUNCTION: MAJOR COMPONENT OF THE VERTEBRATE MYOFIBRILLAR M BAND. BINDS MYOSIN, TITIN, AND LIGHT MEROMYOSIN. THIS BINDING IS DOSE DEPENDENT.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 7 FIBRONECTIN TYPE III-LIKE DOMAINS.
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DR EMBL: X69090; CAA48833.1; -

DR MIM: 603508; -

DR PFAM: PF00041; f03; 5.

DR PFAM: PF00047; f03; 3.

DR PRINTS: PR00014; FNTYPEIII.

KW Immunoglobulin domain: Muscle protein. Thick filament; Repeat.

FT DOMAIN 46 81 6 X 6 AA TANDEM REPEATS.

FT REPEAT 46 51 1.

FT REPEAT 52 57 2.

FT REPEAT 58 63 3.

FT REPEAT 64 69 4.

FT REPEAT 70 75 5.

FT REPEAT 76 81 6.

FT DOMAIN 156 289 FIBRONECTIN TYPE-III.

FT DOMAIN 290 384 FIBRONECTIN TYPE-III.

FT DOMAIN 385 511 IG-LIKE C2-TYPE DOMAIN.

FT DOMAIN 512 612 IG-LIKE C2-TYPE DOMAIN.

FT DOMAIN 613 711 IG-LIKE C2-TYPE DOMAIN.

FT DOMAIN 712 816 IG-LIKE C2-TYPE DOMAIN.

FT DOMAIN 817 917 IG-LIKE C2-TYPE DOMAIN.

FT DOMAIN 918 1023 FIBRONECTIN TYPE-III.

FT DOMAIN 1024 1137 FIBRONECTIN TYPE-III.

FT DOMAIN 1138 1239 FIBRONECTIN TYPE-III.

FT DOMAIN 1240 1352 FIBRONECTIN TYPE-III.

FT DOMAIN 1353 1451 FIBRONECTIN TYPE-III.

FT SEQUENCE 1451 AA: 162452 MW: 35293FE6C5FEFFD10 CRC64;

Query Match 5.3%; Score 123.5; DB 1; Length 1451;

Best Local Similarity 19.8%; Pred. No. 0.19; Indels 121; Gaps 21;

Matches 91; Conservative 67; Mismatches 181; Indels 121; Gaps 21;

QY 43 DNFILMNRNSDESVDN-VTFSEFYOKTGMNWKILSGCONITSTKCNFSKLNYEEI 100

DB 388 DYIIISMKQPAVDGSGPIIGFYDKCEVGTDSW-----SCQNTGPKFAFPPT 436

QY 101 KL-----RIAREKNTSSW-----YEYDSFTPRKKAIGPEVHLAEADKAIVIHIS 147

DB 437 GIEGRSYIFRYAVAKMKIGFPRSEVAALDPAEKARKLSP--LSTLDMTVIVTEE 493

QY 148 PGKDSVMAALDGLSFT-----YSLILMK-----NSSGVEERIENTYS----- 186

DB 494 EPESEGIYPPPTDLSTYETRTYVLSMPPGORGHEGIMYFEKCEAGTEMQRVNTL 553

QY 186 -----RHKIYKLSPEYTYCLKYKAAALTSKIGVSPVHCIRTV-----ENELP 230

DB 554 PVKSPFAFLDLAEKSGYCFVRRC-----SNSAGVGEPSATETVVGDKLDIPKAPKII 609

QY 231 PRENIEVSQNONVYLKMD-----YYANNTFOYOLHAFKRNPGNHLKYWK 278

DB 610 PARNMDFSV-----VVSWEESDKAKELVYVEANVAGSKKPEPC--NNNPVKTRHF-- 660

QY 279 QIPDENVTQOCVPQONFQKGIYLLRYQASDGNNTSMSEIKFDEIOAFLLPP-- 336

DB 660 -----TCHGLVITGOS-----YIFRRAYNAAGLSLEYSDSE--AIYVKAIAIAPSPFP 704

QY 336 --VFNIKSLDSFHYIGAPKOSGNTPTVIOYPLIYEI-----FWENTSNAERKITEK 388

DB 705 CDITCESEFRSDMVLGKMPDKTGAEITGYVNVREYIDVGPQKWR--EANNKAVRBE 761

QY 389 TDVTVPNLKPLTVYCVKAKAHHMDEKLKSSVFSDAVCKX 428

DB 762 A-YKISNLKENNVYIOFOVAAMNAGIGADSAVSECFCEE 800

AC P15127; P97681;

DR 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DE 15-JUL-1998 (Rel. 36, Last annotation update)

GN INSULIN RECEPTOR PRECURSOR (EC 2.7.1.12) (IR).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RN [1] SEQUENCE FROM N.A.

RA MEDLINE: 90231337.

RL "The rat insulin receptor: primary structure and conservation of

RL tissue-specific alternative messenger RNA splicing.";

RL Mol. Endocrinol. 4:235-244(1990).

RC PARTIAL SEQUENCE FROM N.A.

RA Liu Y., Tam J.M.O.;

RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THIS RECEPTOR BINDS INSULIN AND HAS A TYROSINE-PROTEIN

CC KINASE ACTIVITY.

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +

CC PROTEIN TYROSINE PHOSPHATE.

CC -1- ENZYME REGULATION: AUTOPHOSPHORYLATION ACTIVATES THE KINASE

CC ACTIVITY.

CC -1- SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE

CC BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-

CC BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINASE DOMAIN.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-

CC PROTEIN KINASES.

CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -----

DR EMBL: M29014; AAA41441.1; -

DR EMBL: AF005776; AAB61414.1; -

DR EMBL: AF005777; AAB61415.1; -

DR EMBL: U80633; AAB38746.1; -

DR EMBL: U80632; AAB38968.1; -

DR EMBL: U80631; AAB38968.1; JOINED.

DR EMBL: U80630; AAB38967.1; -

DR EMBL: U80629; AAB38967.1; JOINED.

DR PIR: A36080; A36080.

DR HSSP: P06213; IIRK.

DR PRINTS: PR00014; FNTYPEIII.

DR PROSITE: PS00107; PROTEIN KINASE.

DR PROSITE: PS00109; PROTEIN KINASE.

DR PROSITE: PS00109; PROTEIN KINASE.

DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II.

DR PROSITE: PS50011; PROTEIN_KINASE_DOM.

DR PFAM: PF00041; f03; 1.

DR PFAM: PF00069; pkinase; 1.

DR PFAM: PF00757; Furin-like; 1.

DR PFAM: PF01030; Recep-like; 1.

DR Transposase: Tyrosine-protein kinase: Receptor: Transmembrane;

KW Glycoprotein; ATP-binding; Phosphorylation; Signal; Repeat.

FT SIGNAL 1 26

FT CHAIN 27 760

FT PROPEP 761 763

FT CHAIN 764 1383

FT DOMAIN 764 957

FT TRANSEM 958 978

FT DOMAIN 979 1383

FT DOMAIN 619 848

FT CYTOPLASMIC (POTENTIAL).

FT FIBRONECTIN TYPE-III.

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FT DOMAIN 849 949 FIBRONECTIN TYPE-III.
FT NP_BIND 1024 1299 PROTEIN KINASE.
FT BINDING 1030 1038 ATP (BY SIMILARITY).
FT ACT_SITE 1058 1058 ATP.
FT MOD_RES 1190 1190 PHOSPHORYLATION (AUTO-).
FT ACT_SITE 1000 1000 IMPORTANT FOR BIOLOGICAL ACTIVITY.
FT DISULFID 461 494 BY SIMILARITY.
FT DISULFID 550 550 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 42 42 POTENTIAL.
FT CARBOHYD 51 51 POTENTIAL.
FT CARBOHYD 104 104 POTENTIAL.
FT CARBOHYD 137 137 POTENTIAL.
FT CARBOHYD 241 241 POTENTIAL.
FT CARBOHYD 281 281 POTENTIAL.
FT CARBOHYD 321 321 POTENTIAL.
FT CARBOHYD 363 363 POTENTIAL.
FT CARBOHYD 423 423 POTENTIAL.
FT CARBOHYD 444 444 POTENTIAL.
FT CARBOHYD 540 540 POTENTIAL.
FT CARBOHYD 634 634 POTENTIAL.
FT CARBOHYD 652 652 POTENTIAL.
FT CARBOHYD 699 699 POTENTIAL.
FT CARBOHYD 770 770 POTENTIAL.
FT CARBOHYD 783 783 POTENTIAL.
FT CARBOHYD 921 921 POTENTIAL.
FT CARBOHYD 934 934 POTENTIAL.
FT CONFLICT 1119 1119 L -> M (IN REF. 2).
SO SEQUENCE 1383 AA; 156756 MW; 4B919566902A944A CRC64;

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Query Match 5.1%; Score 119; DB 1; Length 1383;
Best Local Similarity 19.2%; Pred. No. 0.38;
Matches 89; Conservative 52; Mismatches 151; Indels 172; Gaps 20;

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QY 43 DNFIKMRNSDSGVNFTSPFYOKTGMDN-----WIKISGCON 81
DB 481 NDIAKLTNGDAQSCNELKFSFIRISFKILLRMEPPWPDPFRLGFMFLYKAPYON 540
QY 82 IT-----STKCNFSSIKLNYEIKLIRAEKENTSSWYEFSTPFKRAQIGPPEVHLEA 137
DB 541 VTEFGGQDAC-----GNSMTYVD-----IDPPQ---RS 566
QY 138 EDKAIIVHISPTKDSVMWALDGLFTYSLLIMKNSGVEERIEINYSRHKIYKLSPEET 197
DB 567 NDPKSGTPSPG-----WLMRG-----LKPWTQ 589
QY 198 YELKTKAALLTSMK---IGVYSPVHCITKTVENELPPPENIEVSQONQYVLUK---DYT 251
DB 590 YAIFFKTLVTFSDERTYGAKSDDIYVQDANPSVPLDPISVSNSSQIILKMKPPSDP 649
QY 252 YANMTFOYQWHLAFLKRNPNGLYKW-KQIPCCENVKTQGVFPQWVQKGIYL-----305
DB 650 NGNIT-----HLYVWERKADESELEFDYCL-----KGLKLSRWS 687
QY 305 --LRVQASDGNTSPWSEIEI-----KEDIEIOAFLPPVENISLSDSFHIIYGAPKO 355
DB 688 PPFESDDSGKHNGSEYEDDASCCGCPKTDQSLKLELESSPR-KTFEEDYLNWVYFPRK 746
QY 356 --SGN-----TPVIOYDPLIYEITFEWNTSAEKIIEK---388
DB 747 TSSGGAEDTPSRKRRLSEEVGNVYATPTLPDPPNISSTI--APTSHHEHRPEFEKYVN 804
QY 388 KIDVTVPNLKPLTVYCVKRAHTMDKLNKSSVFSDAVCEKTP 431
DB 805 KESLVIISGLRHFTGTRIELQACNDSPEERSGV-AAVYSARWTP 847

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RESULT 9
INGR_HUMAN STANDARD: PRT; 489 AA.
AC P15260;
DT 01-APR-1990 (rel. 14, Created)

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DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119).
GN IFNGR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NC [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89003065.
RA Aguet M., Dombic Z., Merlin G.;
RT "Molecular cloning and expression of the human Interferon-gamma
RL receptor.";
RL Cell 55:273-280(1988).
RN [2]
RP DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.
RX MEDLINE: 93183911.
RA Stueder D., Friedlein A., Pountoulakis M., Lahn H.-W., Garotta G.;
RT "Alignment of disulfide bonds of the extracellular domain of the
RT Interferon gamma receptor and investigation of their role in
RL biological activity.";
RL Biochemistry 32:2423-2430(1993).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.
RX MEDLINE: 95342235.
RA Walter M.R., Windsor W.T., Nagabhushan T.L., Lundell D.J., Lunn C.A.,
RA Zaudowy P.J., Narula S.K.;
RT "Crystal structure of a complex between interferon-gamma and its
RT soluble high-affinity receptor.";
RL Nature 376:230-235(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 COMPLEX WITH ANTIBODY.
RX MEDLINE: 98035727.
RA Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A.,
RA Winkler F.K., Robinson J.A.;
RT "Neutralizing epitopes on the extracellular interferon gamma receptor
RT (Irngamma) alpha-chain characterized by homolog scanning mutagenesis
RT and X-ray crystal structure of the A6 fab-IrngammaR1-108 complex.";
RL J. Mol. Biol. 273:882-897(1997).
CC -1- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
CC INTERFERON-GAMMA DIMER.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PM: PHOSPHORYLATED AT SER/THR RESIDUES.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J03143; AAA52731.1; -
DR PIR: A31555; A31555.
DR PDB: 1JRH; 25-MAR-98.
DR MIM: 107470; -.
DR MIM: 209950; -.
KW Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;
KW Immunoglobulin domain; 3D-structure.
FT SIGNAL 1 17
FT CHAIN 18 489 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
FT DOMAIN 18 245 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 246 266 POTENTIAL.
FT DOMAIN 267 489 CYTOPLASMIC (POTENTIAL).
FT DISULFID 77 85
FT DISULFID 122 167
FT DISULFID 195 200
FT DISULFID 214 235
FT CARBOHYD 34 34 POTENTIAL.

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Db 310 GFFNASHPSQCSKCP-----HSYTHEASTCVCEDKDYFRNESPPTMACRCP 359
Oy 232 ---PENIEVSVOONQNYLVK-----DYVAMTFQVOWLHAFKRNPNGLXKWK 278
Db 360 PSABRNALSNVENSVEFLEMIPADTGGKDVSYILCKCN-SHAGVCECGGHYR--- 416
Oy 279 QIPDCENKTKQCFPPQVFOKGIYLLNVAQSDGNNTSFWSDEIKFDIEIQAFLPLPVFN 338
Db 416 -----XLPQDGLKNTSVMMADPLAHNTYF-----EIRA-----VNG 448
Oy 339 IRSLSDFHIYIG--ARKSGNTPVIG-----DYP-----LITEIIF 373
Db 449 VSDISPGTRQYVSVNVTNNQAPSPVTVYVKKGIKKNISLSWQEPDNPNGIILEYIKY 508
Oy 374 WENTSNAERKIE-KTQDVTPVNLKPLTVYCVKARAH 410
Db 509 FEKQDETSITLIKSEETITAEGLKPAVYVFOIARH 546

RESULT 11
ID 110R MOUSE STANDARD; PRG: 575 AA.
AC 061727:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
GN IL10RA OR IL10R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6 X AJ F1; TISSUE=HEMATOPOIETIC;
RX MEDLINE; 94068585.
RA Ho A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;
RT "A receptor for interleukin 10 is related to interferon receptors.";
RC Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).
CC -1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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DR EMBL; L12120; AAA16156.1; -.
DR MGD; MGI:96538; IL10RA.
DR Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 575 INTERLEUKIN-10 RECEPTOR.
FT DOMAIN 17 241 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 242 262 POTENTIAL.
FT DOMAIN 263 575 CYTOPLASMIC (POTENTIAL).
FT DISULFID 204 225 POTENTIAL.
FT CARBOHYD 50 50 POTENTIAL.
FT CARBOHYD 66 66 POTENTIAL.
FT CARBOHYD 113 113 POTENTIAL.
FT CARBOHYD 182 182 POTENTIAL.
FT CARBOHYD 238 238 POTENTIAL.
SQ SEQUENCE 575 AA; 64248 MW; 820B96CD576F686B7 CRC64;

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Db 9 LVTTSSLSLEPIAAGTLLPSPSYVWFARFQHTLHKKPLPNQSESYVEVAL----KQY 64
QY 69 GMDNMKILSGQONTSTKCNFSSLSKLINVEE---IKLIRIA-EKENTSSWEYDS-FTPF 123
Db 65 GNSFMNDIHICRKAQALSCDLTFTEFLDLYHRSYGXRVARVADVNSQSNMTTETRET-- 123
QY 124 RKAQIGPEVHLEADKAIIYHISPGKRDY-KMALDGLSFYTSLLIKNKSQVEEEN 182
Db 123 -----VDEVIL-----TVDSVTLKAMGIIYGIHPRPRTTPAGDEYQ 162
QY 183 IYSRHKIKYKLS-----PET-----TYCLVKKAALLTSWKIGVYSQ 217
Db 163 VFKDLRIYKIKIRFSEKNAKTRVKQETFLTYPIGVKRFVCVAVLPRLSRIRKAEKSE 222
QY 218 VHCIKTVEENLPPPENIEVSQNONVYLKMDYTYAMTQYV-----QWL 262
Db 223 EQCLLITTEQY-----FVYNLSILVISMILFCIGVLVLYQW- 261
QY 263 HAFLEKRNFGNHLKYKKQIPDCENKTKTQCVPQN-----VFQKGYILLR 306
Db 261 --YLRHFG-----KLPTLVYRKKHDEFPANPLCPETPDIAHYIVLEVEFPKVSLELR 310
QY 307 VOASDGNNTS-FWSEELKFDTEIDAFLLP 334
Db 311 DSVLHGSDSGFGSKPDLQTESQOFLP 339

RESULT 12
PTPD_HUMAN
ID PTPD_HUMAN STANDARD: PRT: 1912 AA.
AC P23468.
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP-
DE DELTA).
GN PTPD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE: 95204468.
RX Puidlo R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;
RT "Molecular characterization of the human transmembrane
RT protein-tyrosine phosphatase delta. Evidence for tissue-specific
RT expression of alternative human transmembrane protein-tyrosine
RT phosphatase delta isoforms.";
RL J. Biol. Chem. 270:6722-6728(1995).
RN [2]
RP SEQUENCE OF 390-1912 FROM N.A.
RC TISSUE-PLACENTA;
RX MEDLINE: 91006018.
RA Krueger N.X., Streuli M., Saito H.;
RT "Structural diversity and evolution of human receptor-like protein
RT tyrosine phosphatases.";
RL EMBL J. 9:3241-3252(1990).
CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
CC PROTEIN TYROSINE + ORTHOPHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS ARE FOUND IN DIFFERENT
CC TISSUES DUE TO ALTERNATIVE SPLICING.
CC -1- PTV: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
CC FROM THE TRANSMEMBRANE SEGMENT.
CC -1- SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (3 IG-
CC LIKE DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS),
CC AND A CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS.
CC -----
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CC EMBL: L38929; AAC1749.1; -
DR EMBL: X54133; CAA8068.1; -
DR PIR: S12052; S12052.
DR HSSP: P18052; 1YFO.
DR MIM: 601598; -
DR PRINTS: PRO0014; ENTPPE11.
DR PRINTS: PRO0700; PRTPHPTASE.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS00506; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS00505; TYR_PHOSPHATASE_PTP; 2.
DR PFAM: PF00041; fn3; 8.
DR PFAM: PF00047; 1q; 3.
DR PFAM: PF00102; Y.phosphatase; 2.
KM Hydroxylase, Receptor; Glycoprotein; Signal; Transmembrane; Duplication;
KW Immunoglobulin domain; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 1912
FT DOMAIN 21 1265
FT TRANSMEM 1266 1290
FT DOMAIN 1291 1912
FT DOMAIN 23 115
FT DOMAIN 118 225
FT DOMAIN 232 318
FT DOMAIN 320 414
FT DOMAIN 417 513
FT DOMAIN 516 606
FT DOMAIN 609 708
FT DOMAIN 711 822
FT DOMAIN 825 916
FT DOMAIN 918 1017
FT DOMAIN 1020 1137
FT DOMAIN 1137 1618
FT DOMAIN 1619 1912
FT ACT_SITE 1533 1553
FT ACT_SITE 1844 1844
FT SITE 1175 1178
FT CARBOHYD 254 254
FT CARBOHYD 289 289
FT CARBOHYD 724 724
FT CARBOHYD 832 832
FT VARSPLIC 181 189
FT VARSPLIC 226 229
FT VARSPLIC 775 783
FT VARSPLIC 609 1137
FT MUTAGEN 1178 1178
SQ SEQUENCE 1912 AA; 214759 MW; 3AE8CBDC32182E26 CRC64;
Query Match 5.0%; Score 116; DB 1; Length 1912;
Best Local Similarity 21.8%; Pred. No. 0.97; Indels 40; Gaps 11;
Matches 62; Conservative 47; Mismatches 136; Indels 40; Gaps 11;

DB 585 LARSPOGLASTAISARTMSK--PSAPQDISC--TSPESTS 625
RESULT 13
MSF_CHICK STANDARD; PRT; 1450 AA.
AC 002173;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE M-PROTEIN, STRIATED MUSCLE.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-EMBRYONIC PECTORALIS MUSCLE;
RX MEDLINE; 93015907.
RA Noguichi J., Yanagisawa M., Imamura M., Kasuya Y., Sakurai T.,
RA Tanaka T., Masaki T.;
RT "Complete primary structure and tissue expression of chicken
pectoralis M-protein".
RL J. Biol. Chem. 267:20302-20310(1992).
CC -1- FUNCTION: IS A STRUCTURAL CONSTITUENT OF MYOFIBRILLAR M-BAND IN
STRIATED MUSCLE.
CC -1- TISSUE SPECIFICITY: IS EXPRESSED IN PECTORALIS AND CARDIAC MUSCLE.
CC -1- DEVELOPMENTAL STAGE: CAN BE DETECTED BY DAY 10-13 IN OVO. THE
CONTENT IS GRADUALLY INCREASED THROUGHOUT THE OVO DEVELOPMENT AND
REACHED ITS PEAK AFTER HATCHING.
CC -1- SIMILARITY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC EMBL: D11474; BAA02033.1; -
DR PIR: A44027; A44027.
DR HSSP: P56276; 1TLK.
DR PFAM: PF00041; fn3; 5.
DR PFAM: PF00047; 1q; 3.
DR PRINTS: PRO0014; ENTPPE11.
KM Muscle protein; Repeat; Immunoglobulin domain.
FT DOMAIN 142 238
FT DOMAIN 266 364
FT DOMAIN 368 464
FT DOMAIN 496 592
FT DOMAIN 597 693
FT DOMAIN 696 794
FT DOMAIN 797 898
FT DOMAIN 899 990
FT DOMAIN 1002 1095
FT DOMAIN 1126 1205
FT DOMAIN 1225 1312
FT DOMAIN 1333 1427
SQ SEQUENCE 1450 AA; 163400 MW; E313CD39EE6AC7 CRC64;
Query Match 5.0%; Score 115; DB 1; Length 1450;
Best Local Similarity 21.6%; Pred. No. 0.8; Indels 136; Gaps 26;
Matches 92; Conservative 63; Mismatches 134; Indels 136; Gaps 26;

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OY 130 PPEVHLEAED--KAIVIHISPC-----TQDSVMMALDG-----LFTYSL 167
DB 461 EFWALADPDLERTQTQVHDEGRKAIYSKD-----LEGDIQIPGPTNVHASEISKTYV 516
OY 168 LIWKV-----SSGVEREINIS----RKIKYLSSETTYCKLVKAA 205
DB 517 LSWDPVPVPRGPRELTYFEIKSVAGSGMORVNAOVAKSPRAVVDLAGKRPYFRV--- 574
OY 206 LITSMKIGVSPVHCIKTVENEL--PPENIEVSVN--ONYVLKMD-----250
DB 574 -LSANKHGISDSEITEPTQPODIYVPSAPGRVATRTKTSVYQMKPKHEENTLYCY 632
OY 250 YTYANNTFOVQWLAFLKRNPGNHLTKWKOIPDCENVTQCVFQONVFOKG-IYLLRVO 308
DB 633 YIDYSVVGSNMV-----EPANH---KPI-----NYNR-----FVHGLETGEQYIFRYK 673
OY 309 ASDG---NNTSFMSSEIKTDEIQAFLEPVP--NIRSL--DSFHYIG--APKOSGNP 360
DB 674 AVNAVGFSENSESESAIK---VQALITCPSYPHGITLLNCGHSMTLGMAKPKYSGGSP 729
OY 361 VIODY 365
DB 730 ILGY 734

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RESULT 14

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TYO3_RAT
ID TYO3_RAT STANDARD: PRT: 880 AA.
AC P55146:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN
DE KINASE SKY).
GN TYRO3 OR SKY.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RN RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
RX MEDLINE: 96104999.
RA Ohashi K., Honda S., Ichinomiya N., Nakamura T., Mizuno K.;
RT "Molecular cloning and in situ localization in the brain of rat sky
RT receptor tyrosine kinase."
RL J. Biochem. 117:1267-1275(1995).
CC -1- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY
CC IN THE CENTRAL NERVOUS SYSTEM.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN
CC OTHER TISSUES.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC -----
DB EMBL: D37880; BA007119.1; -.
DB HSSP: P11362; IFGI.
DB PROSITE: P500107; PROTEIN_KINASE_ATP; 1.
DB PROSITE: P500109; PROTEIN_KINASE_TYR; 1.
DB PROSITE: P500011; PROTEIN_KINASE_DOM; 1.
DB PFAM: PF00041; f03; 2.
DB PFAM: PF00047; f02; 2.
DB PFAM: PF00069; pkinase; 1.

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KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
KW Transferase; Phosphorylation; Transmembrane; Signal; Repeat;
KW Immunoglobulin domain.
FT SIGNAL 1 30
FT CHAIN 31 880
FT DOMAIN 31 419 POTENTIAL.
FT TRANSMEM 420 440 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3.
FT DOMAIN 441 880 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 131 115 POTENTIAL.
FT DOMAIN 131 200 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 214 301 IG-LIKE DOMAIN.
FT DOMAIN 305 401 FIBRONECTIN TYPE-III.
FT DOMAIN 308 401 FIBRONECTIN TYPE-III.
FT NP_BIND 514 522 PROTEIN KINASE.
FT BINDING 540 540 ATP (BY SIMILARITY).
FT ACT_SITE 645 645 ATP (BY SIMILARITY).
FT MOD_RES 676 676 BY SIMILARITY.
FT CARBOHYD 53 53 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 75 73 POTENTIAL.
FT CARBOHYD 181 75 POTENTIAL.
FT CARBOHYD 181 181 POTENTIAL.
FT CARBOHYD 220 220 POTENTIAL.
FT CARBOHYD 230 230 POTENTIAL.
FT CARBOHYD 283 283 POTENTIAL.
FT CARBOHYD 356 356 POTENTIAL.
FT CARBOHYD 370 370 POTENTIAL.
SQ SEQUENCE 880 AA; 95918 MW; C3751E86A85FA5B CRC64;

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Query Match

4.9%; Score 113.5; DB 1; Length 880;
 Best Local Similarity 22.3%; Pred. No. 0.54; Indels 91; Gaps 17;
 Matches 79; Conservative 53; Mismatches 132;

```

OY 3 VLLGATLLVYAVGPWVLSAAGGKLNKSPQV-----EVDIIDNFIKRW 50
DB 15 LLLAASLLLP-----SAAAGLKMGAIPKVMVSGQPKVLCNSVEGMDPDI-HM 67
OY 51 RSDSEVGN--VTSEFDYQKGMNWKILSGCQNTSTKCNFSSKLNVYEIKRITAE 107
DB 68 KGAVVQNAQSVSISBQ-----NMIGLLSIKSAERSDAGLYWCQVDGETKI----- 118
OY 108 KENTSSWYEVDG--FTFPRKAQIGPREVHLEAEKKAIVIHISPTKQSVK--ALD 159
DB 118 --SQSVLTLVEGVPFTPEPDLAIVPVPOLSCA-----VGPEPYTITMWRGPTVVG 171
OY 160 GLSFETSLIMKNSGVEREINISRKIKYLSSETTYCKLVKAAFLTSMKIGVSPVH 219
DB 172 GRASSPSVL--NTGVAQRTFEFSCAHNINGLAISRRAIRLQA-----214
OY 220 CIKTTVENELDP--PENIEV--SVONQNYVLK--DYTYANNTFOVQWLAFLKRNPN 272
DB 214 -----PPAEPFNITVTITSSNSASVAVMPGADLALLSCTGVVAHA-----PG- 258
OY 273 HLYKKQIPDCENVTQCVFQONVFOKGIYLLRVOASDGNNTSWSSEIKFQDE 327
DB 258 ---EWEALAVVVPVPPFTCLL-RNLAPATNLSLRVCANALGPSYGDWVPQTK 308

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RESULT 15

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DCC_MOUSE
ID DCC_MOUSE STANDARD: PRT: 1447 AA.
AC P70211:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.
GN DCC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RN RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-BRAIN:
RX MEDLINE: 96112625.

```

RA Cooper H.M., Armes P., Britto J., Gad J., Wilks A.F.;
RT Cloning of the mouse homologue of the deleted in colorectal cancer
RL gene (MDC) and its expression in the developing mouse embryo.;
RN Oncogene 11:2243-2254(1995).
RP REVISIONS.
RC STRAIN-BALB/C; TISSUE-BRAIN;
RA Cooper H.M.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN ARE PRODUCED FROM
CC THE SAME GENE BY THE USE OF ALTERNATIVE INITIATION SITES. A THIRD
CC FORM WHICH IS EXPRESSED ONLY IN THE EMBRYO IS PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED AT HIGH LEVELS IN THE
CC DEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED IN
CC BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS.
CC -1- DEVELOPMENTAL STAGE: LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS
CC EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION
CC AND REMAIN AT THIS LEVEL IN THE ADULT.
CC -1- SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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CC
DR EMBL: X85788; CAA59786.1; -
DR HSSP: P56276; ITLK.
DR MGD: MGI:94869; DCC.
DR PRAM: PF00047; fn3; 6.
DR PRAM: PF00047; fn3; 6.
DR PRINTS: PR00014; FNTYPEIII.
KW Glycoprotein; Immunoglobulin domain; Transmembrane; Signal;
KW Anti-oncogene; Alternative initiation; Alternative splicing.
FT SIGNAL 1 25
FT CHAIN 26 1447
FT CHAIN 85 1447
FT DOMAIN 26 1097
FT TRANSMEM 1098 1122
FT DOMAIN 1123 1447
FT DOMAIN 54 124
FT DOMAIN 154 219
FT DOMAIN 254 317
FT DOMAIN 345 407
FT DOMAIN 426 522
FT DOMAIN 525 618
FT DOMAIN 619 716
FT DOMAIN 722 816
FT DOMAIN 840 940
FT DOMAIN 941 1042
FT DISULFID 61 117
FT DISULFID 161 212
FT DISULFID 261 310
FT DISULFID 352 400
FT CARBOHYD 60 60
FT CARBOHYD 94 94
FT CARBOHYD 299 299
FT CARBOHYD 318 318
FT CARBOHYD 478 478
FT CARBOHYD 628 628
FT CARBOHYD 702 702
FT VARSPLIC 819 838
SO SEQUENCE 1447 AA; 158298 MW; 0D1F1097C22D5B9F CRC64;

Query Match 4.8%; Score 111.5; DB 1; Length 1447;
Best Local Similarity 21.4%; Pred. No. 1.5;

Matches 106; Conservative 63; Mismatches 174; Indels 153; Gaps 29;
QY 32 SPQKVVVDIIDNFI-LRKNRSDSEGVN-FTSPFYQKGMNWKLSGCCQNTSTKCNF 89
DB 431 APRDVLPLVSSRFVRLSRPPEAKGNIGTTFVFSREGDNRERALNTQD----- 483
QY 90 SSLKL---NVEEIKLRIRAEKENTSSWEVDSFTPFKKA-----QIGPEVHLAEADKA 141
DB 483 GSIQLVGNLKRKEAMTFEYVAVN--EMGPGSSQPIKVAQPELOVPGPVENLHA----- 537
QY 142 IYHISPGKDSVMAA---LDGLSTYSLLIMKSSGVEERIEINYSRHKTYKLSPEPT 197
DB 537 --VSTSP-TSIIITWEPAYANGPVQGYRIFCTEYSTGKEQNIIEVDGLSKLEGKKEFE 593
QY 198 YCLKVAALLTSMKIGVSPVHCITVTVENLPPEINIEVSQN-----Q 242
DB 594 YTRFLA--YNRGPGVSTDTITVTLSDVPAPPNISLEVYNSRSIKVSLPPSGTQ 651
QY 243 N---YVLR-----WDYTYANN-----TFQV-----QW 261
DB 652 NGFITGKIRHKKTRRGEMETLEPNLNL-YLTGLEKGSQSFVYSMTVNGTGPSSW 710
QY 262 LNAFLKRNQNLKWKQIPDCEV---KTQCVPQO-----NVFQKGIYLLRQAS 310
DB 711 --YTAETPNDLDE-SQVPDQPSLHVRPQTNCIIMSTPPLNPNIVRG-YIIGYGVG 765
QY 311 DGNNTFSWSEELKPDTEIQAFLPPVFNRSLSDSPHII-----GAP-RQSGWT 359
DB 766 ----SPIAEYRVDSKQ-----YSTERLESSHYISLKAENNGEGVPLYESATT 814
QY 360 PVIOD-----YPLIEIIEFMENTSNAERKIEKTDVTPNLPVYCV-----XAR 407
DB 815 RSLTDPDTPVDYPLDDE---PTSG-----PDVSTPLMDPVGQVALHHEAVR 861
QY 408 AHFMDEKLKSSVFS 423
DB 862 VSMADNSVPKQKTS 877

Search completed: June 1, 2000, 10:24:04
Job time: 20622 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:38:55 ; Search time 17.42 Seconds
(without alignments)
1735.343 Million cell updates/sec

Title: US-09-240-675-2

Perfect score: 2313
Sequence: 1 MMVLLGATTLVAVGPVY.....KSSVSDAVCEKTPQNTSK 436Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

SPTREMBL.12.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plant:*
10: sp_protist:*
11: sp_virus:*
12: sp_vertebrate:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	686.5	29.7	569	13	Q9YHWO gallus gall
2	222.5	9.6	349	11	Q61190 mus musculu
3	203	8.8	332	11	Q63953 mus musculu
4	189.5	8.2	341	13	Q9YGC8 gallus gall
5	138.5	6.0	918	13	Q9W6U9 gallus gall
6	131	5.7	508	13	Q9YHV9 gallus gall
7	130	5.6	1493	11	P97798 mus musculu
8	129	5.6	1375	5	Q94537 drosophila
9	129	5.6	1526	5	Q94538 drosophila
10	127.5	5.5	1443	13	Q90610 gallus gall
11	123	5.3	873	13	Q98949 gallus gall
12	122.5	5.3	1461	4	Q92859 homo sapien
13	122.5	5.3	1461	4	Q00340 homo sapien
14	117.5	5.1	1427	13	Q91562 xenopus lae
15	117.5	5.1	1585	5	Q17859 caenorhabd
16	117.5	5.1	2214	4	Q92673 homo sapien
17	117	5.1	484	4	Q14936 homo sapien
18	117	5.1	817	13	Q07784 gallus gall
19	116.5	5.0	1264	5	P91767 manduca sex
20	115.5	5.0	658	5	Q09946 caenorhabd

21	115.5	5.0	1377	11	P97603	P97603 rattus norv
22	115	5.0	2626	4	Q10466	Q10466 homo sapien
23	113.5	4.9	1040	13	Q9W675	Q9W675 brachydanio
24	113	4.9	1767	5	Q24495	Q24495 drosophila
25	113	4.9	1898	11	Q64604	Q64604 r protein-t
26	113	4.9	6048	5	Q23020	Q23020 caenorhabd
27	113	4.9	6831	5	Q23550	Q23550 caenorhabd
28	113	4.9	7160	5	Q23551	Q23551 caenorhabd
29	112	4.8	572	6	Q29117	Q29117 sus scrofa
30	111.5	4.8	1445	11	Q63155	Q63155 rattus norv
31	111.5	4.8	1571	4	Q60469	Q60469 homo sapien
32	111.5	4.8	1896	4	Q60468	Q60468 homo sapien
33	110	4.8	2213	6	Q95209	Q95209 oryctolagus
34	109	4.7	416	5	Q18094	Q18094 caenorhabd
35	109	4.7	427	4	Q95646	Q95646 homo sapien
36	108.5	4.7	1028	11	Q62682	Q62682 rattus norv
37	108.5	4.7	2033	11	Q54711	Q54711 mus musculu
38	108.5	4.7	2215	11	Q88307	Q88307 mus musculu
39	107	4.6	1651	4	Q916N7	Q916N7 homo sapien
40	106.5	4.6	1894	11	Q64487	Q64487 mus musculu
41	105.5	4.6	1825	5	Q61210	Q61210 caenorhabd
42	105	4.5	777	4	Q9Y2H6	Q9Y2H6 homo sapien
43	105	4.5	1948	4	Q13332	Q13332 homo sapien
44	105	4.5	13055	5	Q09165	Q09165 caenorhabd
45	104	4.5	1239	5	Q61541	Q61541 drosophila

ALIGNMENTS

RESULT	1	ALIGNMENTS
Q9YHWO	PRELIMINARY;	PRT; 569 AA.
Q9YHWO	Q9YHWO;	
AC	Q9YHWO;	
DT	01-MAY-1999 (TREMREL. 10, Created)	
DT	01-MAY-1999 (TREMREL. 10, Last sequence update)	
DT	01-MAY-1999 (TREMREL. 10, Last annotation update)	
DE	INTERFERON ALPHA/BETA RECEPTOR 1.	
GN	IFNAR1.	
OS	Gallus gallus (Chicken).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;	
OC	Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=LIVER.	
RA	REBOUL J., GARDINER K., MONNERON D., UZE G., LUTPALLA G.;	
RT	"Comparative genomic analysis of the Interferon/Interleukin-10	
RT	receptor gene cluster.";	
RL	Genome Res. 0:0-0(1999).	
DR	EMBL; AF082664; AAD13669.1; -	
KW	Receptor.	
SQ	SEQUENCE 569 AA; 64055 MW; F99BC099 CRC32;	
Query Match	29.7%;	Score 686.5; DB 13; Length 569;
Best Local Similarity	37.6%;	Pred. No. 8.5e-47;
Matches 167; Conservative 78; Mismatches 172; Indels 27; Gaps 12;		
QY	7 GATTLVAVGPVWLSAAGGKNLSPKVEVDIIDNFILRMNSDESQVTFSPDYQ 66	
Db	9 GRLAVALICLVVYVSRCCAGOTNLKSPODIOYVAVNNFTLMWYTGDF-NTVFSQYQ 67	
QY	67 -----KTGMDMKIKLSCGNTSTKCNFSSIKLVYEIKLRIRAE-KENTSSVYEDSF 120	
Db	68 CFDDLQTSPEPKELSGCONVSHTECFSSAITAYDTHIRIRAREKSPSSIFEM 127	
QY	121 TPFKAQGPPEVHLEADKIVIRISPGTDSV--KMAIDGLSFTTSLIKKSSGYEE 178	
Db	128 IPIYIAQGPPEIAQSLNGAIKINISPPKANQVRKM-LISVEFKYNVVIMDSSNV-E 185	
QY	179 RIENYSKRIYKLSPEPTCYLAKVKAALLTSKIGVSPVHCITTYE-NELPPENIEY 237	
Db	186 KVRSLPIADVINDLAPETTYCLKQVATVPLEDKGLSPHICITRTKRVNDLLCPTNVRV 245	

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OY 238 SVONQNVYVKMDYTY-ANMFOYQWLHAFILKRNPGNHLTKMKQIPDCEVNTKTC----- 292
DB 246 FALNMKFYLLMNHNEHETTYVQYILTKLNYIDYSSKMWKVSCEINTSKMCLSSV 305
OY 292 VEPONVFOKGIYLLRVOASDGNNTSFMSEIKFDEIOAFLLPPVNIISLSDFIYIG 351
DB 306 IKRTS---ASYFRVQANNEYSKSLKNDVEPDVPTNEIGPDKVIDSLYLHIKIT 361
OY 352 APOGSGNTPIYODIPLIYEIIFEMTSNAERKIEKTD--VTVPNLKPLVYCVKARA 408
DB 362 PPGGPNKIMSDLYDSFYQILYWKNSDNEEYKMKETOTIATVSDLAPOSTLYCVKVOA 421
OY 409 HTMDEKLKSVSDAVCEKTRPG 432
DB 422 --FSEAYNKSSDFSEECIGTAGG 443

RESULT 2
061190 PRELIMINARY: PRT: 349 AA.
AC 061190;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE CYTOKINE RECEPTOR FAMILY 2, MEMBER 4 (CLASS II CYTOKINE RECEPTOR 4).
GN IL10RB OR CRF4 OR CRF2-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97199375
RA GIBBS V.C., PENNICA D.;
RT "CR2-4: Isolation of cDNA clones encoding the human and mouse
RT proteins."
RL Gene 186:97-101(1997).
DR EMBL: U53696; AAC53062.1;
DR MGD: MGI:109380; Il10rb.
DR PFAM: PF00041; fn3; 1.10rb.
SQ SEQUENCE 349 AA; 39774 MW; 4AC1802A CRC32;

Query Match 9.6%; Score 222.5; DB 11; Length 349;
Best Local Similarity 26.2%; Pred. No. 3.9e-10;
Matches 56; Conservative 47; Mismatches 82; Indels 29; Gaps 9;

OY 229 LPPENIEVSVONQNVYVKMD--YTYANMFOVQWLHAFILKRNPGNHLTKMKQIPD-CE 284
DB 21 IPPEKVRMNSVFNKNILOEVPAPFKTNLTFAQY-----ESYRSFQDHCK 67
OY 285 NVKTTQCVFPONVFOKGIYLLRVOASDGNNTSFMSEIKFDEIOAFLLPPVNIISLSD 344
DB 68 RTASTQCDP-SHLSKYGDTVRRAELADEHSEM-VNVTFCPEYEDTITGPENQIESLAE 125
OY 345 SFHIYIGAKPOGSGNTPIYODIPLIYE----IIFEMTSNAERKIEKTDVTPNLKPL 399
DB 126 SLHLRSAP-QIENEPEYTLKNIYOSMAVRQYKNGINEKQVSPIDSEVLRNLEPM 184
OY 400 TYVCVARRAHTMDEKLKSVSDAVCEKTRPGN 433
DB 185 TTYCIOVOGFLDQ--NRIGEMSEPICERT--GN 214

RESULT 3
063953 PRELIMINARY: PRT: 332 AA.
AC 063953;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA RECEPTOR BETA SUBUNIT).
GN IFNGR2.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94170381.
RA HEMMI S., BOHNI R., STARK G., DI MARCO F., AGUET M.;
RT "A novel member of the interferon receptor family complements
RT functionality of the murine interferon gamma receptor in human
RT cells."
RL Cell 76:803-810(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-128SV/7.
RX MEDLINE: 97128072.
RA EBENSPEGER C., RHEE S., MUTHUKUMARAN G., LEMBO D., DONNELLY R.,
RA PESTKA S., DEMBIC Z.;
RT "Genomic organization and promoter analysis of the gene Ifng2
RT encoding the second chain of the mouse interferon-gamma receptor."
RL Scand. J. Immunol. 44:599-606(1996).
DR EMBL: U69599; AAC52938.1; JOINED.
DR EMBL: U69594; AAC52938.1; JOINED.
DR EMBL: U69595; AAC52938.1; JOINED.
DR EMBL: U69596; AAC52938.1; JOINED.
DR EMBL: U69597; AAC52938.1; JOINED.
DR EMBL: U69598; AAC52938.1; JOINED.
DR EMBL: S69336; AAB30165.1; JOINED.
DR MGD: MGI:107654; Ifng2.
DR PFAM: PF00041; fn3; 1.
SQ SEQUENCE 332 AA; 37471 MW; 0BF24E9E CRC32;

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Query Match 8.8%; Score 203; DB 11; Length 332;
Best Local Similarity 30.1%; Pred. No. 1.3e-08;
Matches 69; Conservative 38; Mismatches 86; Indels 36; Gaps 13;

OY 21 ISAAAGC---KNLSPQKVEVDIDNFIKRNNSDES-----VGNVTFSDYQKGM 70
DB 16 LGAAASPSDFSQALAPNPRHLNDBOILTWEPSPSNDPRVYGVESF-----I 69
OY 71 D-NWIKL--SGQNTITSKCNFS--LKLNYE-EIKLRIRAKEN-TSSWYEDSFT 122
DB 70 DGSWRLLEPNCTDITTEKCDLTGGGRLLKLPHPPTVFLRVRAKGNLTSKWVGLEPQH 129
OY 122 FPKAIDGPPV-VHLAEADKAIYIHISPTKSYMAALDGLSTYLLTKMSSGVIEIE 181
DB 130 YENVTVGPPKNISVPPGSLVIFHSPDPD-----VFHGATFYLVHYWKSSETOOEVE 184
OY 182 NIYSRHKIY--KLSPETTYCLKVKAL-LTGWKI--GVSPVHCIKTT 224
DB 185 GPFKNSIYLGNLKRYRYCLOTENQILKKKKIRPHOLLSNVSCHETT 233

RESULT 4
09YGC8 PRELIMINARY: PRT: 341 AA.
AC 09YGC8;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR 2.
GN IL10R2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RA REBOUL J., GARDINER K., MONNERON D., UZE G., LUTFALLA G.;
RT "Comparative genomic analysis of the interferon/interleukin-10
RT receptor gene cluster."
RL Genome Res. 0:0-0(1999).
DR EMBL: AF082667; AAD13678.1;
DR EMBL: AF082666; AAD13671.1;

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KM Receptor.
SQ SEQUENCE 341 AA: 39062 MW: 7433D364 CRC32;

Query Match 8.2%; Score 189.5; DB 13; Length 341;
Best Local Similarity 27.1%; Pred. No. 1.6e-07;
Matches 60; Conservative 41; Mismatches 93; Indels 27; Gaps 10;

OY 220 CIRTVENELPPENIEVSQNONVYLKMD---YTYANNTFOVOMLHAFKRNPNHLYK 276
DB 12 CULLCVSGIVPKPRNARISVNFRLMLMDPPGVKRGNSLYVOAKSIFPKQNNF--- 68
OY 277 WKQIDPCENVKTQC-VFPONVFOKGIYLLRVQASDGNNTSFWSSEIKFDTIOAFLLP 335
DB 68 -----VTNLTNTECDVSSLSY--GAYLVLRVTEWEDHSDMA-VYRFRPMADTVIGPP 119
OY 336 VENISLSDSFHIYIGAP---KQSGNTPIQDY-PIYELIEMNTSNAERKIE---RK 388
DB 120 SYNVSSEGTLVHVDFTGPAADREHDKMSLKQYGSWYILYWKKGSN--KQVITHDTKH 177
OY 389 TDVTVPNLKPLTVYCVKARAHMDEKLKNSVSFSDAVCEKT 429
DB 178 NSEILSQLEPMTIYCIQVGG--VIPRMNKTGERSQELCEOT 216

RESULT 5
OY6U9 PRELIMINARY: PRT: 918 AA.

ID OY6U9: 01-NOV-1999 (TREMBLrel. 12, Created)
AC OY6U9: 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE GLYCOPROTEIN 130 PRECURSOR.
GN GPI30.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-EMBRYONIC HEART PRIMARY CULTURE (E7, E8);
RX MEDLINE: 99026068
RA GEISEN M., HELLER S., PENNICA D., ERNSBERGER U., ROHRER H.;
RT "The specification of sympathetic neurotransmitter phenotype depends
on gp130 cytokine receptor signaling";
RL Development 125:4791-4801(1998).
DR EMBL: AJ011688; CAB42084.1; -
KW signal.
FT SIGNAL. 1 26 POTENTIAL.
SQ SEQUENCE 918 AA: 102495 MW: 9DC128C3 CRC32;

Query Match 6.0%; Score 138.5; DB 13; Length 918;
Best Local Similarity 20.2%; Pred. No. 0.0069;
Matches 92; Conservative 76; Mismatches 168; Indels 119; Gaps 24;

OY 19 WVL5AAGCKN-----LKSPQ---KVEVDIIDNFIKRN-NRSDSVGNVTF 61
DB 202 WVEAANALGKAESDHLVDFPIELVKPPPNLNVNSGILPTVLKLSMENQISIVVMELKF 261
OY 62 SFPIYQTMGNMIRKLSGCONITSTKCNFSSKLNVYEILRIRAEKN-----TSSMYEV 117
DB 262 NIKYRISSDTNMMEVPP-EDTASPRTSFSIOGLRPTEYVFSIRCKMEDGVGWSWSE- 320
OY 118 DSFTPRKAOIGPPEVLEADKAIVHISPGTKDSVMALDGLS-----FTYSLLIWK-- 172
DB 320 -----EIG-----VTTEDKP-----SKGPIWTITIDVSPSPATWIVIRLMKAL 358
OY 172 -----NSSGV-----EERENIYSRAKIYKLS-----PETTYCLKVKAALLTSWKIG 213
DB 359 EPEEANGVILQYEVITIRAKPPLSHPSRYNVTTSLTLKLPNGY-----EVTVAHNRVQ 414
OY 214 VSPVPHCKITVENELPPENIEVSQNONVYLKMDVTYANMTFOVOMLHAFKRNNGNH 273

DB 415 A-SPPSVLLIPSSNSKAPVKNIRTLPKDKILMGTAPNANVLKYIEMC---LMSNSDC 470
OY 274 LYKMKQIDPCENVKTQCVFPONVFOKG-----IYLLRVOA--SDGNNTSFWSSEIKF 325
DB 471 ITWQTEBG-NI-----QGTLYKGDIKPFKCYLITVPLRADGGSG----- 512
OY 326 TEIOAFLLP-----PVNISLSDSFHI-----YIGAKQSGNPNVIODYPLIYIIFWE 375
DB 512 OSVKAYLQOGRPSKGPVQTKKVGKAEVILTMNHLTVDEONG---FIRSYTLKYTVQDN 568
OY 376 NTSNAERKIEKTDVTVPNLKPLTVYCVKARAH 410
DB 569 ETASV---VDSKTEIYTLSDTLTYTVRMAYT 600

RESULT 6
OY9HV9 PRELIMINARY: PRT: 508 AA.

ID OY9HV9: 01-MAY-1999 (TREMBLrel. 10, Created)
AC OY9HV9: 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE INTERFERON ALPHA/BETA RECEPTOR 2.
GN IFNAR2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RA REBOUL J., GANDIER K., MONNERON D., UZE G., LUTPALLA G.;
RT "Comparative genomic analysis of the Interferon/Interleukin-10
receptor gene cluster";
RL Genome Res. 0:0-0(1999).
DR EMBL: AF082665; AAD13670.1; -
KW HSRP; P13726; ITRH.
KM Receptor.
SQ SEQUENCE 508 AA: 57049 MW: 2DC4E498 CRC32;

Query Match 5.7%; Score 131; DB 13; Length 508;
Best Local Similarity 21.1%; Pred. No. 0.012;
Matches 106; Conservative 69; Mismatches 149; Indels 178; Gaps 29;

OY 2 MYVLIGAT---TLVLVAVGPVYLSAAGKMLKSPQKY--EVDIIDNF--ILRW-NR 52
DB 1 METLWGGPLRFYQVLFVSI---LCAACYSLSSEKIPREPPDNILQMTSNFQHILSMRAHS 57
OY 53 DESVC---NVTTSFDYQKTMGNMIRKLSGCONITSTKCNFSSKLNVYE-----IKLRIR 105
DB 58 DPTVPTYYRVLYS-----SHSNMKIRAKOCSRIYQPFCLTDDFOVVSDEYSAFVQSFG 111
OY 106 AEKENTSSWEVDSFTPRKAOIGPPEVLEADKAIVHIS-PGT---KDSVMALDGL 161
DB 112 TEVFNSSLH---FSPLETFGLPPEFNLSCVHCINITTLPLPHLRKNGKL----- 162
OY 162 SFYSLLIWKNSGVEERENIYSRAK-----IYKLSPEYYCLKY----- 203
DB 162 ---LSLFDIYNKYVNEIILRTVGEHKRSPKRYTEPEFSIYELIYLPNNKVCVSVWVAS 218
OY 203 --KAALLTSWKIGVSPVCIKTYVENELPPENIEVSQNONVYLKMDVTYAN----- 255
DB 219 LNHHSIPSAWK-----CITTD-----SVAEKDY--YGITTAGAICFSI 254
OY 255 -MTFOVOMLHAFKRNPNHLYKMKQIDP-----CENYKQTCVFPQNV 297
DB 255 ILVILAKCLHL-----GGYILHKSLSPDTLVFTKMFSLPTFBECEITISVEIILY-KEV 307
OY 298 FOKGIYLLRVQASDGNNTSFWSSEIKFDTIOAFLLPVPFNIRLSDSFHIYI-----G 351
DB 308 KKK-----AEGSVGAVSSEDDSDDESAM-----SNHDTYRRDIYVR 345
OY 352 AKPOSGNTPIYI-----QDYPIYELIEMNTSNAERKIEKKTVO 391


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DB 346 APSSDTSPEVFGHSTSSGDCSSSWVSONPDGPEVFE-----ENEMDAFE---EKDTS 398
QY 392 TYPNKKPLT---VYCVKARAH 409
DB 399 EL--LSPLSKVNCTYSLSRSRN 418

RESULT 7
P97798
ID P97798 PRELIMINARY; PRT; 1493 AA.
AC P97798;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-NOV-1997 (TREMBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE NEOGENIN (NEOGENIN PROTEIN).
GN NEO1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RP [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 9740761.
RA KEEBING S.L., GAD J.M., COOPER H.M.;
RT "Mouse Neogenin, a DCC-like molecule, has four splice variants and is
RT expressed widely in the adult mouse and during embryogenesis."
RL Oncogene 15:691-700(1997).
DR EMBL; 109535; CAA70727.1; -.
DR HSSP; P02751; ITTG.
DR MGD; MGI:1097159; Neol.
DR PFAM; PF00041; fn3; 6.
DR PFAM; PF00047; fn3; 4.
DR PRINTS; PR00014; FNTYPEIII.
SQ SEQUENCE 1493 AA; 163159 MW; 98F26676 CRC32;

Query Match 5.6%; Score 130; DB 11; Length 1493;
Best Local Similarity 21.4%; Pred. No. 0.063;
Matches 89; Conservative 75; Mismatches 191; Indels 60; Gaps 20;

QY 21 LSAAGGKNIKSPQKVEVDIIDNFI-LRWN--RSDESGVNTFSFDYOKTGMDNIKLS 77
DB 461 LAPATGPLPSAPRDVVASLVSRTFIKLTWRTPASDPHGDNLTYSVFYTKEGVDR----E 516
QY 78 GCONITS-----TKCNFSLKLVYVEIKLRIRAKENTSSWYEDSTPFKACIGCP 131
DB 517 RVENISOPGEMOYTIONLMPATYIF-----KVMAQNKHGSG---ESSAPLEVER--OP 565
QY 132 EVHLEAEDKAIVHISPGTKDSVMAL----DGLSFTYSLILWKNSSGVEERIENTYSRH 187
DB 566 EVQGLPPAPANIRAYATSPISITYTWETPLSGNGEIONKLYMEKTDKEDIDVSSHRY 625
QY 188 KIYKLSPEPTYCLKVKAAALTSKIGVSPVHCITTVENELPPENIEVSON-ONYVL 246
DB 626 TINGLKRYTEYSERYVA--YKNHGPSTQDVAVRFLSDVPSAAPQNLSELVANSKSIYI 683
QY 247 KM---DYTYAN--MTFOVOMLHAFKRNPNHLYKKKQIIPDCENKTKTQCVPQVAFK 300
DB 684 HHQPPSTQNGOITGKIRYKRSKSDVTELTGTGL-----SGLI--EGLDGG 733
QY 301 GIYLLRQASDGNNT---SFWSEELKFDTEIOAFLLPV---FNIRSLDSFHIYGAPK 354
DB 734 TENENFVALIYNGTGPALDWLSAEFFESDLDETRIVEPSSLHAYPLVTSI-VVSWTPP 792
QY 355 QSGNTPVADYPLIYIIFWMENTSNAER-KIEKKTQDVTPNKKPLTYVCVAKARA 408
DB 793 ENONI-VVGRGAIYGI-----GSPHAQTIKVDYKQRYTYIENLDPESHVITLKA 842

RESULT 8
Q94537
ID Q94537 PRELIMINARY; PRT; 1375 AA.
AC Q94537;
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DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE FRAZZLED.
GN FRAZZLED.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophillidae; Drosophila.
RP [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97015076.
RA KOLODZIEJ P.A., TIMPE L., MITCHELL K.J., GOODMAN C.S., FRIED S.,
RA JAN L.Y., JAN Y.N.;
RT "Frazzled encodes a Drosophila member of the DCC immunoglobulin
RT subfamily and is required for CNS and motor axon guidance."
RL Cell 87:197-204(1996).
DR EMBL; U71001; AAC47314.1; -.
DR FLYBASE; FBgn0011592; fra.
DR PFAM; PF00041; fn3; 6.
DR PFAM; PF00047; fn3; 6.
DR PRINTS; PR00014; FNTYPEIII.
SQ SEQUENCE 1375 AA; 151692 MW; 43806DBC CRC32;
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Query Match 5.6%; Score 129; DB 5; Length 1375;
Best Local Similarity 16.4%; Pred. No. 0.068;
Matches 102; Conservative 68; Mismatches 184; Indels 268; Gaps 22;

QY 26 GGNKLS-----POKVEVDIIDNFI-LRW-----NRSDSV 56
DB 447 GKKPLDSGLQRLPSQPDVLAQIKSRFVLSWVEPQNGADVYVYVYKMNSEREQ 506
QY 57 GNVTFSDYOKTGMDNIKLSGCONITSTKCNFSS-----LKNVYEIKLR----- 104
DB 507 KMYTSHDDQVNIQSLPGRTRQFRVEANNFSGASAPLVESTQEVNIAQPPRME 566
QY 104 --IRAKENTSSWY-----Y 117
DB 567 GYARSHKEIYVKEEPTVYNGEILKRYVYENDSGADLYHDSALAEVLTSLRPHDYV 626
QY 118 DSFTPFRAQIG-----PPEVHLE-AEDKAIYHISPGTKDSVMAL 158
DB 627 ISVVPFNNGMGDSAEIRVKTFSSTSEPPNNNTVLETSSSITVHPEPAEDRNGOI 686
QY 159 DGLSTYSLILWKNSSGVEERIENTYSRHKLYKLSPEPTYCLKVKALL-----TSWKI 212
DB 687 TGYKIRYRK--FKDAPQVKTSPANI-RYFELSNDRNAEYQVKIAAMTVNGSGPTEWNR 743
QY 213 GYSPVHCKITTVENELP-----PPENIEVSONONYVLK 247
DB 744 A-----NTLENDLDETQVPGKPIWISIHPGANNIALHMGPPHPEIKI--RNYVLG 792
QY 248 W-----DY----- 251
DB 793 WGRGIPDENTIELEKTERHYHLKNDLESMDVYSLARANVAGDPPITYDNKTRDEEYD 852
QY 251 -----TYANMFOVOMLHAFKRN-----PGNHLYKKWQIP 281
DB 853 APTPLEVPGRLATIMSSSIIVYWIIDMLKNKHVTDNRHYTVSYGIGTSNRKYR---- 909
QY 282 DCENKTKTQCVPQVAFKQGIYLLRQASDGNNTSFWSEELKFDTEIOAFLLPVFNIRS 341
DB 909 --HNTDLCMI--NDLRNTQYEFRAVKYKGRRESSMSVLSNSTYONVPTPP----- 960
QY 342 LSDSEHIYIGAPKQSGNTPVADY-----LIYEIIFWMENTSNAER-----KIEKK 388
DB 960 ----REVTVRLDENMNPPIYIQWIPKHTLGQITGINIYITDTTKKDRDMSVAFAGEE 1015
QY 389 TDVTPNKKPLTYVCVAKARAHT 410
DB 1016 TMLMLPNLKPYYTFYFKVQART 1037
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RESULT 9
ID Q94538 PRELIMINARY; PRT: 1526 AA.
AC Q94538;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE FRAZZLED.
GN FRAZZLED.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Prorygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97015076.
RA KOLODIEJ P.A., TIMPE L., MITCHELL K.J., GOODMAN C.S., FRIED S.,
JAN L.Y., JAN Y.N.;
RT "Trazzled encodes a Drosophila member of the DCC immunoglobulin
subfamily and is required for CNS and motor axon guidance."
RL Cell 87:197-204(1996).
DR EMBL: U71002; AAC47315.1;
DR FLYBASE: FBgn0011592; fra.
DR PFM: PFM0047; fn3; 6.
DR PFM: PFM0047; 19; 3.
DR PRINTS: PFM0014; FNTYPEIII.
SQ SEQUENCE 1526 AA; 168787 MW; F17B1EC9 CRC32;

Query Match 5.68; Score 129; DB 5; Length 1526;
Best Local Similarity 16.48; Pred. No. 0.078;
Matches 102; Conservative 68; Mismatches 184; Indels 268; Gaps 22;

QY 26 GGNKLS-----POKEVDIDDNFI-LRW-----NRSDSV 56
DB 598 GKKPLDSGLQARLPSPQPDVAQIKSRFVILSWEPLOMGDVYVYVYKMNSEHQ 657
QY 57 GNVTFSPDYOKTGMNWKILSGCONITSTKCNFS-----LKLNVYEBIKR----- 104
DB 658 KMTKSHDDQVNIQSLPLGRTYQPRVEANTNFGSGASAPLEVSTOPEVNAGPPRNE 717
QY 104 --IRAEKENTSSWE-----Y 117
DB 718 GYARSHKELYYKMEEPYVNGEILKYRYYSSENDGADLYHDSALEAVLELRPHDYV 777
QY 118 DSFTFERRAOIG-----PEVHLE-AEDKAIYIHISPGTKDSVMAL 158
DB 778 ISVVFNRNGMGDSAEIRVKTFSSPTSEPPNNVLEVTSSSIVHMPRAEDRNGI 837
QY 159 DGLSFTYSLILWKNSSGVEERIENTYSRHKIYKLSPEPTYCLKVKAAL-----TSWKI 212
DB 838 TGYKIRYKR--FKDAPQVSTPANI-RYFELSLNDRNAEYQYKIAMTVNGSGPTEWNR 894
QY 213 GYTSVYHCKTIVENELP-----PENIEVSQONQNYLK 247
DB 895 A-----NTLENDLETOVGRKPIWISHPGANNIALHWGPQHPKIKI--RNYVLG 943
QY 248 W-----DY----- 251
DB 944 WGRGIDPENTIELKETERHILKLNESNNDYVYSLARNVKGDGPIYINIKTRDEPVD 1003
QY 251 -----TYANNTFOVOMLHAFLEKRN-----PGNHLKWKQIP 281
DB 1004 APTPLEVPYGLRAITFMSSSIYVYVWIDTMLNKNQHVTDNRHYTVSYGIGSRNRYR---- 1060
QY 282 DCENKTTQCVFPQVFOGIIYLLRYQASDGNNTSFWSEIKFDTIQAFLLPVENIS 341
DB 1060 --HNTDLNCKMI-NDLRPTQYEFAYKVKYGRRESMSKSVNSTQNVPTPP----- 1111
QY 342 LSDSFIIYIGAPROSGNTPIVDY-----LIYEIIFMENTSNAER-----KIIKK 388
DB 1111 ----REVYRLDEMPPIYIVQWIPKHLGQITGINITYTTDTTRDQMSYEAFAEE 1166

QY 389 TDVTPNKLKPLTYCYKARAH 410
DB 1167 TMLLPLMKPITYYFVQVART 1188

RESULT 10
ID Q90610 PRELIMINARY; PRT: 1443 AA.
AC Q90610;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE NEOGENIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-WHITE LEGHORN; TISSUE-BRAIN;
RX MEDLINE: 95105243.
RA VIELMEYER J., ROMAN J.M., DREYER W.J.;
RT "Neogenin, an avian cell surface protein expressed during terminal
neural differentiation, is closely related to the human tumor
suppressor molecule deleted in colorectal cancer."
RL J. Cell Biol. 127:2009-2020(1994).
DR EMBL: U07644; AAC59662.1;
DR HSSP: P80362; 1WTL.
DR PFM: PFM0041; fn3; 6.
DR PFM: PFM0047; 19; 4.
DR NON-TER 1 1
SQ SEQUENCE 1443 AA; 158050 MW; 270B77DC CRC32;

Query Match 5.58; Score 127.5; DB 13; Length 1443;
Best Local Similarity 22.28; Pred. No. 0.095;
Matches 92; Conservative 61; Mismatches 201; Indels 61; Gaps 19;

QY 21 LSAAGKKNLSPKVEVDIDDNFI-LRWNR--SDSEVGNVTFSPDYOKTGMNWKILS 77
DB 416 LAPATTGPLPAPDVAVATLVSTFRILRTWTPVSDQGDULTYSIFTYEG-----INRE 471
QY 78 GCONITSTKCNFSILKNVYEIKLRIRAEKENTSSWYEVDSFTFERRAOIGPEVHLEA 137
DB 472 RVEN-TSRPGTQVNIQMLPEYVYFRVYVQNHGCE--SNAPLAVAT--QREVQLPG 526
QY 138 EDKAIYIHISPGTKDSVMAL-----DGLSFTYSLILWKNSSGVEERIENTYSRHKIYKLS 193
DB 527 PAPINRAVAGSPTSVYTWETPLSGNGBIQNYKLYMEKGDSQDQDVAGLSTITGLK 586
QY 194 PETTYCLKVKAALLSMKIGYSYVHCKTIVENELPPEPIEVSQONQNYLKMDYTY 252
DB 587 KYTESFQVVA--YKNHQPVSQTDVYVRLSDVPSAAPQMLTEARSKSIMLHWOPPP 644
QY 253 ANMTFOVOMLHAFLEKRNPNL-----YKWKQIPDCENKTTQCVFPQVNEQ--KGI--- 303
DB 645 A-----GTHSGQITGKIKIRKYSRKSQDTEVSGQLFOLLBLELGG 687
QY 303 --YLLRQASDGNNT--SFWSEIKFDTIQAFLLPV--FNIRISDSFHIYIGAPK 354
DB 688 TEYNRIAMVNGSPATDVASATFESDDESRRVPSLSLHVRLPVTISI-VVSWTPP 746
QY 355 QSGNTPIVDYPLIYEIIFMENTSNAER-KIIKKTDVTVNKLPLTYCYKAKA 408
DB 747 ENONI-VVGRYAIGIGI--GSPRAQIKYDQRYTYIENLDPSSSHVITLKA 796

RESULT 11
ID Q98949 PRELIMINARY; PRT: 873 AA.
AC Q98949;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)

DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE AXI-RELATED RECEPTOR TYROSINE KINASE.
 GN REX.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 CC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97067156.
 RA BISCARDI J.S., DENHEZ F., BUEHLER G.F., CHESNUT D.A., BARAGONA S.C.,
 O'BRYAN J.P., DER C.J., FIORDAISI J.J., FUTIS D.W., MANESS P.F.;
 RT "Re", a gene expressed in retina and brain, encodes a receptor
 RT tyrosine kinase of the Ax1/Tyro3 family."
 RL J. Biol. Chem. 271:29049-29059(1996).
 DR EMBL: U70045; AAC60041.1; f3; 4.
 DR HSSP: P00041; f3; 2.
 DR PROSITE: P50107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: P80109; PROTEIN_KINASE_TYR; 1.
 DR PFAM: PF00047; f3; 1.
 DR PFAM: PF00069; pkinase; 1.
 SO SEQUENCE 873 AA; 96402 MW; 2918D550 CRC32;

Query Match 5.3%; Score 123; DB 13; Length 873;
 Best Local Similarity 22.5%; Pred. No. 0.11;
 Matches 102; Conservative 58; Mismatches 151; Indels 142; Gaps 25;

OY 13 LVAVGPWVL-----SAAAGKMLSPQKVEY-----DIIDNFILRMNSDES 55
 DB 12 LLLGLMAALRDGAVAAAMKFTGSIKLVKSGOPVKVCLSGEEDPEML-WIKD-- 68
 OY 56 VGNVTFSPD--YOKTGMNDWIKLSCGQNTSTKCNFSSKLNVYEIKRIAEKENTSS 113
 DB 68 -GAVOSVDQVYIIPVDEDMW-----GFLSLK-----SVERTDS 100
 OY 114 ---WYEVDSFTPFRAQ-----IGPPEVHLEAEDEKAIYIHISPTKDSVMALDGLST 164
 DB 101 GKWCQVENGKKESSQWLVIEGVPTVEPED---VSVPNAPFLMCAAAAGPPRP 156
 OY 165 YELLWK-----NSSGVERIENTYSRKITYLSEPTTYCLKVKAALLTS 209
 DB 157 VTIWMMGDSRVGLPDISPILNVSGINOSTMFSEAHNVKGLSSSRATVQIKAMP-- 215
 OY 210 WKIGYSPVHCIKITVENELPPENIEVSQONQVYVLMKYAMTQVOYLHAFKRN 269
 DB 215 -----PLNAVTVS-----QVTSNNS--VWVWPGDGRA 241
 OY 270 P-GNHLVYMKQIPDCENYKTCQVFPQNYFORGI-----YLLRVAQSDGNNTSPWSE 320
 DB 242 PLHSTLVAESPDCQEVSTE--VAPVPFAVYGGLKHTSTNYSVRYGCSNMGSSPTE 299
 OY 321 EIKETELQAFLLPVPFNRSLSDFHYIGAP-----KQSGTTP-VIODYPIITYITW- 375
 DB 300 RYVF-----QTELELP-----SSTPQNIHVIQRDPGLVLEMEGAVPDLKENVLYGR-LEMI 350
 OY 375 -ENTSNAERKITEKTDVTPN-LKPLTV-YCV 404
 DB 351 QDNVTOGEMIVQDTKANLTMPLKDLIIRVCV 383

RESULT 12
 092859 PRELIMINARY; PRT; 1461 AA.
 AC 092859;
 DT 01-FEB-1997 (Tremblrel. 02, Created)
 DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE NEOGENIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN (1)

RP SEQUENCE FROM N.A.
 RA METERHAROT J.A., LOOK A.T., BIGNER S.H., FEARON E.R.;
 RL Oncogene 0:0-0(0).
 DR EMBL: U61262; AAB17263.1; -.
 DR HSSP: P02751; ITTG.
 DR PFAM: PF00041; f3; 6.
 DR PFAM: PF00047; f3; 4.
 DR PRINTS: PRO0014; FNTYPERIT.
 SO SEQUENCE 1461 AA; 159958 MW; 0AB7247E CRC32;

Query Match 5.3%; Score 122.5; DB 4; Length 1461;
 Best Local Similarity 20.7%; Pred. No. 0.24;
 Matches 87; Conservative 80; Mismatches 197; Indels 57; Gaps 20;

OY 11 LVAVGFWVLSSAAGKMLSPQKVEVDIIDNFI-LRNW--RSDESQVNTSPDYOK 67
 DB 425 LILIEHAP-----ATTGFLPSAPRDVVAASLVSTFIKLTWRTPASDPHGNLTVSVYTK 479
 OY 68 TGM--DNWIKLSGQNTSTKCNFSSKLNVYEIKRIAEKENTSSWYEVDSFTPFPRK 125
 DB 480 EGIAERREVENTSHPGEQVITQNLMPATYIF-----RYVAKNKHGSG---ESSAPLRY 530
 OY 126 AQIGPPEVHLEAEDEKAIYIHISPTKDSVMAL-----DGLSTFVSLIMKNSGVEERIE 181
 DB 531 ET--QPEVQLGPRAPNLRAYASPTSTVETWETVSGNGELQNKLYTMEKGTDEKDDVD 588
 OY 182 NITYRHKIYKLSPEPTTYCLKYKAAALLTSWKIGYSPVHCIKITVENELPPENIEVSQON 241
 DB 589 VSSHRTYINGKLYKTERSEFVVA--YKHHGVSTPVAVARTLSDVSAAPQNSLSEVRN 646
 OY 242 -QNVYVLMKD-----YTANMT-FOVQYLHAFKRNPGNHLKMKQIPDCENYKTCQVFP 294
 DB 647 SKSIIHMQPPAPATONGQIIGYKIRYRKASRKSVDVETIVSGTOL-----SGLI-- 697
 OY 295 QNVFQKGIYLLRVAQSDGNNT--SPWSEIKPTELEQAFLLPV---FNIRSLSDSFHI 348
 DB 697 EGLDRGTEYNRVAALNTINGPATDMLSAETESDDETRVPEPSLHRLPVYTI-V 755
 OY 349 YIGAPKQSGNTPIQDYPLIYEIIFMENTSNAER-KIIEKTDVTPNLKPLTVYCYKAR 407
 DB 756 VSMTPPERQNI-VYRGAIIGYI-----GSPHAGIKVDYKORYYTIENLDPSSHYVITLK 810
 OY 408 A 408
 DB 811 A 811

RESULT 13
 000340 PRELIMINARY; PRT; 1461 AA.
 AC 000340;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE NEOGENIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE: 97312699.
 RA VIELMEITER J., CHENG X.N., MISKEVICH F., LANE R.P., YAMAKAWA K.,
 KORENBERG J.R., DREYER W.J.;
 RT "Molecular characterization of human neogenin, a DCC-related protein,
 RT and the mapping of its gene (NEO1) to chromosomal position 15q22.3-
 RT q23."
 RL Genomics 41:414-421(1997).
 DR EMBL: U72391; AAC51287.1; -.
 DR HSSP: P02751; ITTG.
 DR PFAM: PF00041; f3; 6.
 DR PFAM: PF00047; f3; 4.

DR PRINTS: PRO0014: FNTYPE111.
SQ SEQUENCE 1461 AA; 160015 MW; 905AE1C4 CRC32;

Query Match 5.3%; Score 122.5; DB 4; Length 1461;
Best Local Similarity 20.7%; Pred. No. 0.24;
Matches 87; Conservative 80; Mismatches 197; Indels 57; Gaps 20;

QY 11 LVLVAVGPWLSAAGKNEKSPQKVEVDIIDNFI-LRNN--RSDSVGNVTFSEFYOK 67
DB 425 LILLEHAP-----ATGGLPSPADVDVAALVSTRFIKLTWRTPASDHPGDLTYSEFYTK 479
QY 68 TGM--DWIKISGCONITSTFCNSSLKLNVEEIKLRREKENTSSWVEVDSEFTPRK 125
DB 480 EGIARERVENTSHPEGMOVTIQNLMPATVYLF-----RYMKNKHGSG---ESSAPLV 530
QY 126 AOIPPEVHLAEEDKAIYIHISPGTKDSVMAL-----DGLSFTYSLIMKSSGVEERIE 181
DB 531 ET--QPEVQLPGPAPNLRAYASPTSTVYETPVSNGEIQNKLYNMEKGTREKQDQVD 588
QY 182 NIYSRHKIKYKLSPEPTYCLKYKAAALLTSWKIGVYSPVHCITTVENELPPENIEVSYON 241
DB 589 VSSHVYTINGLKKYTESFRVYA--YXKHGPGVSTPDVAVRTLSDPSPADQNLISLEYRN 646
QY 242 -QNVYLRND-----YTYANMT-FOYQMLHAFLRNPGNHLKKNQIIPCCENVKTTQCVFP 294
DB 647 SKSIIHQPAPAPATONQOITGYKIRYKASKSDVETETLVSGTQL-----SGLI-- 697
QY 295 QNVFQKGYLLRVQASDGNNT---SFWESEIKFDEIOAFLLPY---FNIRLSDSFHI 348
DB 697 EGLDRGTENFRVALLTNGTGPATDLSAEFESDLDETREPEVPSLLHVRPLVTST-V 755
QY 349 YIGAKQSGNTPIVDYDPIYELIIFMENTSNAER-KIIEKTDVTPNKLPLTYCVKAR 407
DB 756 VSWPEPEPQNI-VVRGVAIGGVI-----GSPHQITIKVDYKQXYIENLDPSSHVYITLK 810
QY 408 A 408
DB 811 A 811

RESULT 14
Q91562 PRELIMINARY: PRT: 1427 AA.
AC Q91562;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DR 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE TUMOR SUPPRESSOR.
GN XDCCA.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae; Xenopodinae;
OC Xenopus.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE; 9511183.
RA PIERCELL W.E., REALE M.A., CANDIA A.F., WRIGHT C.V., CHO K.R.,
RA FEARON E.R.;
RT "Expression of a homologue of the deleted in colorectal cancer (DCC)
RT gene in the nervous system of developing Xenopus embryos."
RL Dev. Biol. 166:654-665(1994).
DR EMBL; 010986; AAA70168.1;
DR HSSP; P56276; TLTK.
DR PFAM; PF00041; fn3; 6.
DR PFAM; PF00047; 19; 4.
DR PRINTS; PRO0014; FNTYPE111.
SQ SEQUENCE 1427 AA; 156533 MW; E5087475 CRC32;

Query Match 5.1%; Score 117.5; DB 13; Length 1427;
Best Local Similarity 22.2%; Pred. No. 0.59;
Matches 93; Conservative 70; Mismatches 163; Indels 93; Gaps 22;

QY 32 SPQKVEVDIIDNFI-LRNNRSDSEVGNV-TESFDYOKTGMWIKISGCONITSTKCNF 89
DB 431 APRDVPVVLVSSRFRLSRPVESSKNGIOTTYVFSKQGVORRAVNTSOTI----- 484
QY 90 SSKLNV-----YEEKLRIRAEKENTSSWVEVDSEFTPR-----KAQIGPEVHLAED 139
DB 484 -SLQITVGNLTPEETYNFRVAANE-----WGPESSQEVKVVYTOPLOYGPGVENLQ--- 536
QY 140 KAIVHISPGTKDSVMALDGLSFT-----YSLIMKSSGVEEIEENIYSRHKIKYKS 193
DB 536 ---VSTIAP---TSVLISMPPRAYANGPVQGYRPFCAETFSGREGQNIEDVGIYRLGGR 589
QY 194 PETTYCLKYKAAALLTSWKIGVYSPVHCITTVENELPPENIEVSYONQNVYLRKMDYTA 253
DB 590 KTEYSIRVLA--YNRGPGVSSSEHVTVTLSDVPSAMPQNVSLVAN----- 636
QY 254 NMTFOVQMLHAFLRNPGNHL-----YKMQIPDCENVKTT-----QCVFQNVF----- 299
DB 636 SRGKISVM-----LPPPGTONGFITGK-----IRHRTTRGGELETLEPNMLWYFTG 685
QY 299 -QNGI-YLLRVQASDGNNTSFWESEIKFDT-----EQAFLLPPVFNISLSDSRHIYI 350
DB 686 LEKSGQSFQVAAMTVNGTSPSSDMYTAETPENDLDESQVDPDPSLLHVRPLVTSTI-IMS 744
QY 351 GAPQSGNTPIVDYDPIYELIIFMENTSNAER-KIIEKTDVTPNKLPLTYCVKARA 408
DB 745 WTPPLPNPI-VVRGVIIGYGV-----GSPVETVRVDSKORYSTIENLEPSSHVYISLKA 798

RESULT 15
Q17859 PRELIMINARY: PRT: 1585 AA.
AC Q17859; Q20137;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DR 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE C09D8.1 PROTEIN.
GN C09D8.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN (1)
RP SEQUENCE FROM N.A.
RA COLES L.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z46811; CAA86842.1;
DR EMBL; Z49338; CAA86842.1; JOINED.
DR EMBL; Z49338; CAA90189.1;
DR EMBL; Z46811; CAA90189.1; JOINED.
DR HSSP; P28827; IRPM.
DR PFAM; PF00044; fn3; 3.
SQ SEQUENCE 1585 AA; 178386 MW; EA03A8BD CRC32;

Query Match 5.1%; Score 117.5; DB 5; Length 1585;
Best Local Similarity 19.7%; Pred. No. 0.68;
Matches 86; Conservative 74; Mismatches 171; Indels 105; Gaps 24;

QY 33 PQKVEVDIIDNFI-LRNNRSDSEV--GNVTFSEFYOKTGMWIKISGCONITSTKCNFS 90
DB 263 PIDVOYEWKKGKIYVSNRPPESEKRNNGIT-SYKAILSAMQ--ATADYEDPVPAPSPSS 319
QY 91 SKLNVYEIKLRIRA-----EKENTSSWVEV---D 118
DB 320 TFEVNVRAVYLFKVAALTMKIGIPYVLTINPDADLIDNNIEEGNODPGATWGE 379
QY 119 SFTPRKAQIGPEVHLAEEDKAIYIHISPGTKDSVMALDGLSFTYSLIMKSSGVEE 178
DB 380 NNPPKRSKRISTADY-----SALHHAEP-----LTHPISAAALAKAPTIGA 423
QY 179 RENIYSRHKIKYKLSPEPTYCLKYKAAALLTSWKIGVYSPVHCITTVENELPPENIEV- 238

Db 424 PMBAPYTTTS-----TBSTLFFOYTLPPMTAMN-----RVTKLETLVGPPTNVRYE 470
QY 238 SYONONTVLKMDYTYANM-TEOVQWLAFLKRNPNHNL--YKMKOIP---DCENYKTIQ 290
Db 471 ATSNSTAVVQWDFESQKADSFVVKYMH-----EPGNMDEKMKQOLPVYSIDKENPKRRA 525
QY 291 CVPQOVFOKGIYLLRVQASDGNNTSEFSEIEKFDTEIOAFLLPVENIRSL-----SD 344
Db 526 VVSDLNHAKP--YAFCVLAVKNNRQGPCSDP---PTVLES--VTPTVMQNLRLVWKTSN 578
QY 345 SFH1---YIGAPKQSG---NTPVIOYPLIYEIIEMENTSNAE---RKIIIEKTDVTPN 395
Db 579 SVQLTWEYNG-PRNVGFYVNHGKRDY-VNHEL--OEKIWSIPFGQDYDEKHREYLMWTN 634
QY 396 LKPLIVYCVKARAHIM 411
Db 635 LRPHMYTIIHGVRTL 650

Search completed: June 1, 2000, 05:54:18
Job time: 4523 sec


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101 LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVal 117
377 TGAGTCAATTACACCATTTGGCAAGCTGATGTCCTCCCAAAATAC 426
117 LAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluValH 134
427 ATTAGAAGCTGAAGATAGCAATAGTATACATCATCTCCGGAACA 476
134 LsLeuGluAlaGluAspLysAlaIleValIleHisIleSerProGlyThr 150
477 AAGATAGTGTATGTGGGCTTTGGATGCTTAAAGCTTACATATAGCT 526
151 LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerIe 167
527 ACTATCTGGAAGAACTCTCAGCTGAGAAAGAAAGATGAAGAAATTT 576
167 uLeuIleTrpLysAsnSerSerGlyValGluGluArgIleGluAsnIleT 184
577 ATTCCAGACATAAAATTTATTAATCTCACAGAGACTACTATTGTCTA 626
184 YrSerArgHisLysIleTyrLysLeuSerProGluThrThrTyrCysLeu 200
627 AAAGTAAAGCAGCAGCTACTACTGATGCAAAATTTGGTGTCTATGCTC 676
201 LysValLysAlaAlaLeuLeuThrSerTrpLysIleGlyValTyrSerPr 217
677 AGTACATTGTATTAAGACACAGCTGAAATGAATCACTCCACCAAGAA 726
217 ovalHisCysIleLysThrThrValGluAsnGluLeuProProGluVal 234
727 ATATAGAAGTCAGTGTCCAAATTCAGACATATGTTCTTAATGGGATAT 776
234 snIleGluValSerValGlnAsnGlnAsnTyrValLeuLysTrpAspTyr 250
777 ACATATGCAAAATGACCTTTCAAGTTCAGTGGCTCCAGCGCTTTTAA 826
251 ThrTyrIleAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeuLys 267
827 AAGGAATCTCGAAGAACCATTTGTATTAATGGAACCAATACCTGACGTG 876
267 sArgAsnProGlyAsnHisLeuTyrLysTrpLysGlnIleProAspLysG 284
877 AAAATGTCAAAATCAACCAAGTGTCTTCTCCAAAACGTTTTCAAAA 926
284 LuAsnValLysThrThrGlnCysValPheProGlnAsnValPheGlnLys 300
927 GGAATTTACCTTCTCCGCTGTAAGCATTCGATGGAATAATACATCTTT 976
301 GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerPh 317
977 TTGGTCTGAAGAGATAAGTTGATGATGAATACAACTTCTCTACTTTC 1026
317 eTrpSerGlnGluIleLysPheAsnProGluIleGlnAlaPheLeuLeuP 334
1027 CTCAGTCTTTTAACTTACATTCCTTAGTATTCATTCATCTATATATC 1076
334 rOProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle 350
1077 GGTGCTCCAAAACAGTCTGGAACACCCCTGTGATCCAGATTTATCCACT 1126
351 GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrProLe 367
1127 GATTATGAAGATTTATTTTGGGAAAAACACTCAAAATGCTGAGAGAAAA 1176
367 uIleTyrGluIleIlePheTrpGluAsnThrSerAsnAlaGluArgLysI 384
1177 TTATCGAAGAAAAAAGTATGATACAGTCTCTAATTTGAAACCACTGACT 1226
384 leIleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
1227 GTATATGTGTGAAGCCAGACGACACACATGATGAAAAAGCGAATAA 1276
401 ValTyrCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnLys 417

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1277 AAGCACTGTTTACTGACGCTGTATGTGAGAAACAAACCAAGGAATA 1326
417 sSerSerValPheSerAspAlaValCysGluLysThrLysProGlyAsnT 434
1327 CCTCTTAA 1334
434 hSerLys 436

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seq_name: A_Geneseq_36:R28495

seq_documentation_block:
 ID R28495 standard; Protein; 436 AA.
 AC R28495:
 DT 31-MAR-1993 (first entry)
 DE Sequence of a soluble form of the interferon (IFN) receptor
 DE with a high affinity for IFN-alpha and -beta.
 KW Interferon receptor; alpha-interferon; beta-interferon.
 OS Synthetic.
 PN M09218626-A.
 PD 29-OCT-1992.
 PR 17-APR-1991; F00318.
 PR 17-APR-1991; WO-F00318.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
 PI Eld P, Gresser I, Luftalla G, Meyer F, Mogenssen KE,
 PI Toyev M, Uze G;
 DR WPI: 97-382110/46.
 DR N-PSDB: Q30532.
 PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
 PT and beta - useful as immunosuppressants, for treating auto-immune
 PT diseases and transplant rejection
 PS Claim 2; Fig 1; 58pp; English.
 CC DNA encoding the water-soluble polypeptide with a high affinity for
 CC IFN-alpha and -beta is isolated by PCR, using appropriate
 CC oligonucleotides as primers and cloned cDNA as template. For example,
 CC bacteriophage lambda ZAP, containing the entire coding sequence of
 CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
 CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
 CC lacks the transmembrane and cytoplasmic domains. Both forms bind
 CC IFN in the same way as antibodies so are immunosuppressants e.g. for
 CC treating autoimmune diseases and graft rejection. They lack the
 CC toxic side-effects of known immunosuppressants such as steroids.
 SQ Sequence 436 AA;

alignment_scores:
 quality: 2313.00 Length: 436
 Ratio: 5.305 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-240-675-1 x R28495 ..

Align seg 1/1 to: R28495 from: 1 to: 436

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27 ATGATGATGCTGCTCTCTGGGCGGAGACCTAGTGTCTGTCGGCGTGG 76
|||||
1 MetMetValValLeuLeuGlnLysAlaThrThrLeuValIleValAlaGln 17
1 MetMetValValLeuLeuGlnLysAlaThrThrLeuValIleValAlaGln 17
17 yProTrpValLeuSerAlaAlaGlnLysLysAsnLeuLysSerProG 34
77 CCCAGGTGGTGTCTCCGACGCGGAGGTGGAATAATCTAAATCTCCTC 126
|||||
34 InLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn 50
177 AGGAGCGATGACTGTGCGGAATGTGACTTTTCATTCGATTACAAAA 226
|||||
51 ArgSerAspGluSerValGlnAsnValThrPheSerPheAspTyrGlnLys 67
227 AACTGGGATGATTAATGGATAAATTTGTCTGGGTGTCAGAAATATTA 276
|||||

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67  sThrGlyMetAspAsnTrpIleLeuSerGlyCysGlnAsnIleHis 84
277  GTACCAATGCAACTTTCTTCACTCAAGCTGAATGTTATGAAGAAAT 326
    |||||||
84  erThrLysCysAsnPheserSerLeuLysLeuAsnValTyrGluGluIle 100
327  AAATGGCGTAAAGAGCAGAAAAAAGAACACTTCTCATGATGATAGGT 376
    |||||||
101  LysLeuArgIleArgIleGluGlyAsnThrSerSerTrpTyrGluVal 117
377  TGACTCTTACACCATTTGCAAGAGCTGATGGCTCCGCCAGAAATAC 426
    |||||||
117  LAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluValH 134
427  ATTTAGAGCTGAAGATAGGAATAGTATGATACATCTCTCCGAGACA 476
    |||||||
134  IsLeuGluAlaGluAspLysAlaIleValIleHisIleSerProGlyThr 150
477  AAAGATAGTGTATGTGGCTTGGATGGTTAAAGTTTACATATAGCTT 526
    |||||||
151  LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerLe 167
527  ACTTATGTGAAAAAAGCTCTCAGGTGTGAGAGAAAGAGATGAAATATT 576
    |||||||
167  uLeuIleTrpLysAsnSerSerGlyValGluGluArgIleGluAsnIleT 184
577  ATTCAGACATATAAATTATTAAGTCTCACAGAGACTACTATATGCTTA 626
    |||||||
184  ySerArgHisLysIleTyrLysLeuSerProGluThrThrTyrCysLeu 200
627  AAAGTTAAGCAGCAGCTACTTACGTCATGAAAAATGGTGTCTATAGTCC 676
    |||||||
201  LysValLysAlaAlaLeuLeuThrSerTrpLysIleGlyValTyrSerPr 217
677  AGTCATGTGTTAAGAAGACACAGTGAAGAAAGAACTCCGCCACAGAAA 726
    |||||||
217  oValHisCysIleLysThrThrValGluAsnGluLeuProProGluVal 234
727  ATATAGAAGTCAGTGTCCAAATACAGAACTGTCTTAAATGGATTAAT 776
    |||||||
234  snIleGluValSerValGlnAsnGlnAsnTyrValLeuLysTrpAspTyr 250
777  ACATATGCAAAACATGACCTTCAAGTTCAGTGGCTCCAGGCCCTTTTAAA 826
    |||||||
251  ThrTyrAlaAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeuL 267
827  AAGGAATCCGTGGAAGAACATTTGTTAATGAGAAACAAATACCTACAGT 876
    |||||||
267  sArgAsnProGlyAsnHisLeuTyrLysTrpLysGlnIleProAspCysG 284
877  AAATGTCAAAACTACCCAGTGTGCTTCTCTCAAAAGCTTTTCCAAAA 926
    |||||||
284  LuAsnValLysThrThrGlnCysValPheProGlnAsnValPheGlnLys 300
927  GGAATTTACCTTCTCCGCGTACAAAGCATCTGATGAAATTAACATCTTT 976
    |||||||
301  GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerPh 317
977  TTGGTCTGAAGAGATAAAGTTGATGATGAGAAATCAAGCTTCTCTACTTC 1026
    |||||||
317  eTrpSerGluGluIleLysPheAspThrGluIleGlnAlaPheLeuLeuP 334
1027  CTCACGTCTTAACTATGATCCCTAGTATGATTCATTCATATATATATC 1076
    |||||||
334  rProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle 350
1077  GGTGCTCCAAAAAGCTGGAACAAGCTGTGATCCAGATTTATCCACT 1126
    |||||||
351  GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrProLe 367
1127  GATTATGCAAAATTAATTTTGGGAAAAACATCAAAATGCTGAGAGAAAA 1176
    |||||||
367  uIleTyrGluIleIlePheTrpGluAsnThrSerAsnAlaGluArgLysI 384

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1177  TTATCGAGAAAAAAAGCTGATGTTACAGTTCCTAAATTGAACCACTGACT 1226
    |||||||
384  leIleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
1227  GTATATTGTGTGAAGCCAGACACACACCATGATGAGAAAGCTGAATA 1276
    |||||||
401  ValTyrCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnL 417
1277  AAGCAGTGTGTTTAGAGACGCTGTATGTGAGAAAAACAAACCGAGAAATA 1326
    |||||||
417  sSerSerValPheSerAspAlaValCysGluLysThrLysProGlyAsnT 434
1327  CCTCTAAA 1334
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434  hrSerLys 436

seq_name: A_Geneseq_36:R11958
seq_documentation_block:
ID      R11958 standard; Protein; 557 AA.
AC      R11958;
DE      18-JUL-1991 (first entry)
DEF     Human alpha-interferon receptor protein.
KW      Human alpha IFN; IFN agonists; antiviral; anti tumour agent;
        drug targeting.
OS      Homo sapiens.
FH      Key
FT      peptide
FT      1..27
        /label= signal peptide
PD      WO9105862-A.
PE      02-MAY-1991.
PR      19-OCT-1990; F00758.
PR      20-OCT-1989; FR-013770.
PA      (CNRS ) CNRS CENT NAT RECH SCI.
PI      Mogensen KE, Uze G, Lutfalla G, Gresser I;
PI      WPI: 91-148740/20.
DR      N-PSDB; Q11701.
PT      New human alpha-interferon receptor protein - useful for testing
PT      interferon agonists and in treatment or diagnosis
PS      Disclosure: fig 4; 30pp; French.
CC      This recombinant human alpha interferon (IFN) receptor protein is
CC      useful for the testing of IFN agonists and for treatment and diag-
CC      nosis of viral diseases and tumours. Antibodies raised against
CC      this protein can be used for blocking the receptor when required,
CC      eg where overexpression of alpha-IFN is harmful. The Abs are
CC      also useful for eg drug targeting. Variants of the protein,
CC      having residue 164 (Thr) replaced by Arg and an Asp inserted
CC      between residues 479 and 480, are also useful.
SQ      Sequence 557 AA;

alignment_scores:
    Quality: 2313.00      Length: 436
    Ratio: 5.305          Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-240-675-1 x R11958      ..

Align seg 1/1 to: R11958 from: 1 to: 557

27  ATGATGTCCTCTCTCTGGGCGGAGACACCTAGTCTGCGCGGTGGG 76
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1  MetMetValValLeuLeuGluGlyAlaThrThrLeuValLeuValAlaValG 17
77  CCATGGGCTTGTGCGGACGCCGAGGTGGAATAATCTAAATCTCCCTC 126
    |||||||
17  yProTrpValLeuSerAlaAlaIleGlyGlyLysAsnLeuLysSerProG 34
127  AAAAAGAGAGGTGAGCATGATGATGACAACTTATCCGAGAGTGAAC 176
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34  InLysValGluValAspIleIleAspAspAsnPhelleuLeuArgTrpAsn 50

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177 AGGACGATGAGCTGTGCGAATGAGACTTTTCATTGATATCAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGln 67
|||||
227 AACTGGATGATAATGGATAAATGCTGCGGTGTCAGATATTACTA 276
|||||
67 sthrlGlyMetAspAsnTrpIleTyrLeuSerClyCysGlnAsnIleTrs 84
|||||
277 GTACCAATGCAACTTTCTTCTACCAAGCTGAATGTTTATGACA 326
|||||
84 ertHrLysCysAsnPheserSerLeuLysLeuAsnValTyrClyGln 100
|||||
337 AAATGCGTATAGAGAGAAAAAGAAAACCTTTCATGGTAGAGCT 376
|||||
101 LysLeuAsnGlyIleAsnGlyAlaGlySerGlnAsnThrSerTyrPyrGly 117
|||||
377 TGACTCATTTACACCATTTCCGAAAGCTCAGATTGGTCTCCAGAA 426
|||||
117 LAspSerPheThrProPheArgGlyAlaGlnIleGlyProProGlyVal 134
|||||
427 ATTTAGAGCTGAGATAGGCAATAGCATACATCTCTCCGGAACA 476
|||||
134 lslGluAlaGluAspLysAlaIleValIleHisIleSerProGlyThr 150
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477 AAAGTACTGTTATGCGCTTTGGATGTTTAAAGCTTACATATAGCT 526
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151 LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSer 167
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577 ACTATCTGGAAGAACTCTGAGGTGTGAAGAAAGATTGAATATTT 576
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167 uleuIleTrpLysAsnSerSerGlyValGlyGlnArgIleGlnAsnIle 184
|||||
577 ATTCAGACATATAATTTATAACTCTACACAGAGACTACTATTGTT 626
|||||
184 YrSerArgHisLysIleTyrLysLeuSerProGlyThrTyrCysLeu 200
|||||
627 AAAGTTAAGCAGCAGCTACTACGTCATGAAATTTGTCATATAGCC 676
|||||
201 LysValLysAlaIleLeuLeuThrSerTrpLysIleGlyValTyrSer 217
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677 AGTACATTGTATAAGACACAGTGAATGAATACCTCCACAGAAA 726
|||||
217 oValHisCysIleLysThrThrValGluAsnGlyLeuProProGly 234
|||||
727 ATATAGAGTCAAGTCTCCAAATCAGAACTATGTTCTTAATGGAT 776
|||||
234 snIleGlyValSerValGlnAsnGlnAsnTyrValLeuLysTrpAsp 250
|||||
777 ACATATGCAACATGACCTTCAAGTTCAGTGGTCCAGGCTTTTAAA 826
|||||
251 ThrTyrAlaAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeu 267
|||||
827 AAGGAATCTGGAAACCATTTGTATAATGGAACCAATACCTGACTG 876
|||||
267 sArgAsnProClyAsnHisLeuTyrLysTrpLysGlnIleProAsp 284
|||||
877 AAAATGCAAAACACACAGTGTCTTCTCTCAAAAGCTTTTCCAAA 926
|||||
284 lAsnValLysThrThrGlnCysValIleProGlnAsnValPheGln 300
|||||
927 GGAATTTACCTTCTCCGCTACAAGCATCTGATGAAATAACATCAT 976
|||||
301 GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSer 317
|||||
977 TTGGCTGAGAGATATAAGTTGATCTGAAATACAAGCTTCTCTACT 1026
|||||
317 ertPserClyGlnIleLysPheAspThrGlnIleGlnAlaPheLeu 334
|||||
1027 CTCAGTCTTACATTAGATCCCTGTAGTGTATTCATCCATATATATC 1076
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334 rOpIroValPheAsnIleArgSerLeuSerAspSerPheHisIleTyr 350

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1077 GGTGCTCCAAACAGTGTGAAACAGCGCTGTATCCAGGATTATCCACT 1126
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351 GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrPro 367
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1127 GATTATGAAATATTATTTTGGGAAAACTTCAAAATGCTGAGAGAAA 1176
|||||
367 uIleTyrClyIleIlePheThrPoliAsnThrSerAsnAlaGlyArgLys 384
|||||
1177 TTATCGAGAAAAAACTGATGTACAGTTCTTAATTTGAAACCCAGT 1226
|||||
384 leriGlyLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
|||||
1227 GTATATGTGTGAAAGCAGACAGCACACCATGATGAAAAAGCTGA 1276
|||||
401 ValTyrCysValLysAlaArgAlaHisThrMetAspGlyLysLeuAsn 417
|||||
1277 AAGCAGTGTTTAGTACGCTGTATGATGGAAGAAACAGGAAAT 1326
|||||
417 sSerSerValPheSerAspAlaValCysGlyLysThrLysProGlyAsn 434
|||||
1327 CCTCTAAA 1334
|||||
434 hrSerLys 436

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seq_name: A_Geneseq_36:R14488
seq_documentation_block:
ID R14488 standard; Protein: 557 AA.
AC R14488;
DT 16-JAN-1992 (first entry)
DE Complete interferon-alpha/beta receptor.
KW IFN; autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 437..457
FT domain 458..557
FT domain /label= cytoplasmic
PN FR2657881-A.
PD 09-AUG-1991.
PF 05-FEB-1990; 001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE.
PI Tovey MG, Uze G.
DR N-PSDB; Q14240.
DR N-PSDB; Q14240.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Discloure; Page 47; 52pp; French.
CC The invention covers derivatives of the interferon-alpha and/or beta
CC receptor obtained by deleting the transmembrane and cytoplasmic domains
CC of the native receptor or by substitution. Potentially immunogenic
CC epitopes are eliminated and the deriv. can be secreted from
CC transformed cells. Soluble deriv.s block the activity of IFN alpha/beta
CC and can be used to treat autoimmune diseases or to inhibit graft
CC rejection. See also Q14239.
SQ Sequence 557 AA;

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alignment_scores:
Quality: 2313.00 Length: 436
Ratio: 5.305 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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alignment_block:
US-09-240-675-1 x R14488 ..

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Align seg 1/1 to: R14488 from: 1 to: 557
27 ATGATGTCGTCTCTGCGCGCAGACCACTAGTCTGTCGCGCGTGG 76
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1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
77 CCCATGGGTGTTCGCCAGCCGACGGTGAAGAAAAATCTAAATCTCTC 126
17 yProripValLeuSerAlaAlaGlyLysAsnLeuLysSerProG 34
127 AAAAGTAGAGTCGACATCATAGATGACAACTTATCTCTGAGGTGAAC 176
34 LysValGlyValAspIleIleAspAspAsnPhelleLeuArgTrpAsn 50
177 AGGAGCGATAGCTCTGGGAATGATGATCTTTCATGATTAATGAAAA 226
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrpGly 67
227 AACTGGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 276
67 sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS 84
277 GTACCAAAATGCAACTTTTCTTCACCTGACGTAATGTTATGAAATTT 326
84 eThrLysCysAsnPheserSerLeuLysAsnValTyrgLugluille 100
327 AAATTCGCTATAGACGAGAAAAGAAACACTTCTTCATGATGATGGT 376
101 LysLeuArgGlyLeuArgAlaGlyLysGluAsnThrSerSerTrpTyrgL 117
377 TGACCTATTACACCATTTTCGCAAACTGACATGCTGCTCCAGAAAGTAC 426
117 LaspSerPheThrProPheArgLysAlaGlnIleGlyProProGluValH 134
427 ATTTAGAGCTGAAGATTAAGCAATAGTGATACATCTCTCTCGAACA 476
134 LsLeuGluAlaGluAspLysAlaIleValIleHisIleSerProGlyThr 150
477 AAGATAGCTGTATGCGGCTTGAGTGGTGAAGCTTTCATGATAGCTT 526
151 LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrgSerLe 167
527 ACTTACTGTGAAAAACTCTTCAGGTGAGAGAAAGATTAATGATTTT 576
167 uLeuIleTrpLysAsnSerSerGlyValGluGluArgIleGluAsnIleT 184
577 ATTCGACACATAAATTTAATTAACCTCTCACGACGACTTATGTGCTA 626
184 ySerArgHisLysIleTyrgLysLeuSerProGluThrTyrgCysLeu 200
627 AAAGTTAAACGACACTACTTACGTCTATGAAAAATGGTGTCTATATCC 676
201 LysValLysAlaAlaLeuLeuThrSerTrpLysIleGlyValTyrgSerPr 217
677 AGTACATGTATTAAGACACAGTGTGAAGAACTACTCTCCACAGAAAA 726
217 oValHisCysIleLysThrThrValGluAsnGluLeuLeuProProGluA 234
727 ATATAGAGTCAGTGTCCAAATGAGAACTATGTTCTTAATGGATTAAT 776
234 snIleGluValSerValGlnAsnGlnAsnTyrgValLeuLysTrpAspTy 250
777 ACATATCGAAACATGACCTTTCAGGTGACGGCTCCACGCTTTTAAA 826
251 ThrTyrgLysAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeuL 267
827 AAGGAATCTGGAACCATTTGATTAATGAAACAAATACCTGCTGTG 876
267 sArgAsnProGlyAsnHisLeuTyrgLysTrpLysGlnIleProAspGly 284
877 AAAATGTCAAAACATACCAAGTGTCTTCTCAAAACGTTTCCAAAA 926
284 LuAsnValLysThrThrGlnCysValPheProGlnAsnValPheGlnLys 300
927 GGAATTTACCTTTCGCGGTACAGCATCTATGAAATACACATCTTT 976
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317 eTrpSerGluGluIleLysPheAspThrGluIleGlnAlaPheLeuLeuP 334
1027 CTCGAGCTCTTAACATTTAGATCCCTAGTGTGATTCATTCATATCATATC 1076
334 rOProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrgIle 350
1077 GGTGCTCCAAAACAGTCTGGAACACGCGCTGTGATCCAGATTAATCCACT 1126
351 GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrgProle 367
1127 GATTTATGAAATTAATTTTGGGAAACACTTCAATCTGAGAGAAAA 1176
367 uLetyrgLuuIleIlePheThrTyrgLysAsnThrSerAsnAlaGluArgLys 384
1177 TTATGAGAAAAAAACGATGTTACAGTTCCTTAATTTGAAACGACTGACT 1226
384 LeIleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
1227 GTATATTGTGTGAAGCCAGACACACACATGATGAAAGCTGAATAA 1276
401 ValTyrgCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnL 417
1277 AAGCAGTGTTTTACTGACGCTGTATGTGAGAAAAACAAACCGAATA 1326
417 sSerSerValPheSerAspAlaValLysGluLysThrLysProGlyAsnT 434
1327 CCTCTAAA 1334
434 hTrSerLys 436

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seq_name: A_Geneseq_36: R28496

seq_documentation_block:
ID R28496 standard; Protein; 557 AA.
AC R28496;
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the interferon (IFN) receptor
DE with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-interferon; beta-interferon.
OS Synthetic.
PN WO9218626-A.
PD 29-OCT-1992.
PE 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
RA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PI Tovey M, Uze G,
PI WP1: 92-382110/46.
DR N-PSDB; Q30533.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
PT and beta - useful as immunosuppressants, for treating auto-immune
PT diseases and transplant rejection
PS Claim 5; Fig 2; 58pp. English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
CC IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template. For example,
CC bacteriophage lambda ZAP, containing the entire coding sequence of
CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
CC lacks the transmembrane and cytoplasmic domains. Both forms bind
CC IFN in the same way as antibodies so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 357 AA;

alignment_scores:
Quality: 2313.00 Length: 436
Ratio: 5.305 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1 x R28496

Align seg 1/1 to: R28496 from: 1 to: 557

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1  MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG 17
77  CCCATGGGTGTGTCCGACGCCGAGGTGAAAAAATCTAAATCTCC 126
    |||||||
17  yProTrrValLeuSerAlaAlaIleGlyLysAsnLeuLysSerProG 34
127  AAAAAGTAGAGTCGACATCATGATGACAACCTTATCCGAGCTGAG 176
    |||||||
34  InLysValGluValAspIleIleAspAspAspAspAspAspAsp 50
177  AGGAGCGATGAGTCTGTCGGAAATGAGCTTTTCATTCGATTATCA 226
    |||||||
51  ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrrG 67
227  AACTGGGATGATTAATTGGATTAATGCTGGGTGTCAAGATTAATCA 276
    |||||||
67  sThrGlyMetAspAsnTrrPileLysLeuSerGlyCysGlnAsnIle 84
277  GTACCAATGCAACTTTCTTCACCTCAAGCTGAATGTTATGAGA 326
    |||||||
84  eThrLysCysAsnPheSerSerLeuLysLeuAsnValIlyrGluGlu 100
327  AAATTCGGTAAAGACGACAAAAAAGAAACACTTCTTCATGTATGAG 376
    |||||||
101  LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrrPrrG 117
377  TGACATTTTACACCATTTGCGAAAGCTGAGATGTCCTCCAGAGTAC 426
    |||||||
117  LAspSerPheThrProPheThrGlySalGlnIleGlyProProGlu 134
427  ATTAGAACCTGAGATAAGCAATAGTATACATCATCTCTCCGTGACA 476
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134  LsLeuGluAlaGluAspLysAlaIleValIleHisIleSerProG 150
477  AAAGATAGTGTATGTGGCTTTGATGGTTTAAGCTTACATATAGCTT 526
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151  LysAspSerValMetTrrPalaLeuAspGlyLeuSerPheThrTyr 167
527  ACTTATCTGGAATAAACTCTTCAGGTGTAGAAAGAAAGTGAATA 576
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167  ULeuIleTrrPlysAsnSerSerGlyValGluGluAsnIleG 184
577  ATTCGACATAAATTTTAAACTCTCAGCAGAGACTACTTATGTCTTA 626
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184  ySerArgHisLysIleTrrLysLeuSerProGluThrThrTrrCys 200
627  AAAGTTAAAGCAGCACTACTTACGTATGAAAAATTTGGTGTATAGT 676
    |||||||
201  LysValLysAlaAlaLeuLeuThrSerTrrPlysIleGlyValTyr 217
677  AGTACATTTATTAAGACACAGCTGAAAAATGACTACTCCACAGAAA 726
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217  oValHisCysIleLysThrThrValGluLysGluLeuProProG 234
727  ATATAGAACTGAGTCCAAAAATCAGAACTATGTTCTTAATGGATTA 776
    |||||||
234  snIleGluValSerValGlnAsnGlnAsnTrrValLeuLysTrr 250
777  AATATGCAACATGACCTTTCAAGTCTGCTGCTCCAGGCTTTTAA 826
    |||||||
251  ThrTrrAlaAsnMetThrPheGlnValGlnTrrPheHisAlaPhe 267
827  AAGGAATCCTGGAAACCATTTGTATAAATGAAACAAATACTGACTG 876
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267  sArgAsnProGlyAsnHisLeuTrrLysTrrPlysGlnIleProAs 284

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877  AAAATGTCAAAATCAACCAAGTGTGTCTTCTTCAAAACGTTTCCAAA 926
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301  GlyIleTrrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSer 317
977  TTGGTCTGAGAGATAAAGTTGATACGAAATACAACTTTCCTACTTC 1026
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317  eTrrPrrGluGluIleLysPheAspTrrGluIleGlnAlaPheLeu 334
1027  CTTCCAGCTCTTACATAGATCCCTTACTGATTCATTCATATCATATC 1076
    |||||||
334  rProValPheAsnIleArgSerLeuSerAspSerPheHisIleTrr 350
1077  GGTGCTCCAAAACAGTCTGAAACACGCGCTGAGATCCAGATTAATCA 1126
    |||||||
351  GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTrrPro 367
1127  CATTTATGAAATTAATTTTGGGAAACACTTCAAAATCTGAGAGAAAA 1176
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367  uIleTrrGluIleIlePheTrrPrrGluAsnThrSerAsnAlaGlu 384
1177  TTATCGAGAAAAAATGATGTACAGTTCTCAATTTGAACCACTGACT 1226
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384  LeIleGluLysLysThrAspValThrValProAsnLeuLysProLeu 400
1227  GTATATGTGTGAAGCCAGACACACATGATGATGAAGACGTAATA 1276
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401  ValTrrCysValLysAlaArgAlaHisThrMetAspGluLysLeuAs 417
1277  AAGCAGTGTTTTACTGACGCTGATGTGACAAAAACAAACAGGAATA 1326
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417  sSerSerValPheSerAspAlaValCysGluLysThrLysProGlyAs 434
1327  CCTTAA 1334
434  hrSerLys 436

seq_name: A_Geneseq_36:R42635
seq_documentation_block:
ID   R42635 standard; Protein; 557 AA.
AC   R42635;
DT   20-APR-1994 (first entry)
DE   Human interferon receptor.
KW   IFN-R; extracellular domain; monoclonal antibody; viral infection;
KW   cell proliferation; allograft rejection; systemic lupus erythematosus;
KW   psoriasis; multiple sclerosis; Behcet's disease; aplastic anaemia;
KW   immunodeficiency; measles virus; interferon alpha-beta.
OS   Homo sapiens.
FH   Key
FT   domain
FT   1..436
FT   /label= extracellular domain
FT   /note= "soluble, immunogenic form of IFN-R"
EP   EP-563487-A.
PD   06-OCT-1993.
PE   31-MAR-1992; 400902.
PR   31-MAR-1992; EP-400902.
PA   (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI   Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG;
DR   P-RSDB; R42635.
DT   Monoclonal antibody to human interferon type-I receptor - having
PT   neutralising activity against human type I interferon, used for
PS   disclosure; Fig 3; 21pp; English.
CC   Monoclonal antibodies produced against soluble forms of the human
CC   interferon alpha-beta receptor based on the full-length human IFN-R
CC   sequence are claimed. The antibodies are useful for treatment and
CC   prophylaxis of disorders involving cell proliferation and/or viral

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CC Infection.
50 Sequence 557 AA:

alignment_scores:

Quality: 2313.00 Length: 436
Ratio: 5.305 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1 x R42635

Align seg 1/1 to: R42635 from: 1 to: 557

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1 MetMeValValLeuLeuClYAlaThrThrLeuValLeuValAlaValG 17
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|||||
17 yProTPValLeuSerAlaAlaValGlyLysAsnLeuLysSerProG 34
127 AAAAGTAGAGTCGACATCATGATGACAACTTATCCTGAGGTGAG 176
|||||
34 LnlYsValGluValAlaPlelleAspAspAsnPhelleuAlaGtrPasn 50
177 AGGACGATGAGTCTGCGGAGATGACTTTTCATTCGATTATCAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrIlnY 67
227 AACTGGGATGATTAATGATAAATTTGCTGGGTCTCAGAAATATTACTA 276
|||||
67 sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrs 84
277 GATACCAAGCAACTTTCTCTCAGCTGAACTGTAATGTTATGAAGAAAT 326
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84 eThrLysCysAsnPheSerSerLeuLysLeuAsnValIlyrGluGluIle 100
327 AATTCGCTATAGACAGCAAAAAAAGAAACACTTCTTCATGCTATGAGT 376
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101 LysLeuAlaArgIleArgAlaGluLysGluAsnThrSerSerTrpIyGluVal 117
377 TGACATCATTTACACCATTTTCGCAAGCTCAGATTGCTCTCCAGAAAGTAC 426
|||||
117 LAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluValH 134
427 ATTTAAGACTGAAGATAAGCAATAAGTGTATACATCTCTCTGGAACA 476
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134 IAsnGluLysAlaGluAspLysAlaIleValIleHisIleSerProGlyThr 150
477 AAAGATAGTGTATGTGGCTTGGATGATTAAAGCTTTACATATAGCTT 526
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151 LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrIySerIle 167
527 ACTTATCTGGAAAACTCTTCAGGCTGAGAGAAAGGATTGAAATATTT 576
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167 uLeuIleTrpLysAsnSerSerGlyValGluGluArgIleGluAsnIleT 184
577 ATCCGACGACATAAATTATTAACCTGCACAGAGACTACTTATTTGCTA 626
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184 yIserTrpHisLysIleTrpLysLeuSerProGluThrThrIyCysLeu 200
627 AAAGTTAAAGCACACTACTTACGTCATGCAAAATGGTGTCTATAGTCC 676
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201 LysValLysAlaAlaLeuLeuThrIleTrpLysIleGlyAlaIySerTr 217
677 AGTACATTTGATTAAGACACAGCTTGAATAATGAACCTCCACAGAGAA 726
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217 oValHISCYsIleLysThrThrValGluAsnGluLeuProProGluA 234
727 ATATAGAAAGTCAGTCCAAATCAGAAATATGTTCTTAATGGATATT 776
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234 snIleGluValSerValGlnAsnGlnAsnTrpValLeuLysTrpAspTyr 250

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777 ACATATGCAAAACATGACCTTTCAGTTCAGTGGCTCCACGCCCTTTTAA 826
|||||
251 ThrYrAlaAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeuLys 267
827 AAGCAATCTGGAACCATTTGTATAAATGGAACAAATACCTGACCTG 876
|||||
267 sArgAsnProGlyAsnHisLeuTrpLysTrpLysGlnIleProAspCysG 284
877 AAATGTCAAAACCTACCCAGTGTCTTCTCCGTCGAAACGTTTCCAAAA 926
|||||
284 LuAsnValLysThrThrGlnCysValPheProGlnAsnValPheGlnLys 300
927 GGAATTAACCTTTCGCCGTACACATCTGATGGAATTAACACATCTTT 976
|||||
301 GlyIleTrpLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerPh 317
977 TTGCTGTGAAGATGAAGTTTGATACAGAAATACAACTTTCCTACACTC 1026
|||||
317 eTrpSerGluGluIleLysPheAspTrpGluIleGlnAlaPheLeuLys 334
1027 CTCACGCTTTTACATTAGATCCCTTAGTATTCATTCATTCATATATC 1076
|||||
334 rOProValPheAsnIleArgSerLeuSerAspSerPheHisIleTrpIle 350
1077 GGTGCTCCAAACAGCTGTGAAACACGCCGTGTGATCCAGATTAATCC 1126
|||||
351 GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrProLe 367
1127 GATTATGAAATATTTTGGGAAACACTCAAACTGAGAGAGAAAAA 1176
|||||
367 uIleTrpGluIleIlePheTrpGluAsnThrSerAsnAlaGluArgLysI 384
1177 TTATCGAGAAAAAACTGATGTTCAGAGTCTCAATTTGAAACACTGACT 1226
|||||
384 lIleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
1227 GATATATGTGTGAAGACACAGACACACACCATGATGAAAGCTGAATA 1276
|||||
401 ValTyrCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnLys 417
1277 AAGCAGTGTTTTATGACGCTGTATGTCAGAAAAACCAAGCAAGAAAT 1326
|||||
417 sSerSerValPheSerAspAlaValCysGluLysThrLysProGlyAsnT 434
1327 CCTCTAAA 1334
|||||
434 hrSerLys 436
seq_name: A_Geneseq_36:R75356
seq_documentation_block:
ID R75356 standard: Protein: 557 AA.
AC R75356:
DE 16-OCT-1995 (first entry)
DE Human IFN receptor.
KW IFN receptor; Interferon receptor; Interferon-alpha;
KW Interferon-beta; monoclonal antibody; immunomodulator; AIDS.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..436
FT /label= Extracellular_domain
PN W09507716-A.
FD 23-MAR-1995.
FE 16-SEP-1994: E03114.
PR 17-SEP-1993: EP-402279.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benizri EJ, Tovey MG;
DR N-PSDB: 086458.
DR Compn. of monoclonal antibodies against Interferon receptor
PT useful as immuno-modulator, eg. for treating AIDS
PS Disclosure: Fig. 3A-2B; 105pp; English.

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CC The amino acid sequence of human Interferon class I receptor is
 CC given in R75356. A recombinant soluble form of the extracellular
 CC domain of this receptor (R71723) has been used to raise
 CC immunomodulatory monoclonal antibodies.
 SO Sequence 557 AA:

Alignment scores:
 Quality: 2309.00 Length: 436
 Ratio: 5.296 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 99.771

Alignment block:
 US-09-240-675-1 x R75356

Align seg 1/1 to: R75356 from: 1 to: 557

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27 ATGATGCTGCTCCTCGGCGGCGACGACCTAGTCTGCGCGCTGG 76
1 MetMetValValLeuLeuGlyAlaThrThrValLeuValAlaValAl 17
77 CCCATGGGTGTTCGCGAGCGAGGGAATAAATCTAATCTCTC 126
17 yProTPrValLeuSerAlaAlaGlyGlyLysAsnLeuLysSerProG 34
127 AAAAAGTAGAGTCGACATCATAGATGACAACCTTATCTGAGTGGAAC 176
34 LntLysValGluValAspLeuIleLeuAspAsnPhelIleLeuArgTrpAsn 50
177 AGGAGCATGAGTGTGCGGAATGTGACTTTTCATTGCTATTCATAA 226
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGln 67
227 AACTGGATGATTAATGATAAATGTCTGGGTGCAGAAATTTACTA 276
67 sThGlyMetCaspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS 84
277 GTACCAATGCACACTTTCTCTACTCAAGCTGAATGTTTATGAGAAT 326
84 eThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGlnIle 100
327 AAATGCGTATAGAGCAAAAAACAACCTTCTTCAATGATGATGAGT 376
101 LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGlu 117
377 TGACTCTTATACACATTTCGCAAGCTCAGATGGTCCCGCAATAC 426
117 LAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 134
427 ATTAGAAGCTGAAGATAGCAATAGTATACATCTCTCGGAAACA 476
134 LsLeuGluAlaGluAspLysAlaIleValIleHisIleSerProGlyThr 150
477 AAAGATAGTGTATGCGGCTTGGATGATTAACTTACATATAGCTT 526
151 LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSer 167
527 ACTTATCTGAAAAACTCTCAGGTGAGTGAAGAAGATGAATAATTT 576
167 uLeuIleTrpLysAsnSerSerGlyValGluGluValGlyIleGluAsn 184
577 ATTCAGACATTAATTAATTAACCTCAGCAGAGACTACTATATGCTA 626
184 ySerArgHisLysIleTyrLysLeuSerProGluThrThrTyrCysLeu 200
627 AAAGTAAACACACTACTTACGTATGAGAAATGGTGTATATGCTC 676
201 LysValLysAlaAlaLeuLeuThrSerTrpLysIleGlyValTyrSer 217
677 AGTACATTGTATAAGACACACAGTGAATGAATGAACTACCGCCGAA 726
217 oValHisCysIleLysThrThrValGluAsnGluLeuProProGlu 234

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727 ATATAGACAGTGTCCAAATATCAGAACTATCTTAAATGGATAT 776
234 snLleGluValSerValGlnAsnGlnAsnTyrValLeuLysTrpAspTyr 250
777 ACATATGCAAAACATGACCTTTCAAGTTCAGTGGCTCCAGCCCTTTAA 826
251 ThrTyrAlaAsnMetThrPheGlnValGlnTrpLeuHisAlaPhePhe 267
827 AAGGAATCCTGGAAACCATTTGTATATGAAACAAATACCTGACTGTG 876
267 sArgAsnProGlyAsnHisLeuTyrLysTrpLysGlnIleProAspCysG 284
877 AAAATGCAAAACTACCCAGTGTCTTCTTCCAAACCTTTTCCAAAA 926
284 LysnValLysTrpThrGlnCysValPheProGlnAsnValPheGlnLys 300
927 GGAATTACCTTCTCCGCTACAGCATGTGATGAAATACACATCTT 976
301 GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSer 317
977 TTGGCTGAAAGATTAAGTTGATACGAAATACAGCTTTCCTACTTC 1026
317 eTrpSerGluGluIleLysPheAspThrGluIleGlnAlaPheLeu 334
1027 CTCAGCTCTTAACATTAGATCCCTAGATGATTCATTCATATATATC 1076
334 roProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyr 350
1077 GGTGCTCCAAACAGTCTGAAACACAGCCTGTGATCCAGATTAATC 1126
351 GlyAlaProLysGlnSerIleLysAsnThrProValIleGlnAspTyr 367
1127 GATTTTGAAATTTATTTTGGGAAAAACCTCAATGCTGAGAGAAAA 1176
367 uIleTyrGluIleIlePheTrpGluAsnThrSerAsnAlaGluArgLys 384
1177 TTATCGAGAAAAAACTGATGTATACAGTCCCAATTTGAAACCATG 1226
384 lLeIleGluLysLysThrAspValThrValProAsnLeuLysProLeu 400
1227 GATATATGTGTGAAAGCCAGACACACACATGATGAAAGCTGAAT 1276
401 ValTyrCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsn 417
1277 AAGCAGTGTTTTATGAGCGCTGTATGAGAAAAACCAAGCAATA 1326
417 sSerSerValPheSerAspAlaValCysGluLysThrLysProGlyAsn 434
1327 CCTCTAAA 1334
434 hrSerLys 436

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seq_name: A_Geneseq_36:W21804

seq_documentation_block:
 ID W21804 standard; Protein: 557 AA.
 AC W21804:
 DT 23-SEP-1997 (first entry)
 DE Transmembrane1 Interferon alpha-receptor.
 KW Interferon alpha-receptor; IFNAR.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 1..436
 FT domain /label= Extracellular_domain
 FT domain 437..457
 FT domain /label= Transmembrane_domain
 FT domain 458..557
 FT domain /label= Intracellular_domain
 AU9475977-A.
 PD 11-MAY-1995.
 PF 20-OCT-1994.
 PR 24-OCT-1993; IL-107378.
 PA (YEDA) YEDA RES & DEV CO LTD.

PA (ABRA) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M:
DR MPI: 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PS inhibiting, modulating or modifying the activities of interferon(s)
CC Disclosure; Fig 7; 46pp; English.
CC Human transmembrane interferon alpha receptor (IFNAR) (W21804)
CC includes a 21-amino acid transmembrane region. Novel, splice-
CC deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected
CC that lack this transmembrane domain. These, soluble non-membrane
CC bound polypeptides can be expressed in host cells and used to
CC inhibit, modulate or modify the activities of interferons alpha
CC and beta in cells, tissues and organisms, or for diagnostic
CC purposes.
SO Sequence: 557 AA:

alignment_scores:
Quality: 2308.00 Length: 436
Ratio: 5.306 Gaps: 0
Percent Similarity: 99.771 Percent Identity: 99.771

alignment_block:
US-09-240-675-1 x W21804

Align seg 1/1 to: W21804 from: 1 to: 557

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27 ATATGTCCTCTCTCGGCGGACACCTAGTCTGCTGCGCGG 76
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGly 17
77 CCATGCGGTGTTCGCGACCGCGAGGTGAAAAATCAAACTCTC 126
17 ProTTPValLeuSerAlaAlaAlaGlyGlyValSerLeuSerProG 34
127 AAAAGTAGAGTGCACATCATGATGACAACTTATCTGAGGTGAAC 176
34 LysValGluValAspIleIleAspAspAspPheIleLeuArgTyrAsn 50
177 AGAGCGATGAGTCTGCGGAGTGTACTTTTCATTCGATTATCAAA 226
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGln 67
227 AACTGGATGATTAATGATTAATGATGATGATGATGATGATGAT 276
67 SerIleGlyMetAspAsnTyrIleLeuSerGlyCysGlnAsnIleThr 84
277 GTACCAATGCACTTTCTTCTCACTCAAGTGAATGTTATGAAGAAT 326
84 SerIleGlySerAspAspSerSerLeuSerLeuSerValTyrGlnIle 100
327 AATTGCGTATAGAGCAAAAAAGAAACATCTTCATGATGATGAT 376
101 LysLeuArgIleArgAlaGlnLysGlnAsnThrSerSerTyrGlnVal 117
377 TGACATTTATACACATTTGCAAGTCAATGATGATGATGATGATGAT 426
117 LysSerPheThrProPheArgLysAlaGlnIleGlyProProGlnVal 134
427 ATTAGAAGTGAAGTAAAGCAATAGTATACATCTCTCGAGACA 476
134 LysLeuGlnAlaGlnLysAlaIleValIleHisIleSerProGlyThr 150
477 AAAGATAGTATATGCGCTTGGATGATGATGATGATGATGATGAT 526
151 LysAspSerValMetTyrPalaLeuAspGlyLeuSerPheThrTyrSer 167
527 ACTATCTGAAAAACCTTCAGGTGAGAGAAAGATGAAAAATTT 576
167 LysLeuIleTyrPalaSerSerSerValGlnGlnLysGlnIleGlnAsn 184
577 ATTCAGACATTAATTAATTAATCTCACAGAGACTACTATATGCT 626

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184 YSerArgHisLysIleTyrLeuSerProGlnThrThrTyrCysLeu 200
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201 LysValLysAlaAlaLeuLeuThrSerTyrLysIleGlyValTyrSer 217
677 AGACATTTGATTAAGCCACCTTGAATGAATGAACTCCACCGAAA 726
217 ValHisCysIleLeuThrThrValGlnGlnGlnLeuProProGln 234
727 ATATAGAGTCACTGTCACAAATCAGAACTATGTTTAAATGAGTAT 776
234 snIleGluValSerValGlnAsnGlnAsnTyrValLeuSerTyrPhe 250
777 ACATATGCAAACTACCTTTCAAGTCAAGTCCACCGCTTTTAAA 826
251 ThrTyrAlaSerMetThrPheGlnValGlnTyrPheHisIlePheLeu 267
827 AAGGAATCCGGAACCATTTGATTAATGGAATGAAATACCTGACTG 876
267 SerAsnProGlyAsnHisLeuTyrLysTyrLysGlnIleProAspG 284
877 AAATGCAAACTACCCAGTGTCTTCTCCCAAACTTTTCCAAAA 926
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301 GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSer 317
977 TTGCTGAGAGATTAAGTTGATGATGATGATGATGATGATGATGAT 1026
317 ThrPheGlnGlnIleLeuSerPheThrGlnIleGlnAlaPheLeuSer 334
1027 CTCAGTCTTTAATTAATGATCCCTAGTATGATTCATTCATATATC 1076
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1077 GGTGCTCAAAACAGTCTGGAACAGCGCTGTATCAGAGATTAAC 1126
351 GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrPro 367
1127 GATTATGAATATTTTGGAAAAACCTTAATGCTGAGAGAAAA 1176
367 ValIleTyrGlnIleIlePheThrPheLysnThrSerAsnAlaGlnLys 384
1177 TTATCGAAAAAAACCTGATGATGATGATGATGATGATGATGAT 1226
384 LeuIleGlnLysLysThrAspValThrValProsnLeuLysProLeu 400
1227 GATATGTTGTGAAAGCCAGAGCACACACCATGATGAAAGCTGA 1276
401 ValTyrCysValLysAlaArgAlaHisThrMetAspGlnLysLeu 417
1277 AAGCAGTGTGTTTACGAGCTGTATGATGAGAAAAAACCAGAAAA 1326
417 SerSerValPheSerAspAlaValCysGlnLysThrLysProGlyAsn 434
1327 CCTCTAAA 1334
434 HisThrLys 436

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seq_name: A_Geneseq_36:R71723
seq_documentation_block:
ID R71723 standard; Protein; 436 AA.
AC R71723.
DT 16-OCT-1995 (first entry)
DE IFN receptor extracellular domain.
KW IFN receptor; interferon receptor; interferon-alpha;
OS Interferon-beta; monoclonal antibody; immunomodulator; AIDS.
PV MO507716-A.

PD 23-MAR-1995.
 PF 16-SEP-1994: E03114.
 PR 17-SEP-1993: EP-402279.
 PA (EUBI-), LAB EURO BIOTECHNOLOGIE SA.
 PI Beniziri EJ, Tovey MG;
 DR WPI: 95-13187/17.
 DR N-PSDB: 086457.
 PT Compn. of monoclonal antibodies against interferon receptor
 PT useful as immuno:modulator, eg. for treating AIDS
 PS Disclosure: Fig. 2A-2B; 105pp; English.
 CC A recombinant soluble form of the human interferon class I receptor
 CC protein extracellular domain, given in R71723, was expressed in
 CC either E. coli or COS cell hosts. The protein was used to raise
 CC immunomodulatory monoclonal antibodies.
 SQ Sequence 436 AA;

Alignment_scores:

Quality: 2304.00 Length: 436
 Ratio: 5.284 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 99.312

alignment_block:

US-09-240-675-1 x R71723

Align seg 1/1 to: R71723 from: 1 to: 436

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27 ATGATGTCCTCCTCCGCGCGACGACCTAGTCCTGCGCCGTGGG 76
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77 CCCATGGGTGTCGCCGCGCGCGAGTGGAAAAATCTAAATCTCTC 126
17 YProTrpAlaLeuSerAlaAlaAlaGlyLysAsnLeuLysSerProG 34
127 AAAAGTAGAGTGCATCATAGATGACAACTTATCTGTGGTGGAGAC 176
34 LInyValGluValAspIleIleAspAspAspIleLeuNhgTrpAsn 50
177 AGAGCGATGAGTGTGCGGAGTGTGACTTTTATTCGATTAACA 226
51 ArgSerAspGlnSerValGlyAsnValThrPheSerPheAspTyrGln 67
227 AACGGGATGATATTTGGATTAATTTGTCGGGTGTGCAATATTA 276
67 StHcIleAspAspAspTrpIleLysLeuSerClyGlnAsnIleTrp 84
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117 LAspSerThrThrProPheArgLysAlaGlnIleLysProProGlnVal 134
427 ATTAGAAGCTGAAGATAGCAATAGTATACATCTCTCGAGACA 476
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151 LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheTrpTyrSer 167
527 ACTATCTGGAAGAACTCTGAGGTGTAAGAAAGATTAATAATTT 576
167 uLeuIleTrpLysAsnSerSerGlyValGlnGlnTrpGlnGlnIle 184
577 ATTCGAGATTAATTTATTAACCTCTCAGACAGACTACTATATGCT 626

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184 YrSerArgHisLysIleTyrLysLeuSerProGlnThrThrTyrCysLeu 200
627 AAAGTAAAGCAGCAGCTACTACTCATGGAATAATGGTGTCTATAGTCC 676
201 LysValLysAlaAlaLeuLeuThrSerTrpLysIleLysValTyrSerTr 217
677 AGTACATGTTATTAAGACACAGTGAATAATGAATCTCCACACAGAAA 726
217 oValHisCysIleLysThrThrValGlnAsnGlnLeuProProGln 234
727 ATTAAGAAGCAGGTCGCAAAATCAGAAATGTTCTTAATGGATAT 776
234 snIleGluValSerValGlnAsnGlnAsnTyrLeuLysTrpAspTyr 250
777 ACATATGCAAAACATGACCTTTCAAGTTCAGTGGCTCCAGCCCTTTAAA 826
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977 TTGCTTGAAAGATTAAGTTGATGATGAAATCAAGCTTCTCTACTTC 1026
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367 uIleTyrGlnIleIlePheTrpGlnAsnThrSerAspAlaGlnArg 384
1177 TTATCGAGAAAAAAGCATGATTAAGTTCCTAATTGGAACAGCACT 1226
384 LelIleGluLysLysThrAspValThrValProAsnLeuLysProLeu 400
1227 GTATATTTGTGAAGCCAGACAGCACACCATGATGAAGTGAATA 1276
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1277 AAGAGTGTTTTATGACCTGTATGTGAAAAACAAACAGGAATTA 1326
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434 hTrSerLys 436

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seq_name: A_Geneseq_36:W21805

seq_documentation_block:

ID W21805 standard; protein; 434 AA.

AC W21805:

DT 23-SEP-1997 (first entry)

DE Spliced-deleted interferon alpha-receptor form 1.

KW Interferon alpha-receptor; IFNAR.

OS Homo sapiens.

FT Key Location/Qualifiers

FT domain 1..427

FT /label= Extracellular domain
FT /note= "comprises amino acids 1-427 of the
FT transmembrane IFNAR"
FT 428..434
FT /label= S_domain
domain
AU9475977-A.
PN 11-MAY-1995.
PF 20-OCT-1994; 075977.
PA 24-OCT-1993; 11-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (ABRAV) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M;
DR MPI: 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Example 2; Fig 7; 46pp; English.
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 1
CC (W21805) is characterised by a new domain (S) which follows an
CC end-deleted extracellular domain when compared to transmembrane
CC IFNAR (W21804). There is no transmembrane domain. The amino acid
CC sequence is predicted from a cDNA clone (see also T73520) obtd.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 and 2 (see also W21806) probably regulate
CC the response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating the activity of the multiple IFN
CC subtypes. They can be expressed in host cells and used to inhibit,
CC modulate or modify the activities of IFNs alpha and beta in cells,
CC tissues and organisms, or for diagnostic purposes.
SQ Sequence 434 AA;

alignment_scores:
Quality: 2260.00 Length: 427
Ratio: 5.305 Gaps: 0
Percent Similarity: 99.766 Percent Identity: 99.766

alignment_block:
US-09-240-675-1 x W21805

Align seq 1/1 to: W21805 from: 1 to: 434

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34 IndysValGluValAlaPheIleLeuPheSerPheIleLeuArgTrpAsn 50
177 AGAGCATGAGTCTGCGGAGATGTGACTTTTCATTCGATATCAAAA 226
51 ArgSerPhePheValGlyAsnValThrPheSerPheAspTrpGln 67
227 AACTGGATGATTAATGATTAATGATGCTGGGTGCAGATATTTCTA 276
67 sThrGlyMetAspAsnTrpIleLeuSerGlyCysGlnAsnIlePheS 84
277 GTACCAATGCAATTTTCTCACTCAAGCGAATGTTTATGAAGAATT 326
84 eThrTrpCysAsnPheSerSerLeuValValTrpGluGluIle 100
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167 uLeuIleTrpLysAsnSerSerGlyValGluGluArgIleGluAsnThr 184
577 ATTCCACACATTAATTTATTAATCTCCACAGACACTACTTATGCTCA 626
184 YSerAlaGlnHisLysIleTrpLysLeuSerProGluThrTrpTrpCysLeu 200
627 AAAGTTAAACAGACACTTACGTCAATGAAATGGTCTCATATGCTC 676
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677 AGTACATTTGATTAAGACACACAGCTTGAAATGAACTACCTCCACAGAAA 726
217 oValHisCysIleLeuThrThrValGluAsnGluLeuProProGlu 234
727 ATATAGAGTCACTGTCCAAAATCAGACACTATGTTCTTAATGGATTA 776
234 snIleGluValSerValGlnAsnGlnAsnTrpValLeuLysTrpAspTr 280
777 ACATATGCAAAACAGCTTCAAGTCAAGTGGCTCCAGCCCTTTTAA 826
251 ThrTrpAlaAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeu 267
827 AAGGAATCTGGAACCACTTGTATTAATGAACAAATACGTAGCTGTG 876
267 sArgAsnProGlyAsnHisLeuTrpLysTrpLysGlnIleProAspCysG 284
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927 GGAATTAACCTCTCGCGGTACAGATCGATGAGAAATACATCTT 976
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977 TTGGTCTGAGAGATTAAGTTTATGATCTGAAATACAGACTTCTCACTTC 1026
317 eTrpSerGluGluIleLeuPheAspThrGluIleGlnAlaPheLeuLeuP 334
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334 rProValPheAsnIleArgSerLeuSerAspSerPheHisIleTrpIle 350
1077 GGTCGTCGAAAACAGCTGGAACACAGCTGTATCCAGATTAATCCACT 1126
351 GlyAlaProLysGlnSerIleGlnAsnThrProValIleGlnAspTrpLe 367
1127 GATTATGAATTAATTTTGGGAAAACACTCAATGCTGAGAGAAAA 1176
367 uIleTrpGluIleIlePheTrpLysAsnThrSerAlaGlnArgLysI 384
1177 TTATCGAAGAAAAACATGATGTTACAGTTCCTTAATTTGAACACCTGACT 1226
384 lIleGluLysIleTrpAspValThrValProAsnLeuLysProLeuThr 400
1227 GTATATGCTGTAAGCCAGACACACACATGATGAAAGCTGAATTA 1276
401 ValTrpCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsn 417
1277 AACCACTGTTTATGACGCTGTATGTAG 1307
417 sSerSerValPheSerAspAlaValCysGlu 427
```

seqName: A_Geneseq_36:W21806

seq documentation block:

ID W21806 standard; Protein: 496 AA.
AC W21806;
DT 23-SEP-1997 (first entry)
DE Spliced-deleted interferon alpha-receptor form 2.
KW Interferon alpha-receptor; IFNAR.
OS Homo sapiens.

FT key 1. 419 Location/Qualifiers
FT domain /label= "Extracellular domain
FT /note= "comprises amino acid residues 1-413 and
FT 422-427 of transmembrane IFNAR".
FT domain 420. 496
FT /label= "intracellular domain
FT /note= "comprises amino acids 481-557 of
FT transmembrane IFNAR".

PN AU9475977-A
PD 11-MAR-1995.
PE 20-OCT-1994. 075977.
PR 24-OCT-1993. IL-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PI (ABRA/) ABRAMOVICH C
PI Abramovich C, Ratovitski E, Revel M;
DR WPI; 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Example 3; Fig 7; 46pp: English.
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2
CC (W21806) is characterised by a double deletion when compared to
CC transmembrane IFNAR (W21804). The extracellular domain is
CC shortened by 6 amino acid residues and is followed by a truncated
CC intracellular domain. There is no transmembrane region. The amino
CC acid sequence is predicted from a cDNA clone (see also T73521) obtd.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 (see also W21805) and 2 may regulate the
CC response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating IFN activities. They can be expressed
CC in host cells and used to inhibit, modulate or modify the
CC activities of IFNs alpha and beta in cells, tissues and organisms,
CC or for diagnostic purposes.
SO Sequence 496 AA.

alignment scores:
Quality: 2208.00 Length: 427
Ratio: 5.282 Gaps: 1
Percent Similarity: 97.882 Percent Identity: 97.882

alignment block:

US-09-240-675-1 x W21806

Align seg 1/1 to: W21806 from: 1 to: 496

27 ATGATGCTGCTCTCTGCGGCGGACGACCTAGTCTGCTGCGGCTGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValAlaValAlaGly 17
77 CCCAGGCTGTGCTCCGACGCGCAGGTGGAATAAATCTAAATCTCTCC 126
|||||
17 yProtrpValLeuSerAlaAlaAlaGlyGlyValAsnLeuLysSerPro 34
127 AAAAAGTAGAGGTGACATCATAGATGACAACTTATCTGAGGTGAAAC 176
|||||
34 InLysValAlaGlyValAlaSerPheIleAspAspPheIleLeuArgTrpAsn 50
177 AGGACGATGAGTCTGCGGGAATGTGACTTTTATCGATATACAAA 226
|||||
51 ArgSerAspGlnSerValGlyAsnValThrPheSerPheAspTyrGlnLys 67
227 AACTGCGATGATTAATGATTAATGCTGCGGTGATATATATATAT 276
|||||
67 sThrLysMetAspAsnTrpLysLeuSerGlySerGlnAsnIleThr 84

277 GTACCAATGCAACTTTCTTCACTCAAGCTGATGTTATGAGAAT 326
|||||
84 erThrLysCysAsnPheSerSerLeuLysLeuValTyrGlnGlnIle 100
327 AATTCGCTTATAGACGAGAAAAAGAAACCTTCTTCATGATAGAG 376
|||||
101 LysLeuArgGlyLeuArgAlaGlnLysGlnAsnThrSerSerTrpTyrGlnVal 117
377 TGACTCATTCACACATTTCCGAAGCTCAGATGGTCTCCGAAAGTAC 426
|||||
117 LysSerPheThrProPheArgLysAlaGlnIleGlyProProGlnValH 134
427 ATTGAGAGCTGAAGATAGGCAATAGTATACATCTCTCTGGAACA 476
|||||
134 LysLeuGlnAlaGlnAspLysAlaIleValIleHisIleSerProGlyThr 150
477 AAGATAGTGTATATGCGGCTTGGATGTTTAAAGCTTACATATAGCT 526
|||||
151 LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerIle 167
527 ACTATCTGGAAGAAACCTCTCAGGTGAGAAAGAGATGAATAATTT 576
|||||
167 uLeuIleTrpLysAsnSerSerGlyValGlnGlnArgIleGlnAsnThr 184
577 ATTCCAGACATAAATTTATTAACCTCTCACAGAGACTTCTTGTCTA 626
|||||
184 YrsrArgHisLysLysIleTyrLysLeuSerProGlnThrTyrCysLeu 200
627 AAGTTAAGCAGACACTTACTGATGATGGAATAATGGTGTCTATAGTC 676
|||||
201 LysValLysAlaAlaLeuLeuThrSerTrpLysIleLeuValTyrSerP 217
677 AGTCATGTTATTAAGACACAGTGAATAATGAACTACCTCCACAGAA 726
|||||
217 oValHisCysIleLeuThrThrValGlnAsnGlnLeuProProGlnAla 234
727 ATATAGAGTCAGTGTCCAAATCAGAACATATGTTCTTAATGGATTA 776
|||||
234 snIleGlnValSerValGlnAsnGlnAsnTyrValLeuLysTrpAspTyr 280
777 ACATATGCAACATGACCTTTCAAGTCACTGCTCCACCCCTTTTAA 826
|||||
251 ThrTyrAlaAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeu 267
827 AAGGAATCTGGAACCATTTGATTAATAAGAAACAATACCTGATG 876
|||||
267 sArgAsnProGlnLysHisIleuTyrLysTrpLysGlnIleProAspCys 284
877 AAATGTCAAACTACCCAGTGTGCTCTTCTCCAAAACGTTTCCAAA 926
|||||
284 LysAsnValLysThrThrGlnCysValAlaPheProGlnAsnValPheGlnLys 300
927 GGAATTAACCTTCTCCGCTGACACATCGATGAGAAATTAACACTTT 976
|||||
301 GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerP 317
977 TTGCTGAGAGATAAGTTGATGACTGAATAACAAGTTCTCTCTCTC 1026
|||||
317 eTrpSerGlnGlnIleLysPheAspThrGlnIleGlnAlaPheLeuLeu 334
1027 CTCGAGCTTTAACATTAGATCCCTTAGTATGATTCATCATCTATAT 1076
|||||
334 ropProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle 350
1077 GGTGCTCAAAACAGCTGGAACAGCCGTGATCCAGATATATACACT 1126
|||||
351 GlyAlaProLysGlnSerGlnAsnThrProValIleGlnAspTyrProLe 367
1127 GATTATGAATATATTTTGGAAAAACACTTCAATGCTGAGAGAAAA 1176
|||||
367 uIleTyrGlnIleIleIlePheTrpGlnAsnThrSerAsnAlaGlnArgLys 384

1177 TATACGAAAAAAGTATGATTCCTATTTGAACACAGTACT 1226
 |||||
 384 lallggluylslysthrasvalthrvalproasnlleuylsppolethr 400
 1227 GTATATGTGTGAAGCCAGACGACACCATGATGAAAGCTGATTA 1276
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 401 ValTTCysVallylsAlaArgAlaHisThrMetLsPdlu..... 413
 1277 AAGCAGTGTTTTATGACGCTGATGTGAG 1307
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 414SerAspAlaValCysGlu 419

seq_name: A.Geneseq_36:W52296

seq_documentation_block:

ID W52296 standard; Protein: 325 AA.
 AC W52296;
 DT 23-JUN-1998 (first entry)
 DE CRFB4 protein.
 KW CRFB4, interleukin-10, IL-10, IL-10 receptor; allograft rejection;
 KW vaccine; photosensitivity; inflammation; autoimmune disease;
 KW septic shock; immune response; organ rejection; gene therapy.
 OS Homo sapiens.
 PN W09802542-A1.
 PD 22-JAN-1998.
 PF 17-JUL-1997: U12455.
 PR 17-JUL-1996: US-683743.
 PA (UIN-) UNITV NEW JERSEY.
 PI Kolenko SV, Pestka SJ.
 DR MPI: 98-110590/10.
 N-PSDB: V19874.
 PT New recombinant DNA - comprises sequences encoding interleukin-10
 and CRFB4 linked to operator, useful, e.g. preventing allograft
 rejection.
 PS Claim 2: Page -: 79pp; English.
 CC This sequence is the human CRFB4 sequence, DNA encoding it is used in the
 CC recombinant DNA (1) of the invention. (1) comprises a sequence (S1)
 CC encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2)
 CC encoding CRFB4, both operably linked to expression control sequences.
 CC Cells containing (1) may be used to identify agonists/antagonist of
 CC IL-10. Agonists are potentially useful, e.g. for preventing allograft
 CC rejection, as vaccine adjuvants, for treatment of photosensitivity,
 CC inflammation, autoimmune disease and septic shock, while antagonists are
 CC potentially useful for increasing immune responses against tumours,
 CC viruses, bacteria and parasites (especially intracellular pathogens) and
 CC for preventing organ rejection. A vector containing (1) is used to
 CC restore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses
 CC a dysfunctional IL10R and is able to bind IL-10 but not to transduce a
 CC signal. Antisense CRFB4 sequences (especially ribozymes), can inhibit
 CC IL-10 activity in cells. Antibodies specific for CRFB4 are used to
 CC measure and localise CRFB4, for diagnosis of defective IL-10 activity.
 CC Fragments of (1) are used as primers or probes to assay CRFB4-specific
 CC RNA. Agonists/antagonists may be administered parenterally, orally or
 CC rectally especially by intravenous injection or directly into a tumour or
 CC allograft.
 SQ Sequence 325 AA.

alignment_scores:

Quality: 228.50 Length: 224
 Ratio: 1.693 Gaps: 8
 Percent Similarity: 60.268 Percent Identity: 29.911

alignment_block:

US-09-240-675-1 x W52296

Align seg 1/1 to: W52296, from: 1 to: 325

81 TGGGTGTTCGCGACCGCGAGTGGAATAATCTAAATCT..... 122
 ||| ||||| ||||| ||||| |||||
 3 TrrperleuglysertrpLeuglyGlyCysleuLeuValSerAlaLeuG1 19
 |||||
 123CCTCAAAAAGTAgAGCTGCATCATATGATGACAACT 159

19 yMetValProProProGluAsnValLrYmetLsSerValAspPheLysA 36
 |||||
 160 TATCCGTAGGTGGAACAGAGACGATGACTGCTCGGAAATGACTTTT 209
 |||||
 36 snlleuglntrpGluSerProAlaPheAlaLysGlyLysnleuthrPhe 52
 |||||
 210 TCATGTCATTATCAAAAACCTGGATGATTAATGGATTAATTTCTGG 259
 |||||
 53 ThrAlaGlyLr.....LeuSerTYrArgLrPheGlnAspLry 65
 260 GTGTCAGATATATATGATACCAATGCAATCTTTTCTGACATGCA 309
 |||||
 65 scYsMetAsnThrThrLeuThrGlyCysAspPheSer.....LeuS 80
 310 ATGTTATGAAAGAAATTAATTCCTATAGACAGAA...AAGAAAC 356
 |||||
 80 erlystYrGlyAspRhlstHrLeuArgValArgAlaGlnPheAlaAspGlu 96
 357 ACTTTTCATGTATAGAGTGTGACATTTTACACCATTTGCGAAAGCTA 406
 |||||
 97 HisSerAspTrpValAsnLe...ThrPheCysProValAspAspRhlx1 112
 407 GATTGGCTCCGAGAGTACATTAGAGCT...GAAGATTAAGGCAATG 453
 |||||
 112 eileGlyProProGlyMetGlnValGlnValLeuAlaAspSerLeuHis 129
 454 TGATACACATCTCTCCGAAACAAAGATAGCTT...ATGTGGCTTG 500
 |||||
 129 eLarPheLeuAlaProLysIleGluAsnGlnLrYrGlnLrThrPrlMet 145
 501 GATGCTTTA.....AGCTTACATATGCTTACTTATCTGAAAAC 544
 |||||
 146 LysAsnValLrYrAsnSerTrpThrYrAsnValGlnLrYrLysAsnG1 162
 545 TTGAGGTGTGAAGAAGGATTAATAATTTTTCGACGACAAATTT 594
 |||||
 162 YThrAspGlnLrYrPheGlnLrThrProGlnLrYrAspPheGlnValLeu 179
 595 ATTAACCTCCACGACACTTACTTATGTCTAAAGTTAAAGCAGCACTA 644
 |||||
 179 rGsnleuglntrpTrpThrThrYrCysValGlnValArgGlyPheLeu 195
 645 CTTACGTGATGGAATATGGTGTCTATGTCACGTCATCTGATTAAGAC 694
 |||||
 196 ProAspTrpGsnLysAlaGlyLrYrPserGlnProValCysGlnLr 212
 695 CAGAGTTGAAGAAGCACTACT 716
 212 TrpHisAspGlnThrValPro 219

seq_name: A.Geneseq_36:R75782

seq_documentation_block:

ID R75782 standard; Protein: 332 AA.
 AC R75782;
 DT 13-NOV-1995 (first entry)
 DE IFN-gamma receptor beta subunit.
 KW Interferon-gamma receptor beta subunit; muIFN;
 KW Interferon-gamma antagonist.
 OS Mus sp.
 FH Key
 FT peptide
 FT 1..18
 FT /label- Sig peptide
 FT 19..242
 FT /label- Extracellular domain
 FT 243..266
 FT /label- Transmembrane anchoring domain
 FT 267..332
 FT domain
 FT /label- Cytoplasmic domain

PD W09516036-A.
 15-JUN-1995
 PF 07-DEC-1994: U14277.

PR 09-DEC-1993; US-164596.
 PA (AGDE/) AGDET M.
 PA (BOEH/) BOEHNI R.
 PA (HEMM/) HEMMI S.
 PI Aguet M, Boehni R, Hemmi S;
 DR MPI, 95-224321/29.
 DR N-PSDB; 090808.
 PT Novel interferon gamma receptor beta chain polypeptide - for
 treatment of inflammatory bowel disease and liver damage
 PS claim 3; Fig. 2a; 86pp; English.
 CC The IFN-gamma receptor beta-subunit encoded by a cDNA clone derived
 from mouse B-cells is given in R75782. Recombinant beta-subunit,
 CC pref. with the transmembrane anchoring domain deleted or
 CC inactivated and with the cytoplasmic domain deleted, may be
 CC used to treat pathological conditions associated with endogenous
 CC IFN-gamma production.
 SO Sequence 332 AA;

alignment_scores:
 Quality: 203.00 Length: 229
 Ratio: 1.471 Gaps: 13
 Percent Similarity: 60.262 Percent Identity: 30.131

alignment_block:
 US-09-240-675-1 x R75782

Align seg 1/1 to: R75782 from: 1 to: 332

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87 TTGCCCCGAGCCGAGGTGA.....AAAATCTAATCTCC 124
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16 LeuLylAlaAlaLeuSerProAspSerPheSerGlnLeuAlaAla 32
125 TCAAAAGTAGAGGTGCAGCATAGATAGACACTTATCTCGAGGTGA 174
|:::|||||:|||||:|||||:|||||:|||||:|||||:
32 oleuAsnProArgLeuHisLeuTyraAsnAspGlnLeuThrTrp 49
175 ACAGAGGAGTACTCT.....GTGGGAATCTGACT 206
|||:|||||:|||||:|||||:|||||:|||||:
49 luProSerProSerSerAsnAspProArgProValIValGln 65
207 TTTTCATTCGATTATCAAAAACGCGATGAT..AATGGATTAAT 253
|||:|||||:|||||:|||||:|||||:|||||:
66 TySerPhe.....IleAspGlySerTrpHisArgLeu 76
254 G.....TCTGGTGTCAAGATATTACTAGTACCAATCAACTTTCT 297
|||:|||||:|||||:|||||:|||||:|||||:
76 uleuGluProAsnCysThrAspIleThrGlnThrLysCysAspLeuThr 93
298 CA.....CTCAAGCTGAATGTTTAAVGA..GAAATTAATGGCT 335
|||:|||||:|||||:|||||:|||||:|||||:
93 lylGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeu 109
336 ATAAGAGAGAGAAAAGAAAC..ACTTCTCATGTTAGTGGTTGACTC 382
|||:|||||:|||||:|||||:|||||:|||||:
110 ValAlaGlyAlaArgGlyAsnLeuThrSerLysTrpValGlyLeuGlu 126
383 ATTATACACATTTGCAAAAGCTCAGATTGTCTCCAGAA..GTACTAT 429
|||:|||||:|||||:|||||:|||||:|||||:
126 oPheGlnHisLysTrpGlnAsnValThrValGlyProTrpLysAsnIleSer 143
430 TAGAAGCTGAAGATAGGCAATAGTATGATACATCTCTCTGAACAAA 479
|||:|||||:|||||:|||||:|||||:|||||:
143 alThrProGlyLysGlySerLeuValIleHisLysPheSerProPheAsp 159
480 GATAGTGTATAGTGGCTTTAGCTTTACATATAGCTTACT 529
|||:|||||:|||||:|||||:|||||:|||||:
160 .....ValPheHisGlyAlaThrPheGlnTrpLeuValHis 171
530 TATCTGAAAAACTCTTCAAGGTAGAGAAAGAGATTAATATTAT 579
|||:|||||:|||||:|||||:|||||:|||||:
171 styLysTrpLysSerGlnThrGlnGlnValGlnValGlnLysProPhe 188

```

580 CCAGACATAAAATTTAT.....AAACTCCACAGAGACTACTATTGT 623
 ::|||:|||||:|||||:|||||:|||||:|||||:|||||:
 188 lylSerAsnSerIleValIleGlyAsnLeuLysProTrpArgValTrpCys 204
 624 CTAAAGTTAAACGACACTA..CTTACGTCATGGAATTT..... 662
 |||:|||||:|||||:|||||:|||||:|||||:|||||:
 205 leuGlnThrGlnLysLeuLeuLeuLysAsnLysGlyIleArgProHis 221
 663 GGGTGTATAGTCGATCATGTATTAAGACCCACA 698
 |||:|||||:|||||:|||||:|||||:|||||:|||||:
 221 sGlyLeuLeuSerAsnValSerCysHisGlnThr 233

seq_name: A.Geneseq_36:W79159

seq_documentation_block:
 ID W79159 standard; Protein: 553 AA.

AC W79159;
 DT 20-NOV-1998 (first entry)
 DE Zcyto7 cytokine receptor polypeptide.
 KW Zcyto7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas;
 KW type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;
 KW agonist; cell proliferation; cell differentiation; renal disease; human;
 KW renal disease; pancreatic disease.
 OS Homo sapiens.
 FH Key
 FT Domain Location/Qualifiers
 FT 30..250 /note="extracellular (ligand-binding) domain;
 FT 275..553 /note="intracellular domain"

FT Domain W09837193-A1.
 FT 27-AUG-1998.
 PF 18-FEB-1998: U03029.
 PR 02-OCT-1997: US-943087.
 PR 20-FEB-1997: US-803305.
 PA (ZIMO) ZIMOGENTICS INC.
 PI Adams RL, Farrah TM, Jellmeberg AC, Kuo CJ, Lok S,
 PI Whitmore TE;
 DR MPI, 98-480798/41.
 DR N-PSDB; V57515.
 PT Novel human Zcyto7 DNA encodes a type 2 cytokine receptor - useful
 for treating renal, neural, pancreatic and prostatic diseases
 PS Claim 1; Pages 55-59; 72pp; English.
 CC This represents the Zcyto7 cytokine receptor. Zcyto7 is a ligand-
 CC binding receptor polypeptide and is a novel member of the type 2 cytokine
 CC receptor family (CRF2). An expression vector containing the Zcyto
 CC polynucleotide, operably linked to transcription promoter, a sequence
 CC encoding a transmembrane and intracellular domain, or both, and a
 CC transcriptional terminator can be used to transform host cells for the
 CC recombinant production of the polypeptide. The sequences can be used to
 CC study the Zcyto7 gene and to isolate ligands binding to it. Zcyto7 is
 CC preferentially expressed in the kidney, pancreas, prostate or nervous
 CC tissue. Agonists of Zcyto7 can be used to stimulate proliferation and
 CC differentiation of cell in these organs. The antagonists and agonists can
 CC also be used in the treatment of renal, neural, pancreatic and prostate
 CC diseases.
 SO Sequence 553 AA;

alignment_scores:
 Quality: 198.00 Length: 433
 Ratio: 0.908 Gaps: 17
 Percent Similarity: 50.346 Percent Identity: 21.016

alignment_block:
 US-09-240-675-1 x W79159

Align seg 1/1 to: W79159 from: 1 to: 553

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57 CTAGTGTCTGCTCCGCGGCCCATGG.....GTGTGTCGACGCCCC 100
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18 LeuLeuLeuLeuLeuAlaAlaProTrpGlyArgAlaValProCysVal 34

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101 AGGTGGAAAAATCTAAATCTCTCAAAAGTAGAGTCGACATCATAG 150
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34 rglgly.....LeuProlyProAlaAsnIleThPheLeuSerIleA 49
151 ATGACACATTATTCAGAGTGAGGAGAGGAGCGATGCTGCGG... 197
    ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
49 snbetyAsnValLeuGlnIleThProProGlnGlyLeuGlnGlyVal 65
198 AATGATCTTTTCATTCGATATCAAAAACGCGGATGATTAATGAT 247
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
66 LysValIleThyThyValGlnIleThyPheIleThyGlyGlnLysIle 82
248 AAAATGCTGGGTGAGATATTAATTAAGTACCAATGCAATCTTCT 297
    ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
82 uasnlySerGlnCysArgAsnIleAsnArgIleThyCysAspLeuSer 99
298 CACTCAAGCTGAATGTTTATGAAGAAATTAATGCTATAGAGCA... 344
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
99 IacIleThySerAspIleGlnIleThyValIleThyValIleValIle 115
345 GAAAAAGAAACACTTCTCATAGTATGAGTGTGACTCATTTACACAT 394
    ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
116 TrpGlyThyLysCysSerIleThyPheIleGlnSerGlyArgPheThy 132
395 TCCCAAGCTCAGATGCTGCTCCAGAGTACATTTAGAGCTGAGATA 444
    ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
132 eLeuGlnIleThyGlnIleIleIleProGlnIleValIleThyThy 149
445 AGCAATAGTATGATACATCTCTCCGAGCAAA..... 479
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
149 ySerIleSerValIleThyThyAlaProGlnIleThyIleValIle 165
480 .....CATAGTGTATGCTGGGCTTGGATGCTTAAAGCTTTAC 517
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
166 GlnAspLeuProValSerMetGlnIleIleThySerAsnLeuIleThy 182
518 AATAGCTACTATCTCGAAACCTTCAGCTAGAGAGAGAGATTC 567
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
182 nValSerValLeuAsnThyLysSerAsnArgIleThyPheGlnCysVal 199
568 AAAATATTATTCCAGACATTAATTTATTA.....CTCTCCAGAG 611
    ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
199 hAsp.....HisThyLeuValLeuThyThyPheGlnProAsn 211
612 ACTACTTATGCTTAAAGTAAAGCAGACCTACTAGCTAGAGAAAT 661
    ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
212 ThrLeuThyCysValHisValGlnSerPheValProGlyProArg 228
662 TGGTCTATAGTCCAGTACATGCTTAAAGACACAGCTGAAAGAA 710
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
228 gAlaGlnProSerGlnLysGlnLysAlaArgIleLysAspGlnSer 245
711 .....CTACCTCCAGAGAA 725
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
245 eGlnPheLysAlaLysIleIlePheThyPheValLeuPro..... 258
726 AATATGAGTCAAGTCCAAATCAAGACTATGCTTAAATGAGATTA 775
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259 ..IleSerIleThyVal.....Phe 264
776 TACATGCAACATGACCTTCAAGT...CAGTGGCCAGCCTTTT 822
    ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
264 eLeuPheSerValMetGlyThySerIleThyArgIleHisValGly 281
823 TAAAGAGATCTGGAACCAATTTATTAATGAAACAAATTAAGTAC 872
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
281 yGlnLysHisProAlaAsnLeuIle..... 289
873 TGTGAAAATGTCAAACTACCAAGTGTCTTCTCAAAAGCTTTTCA 922
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290 .....LeuIleThyGlyAsnGlnPheAs 297
923 AAAGAGATTTACCTTCTCCGGGTAACAGCATGTGATGAATTAACAT 972

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297 pLysArgPhePheVal.....ProAlaGlnLysIleValIleA 310
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973 CTTTGGTGAAGAGATTAAGTTGATGATCAATA.....CAA 1013
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
310 snbHeIleThyLeuAsnIleSerAspSerLysIleSerHisGlnAsp 326
1014 GCCTTCCCTACTCTCCAGCTTTAAACATTAGATCCCTTAGATTCAT 1063
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
327 MetSerLeuLeuGlnLysSerSerAspValSerSerLeuAsnAsp 341
1064 CCATATCTATATGCGTGCCTCCAAACAGCTGGAACAGCCCTGCATCC 1113
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
342 .....ProGlnProSerGlnAsnLeuArgProProG 352
1114 AGCATATCCACGATTTATGAAT..... 1139
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
352 IacIleGlnIleGlnValIleValHisLeuGlyThyAlaSerHisLeuMetGln 368
1140 ATTTTGGGAAAAACACTTCAATGCTGAGAGAAAAATTAAGAGAAAA 1189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
369 IlePheCysAspSerGlnIleAsnThyGlnGlyThySerPheThyGln 385
1190 AACTGATCTT.....ACAGTCTCTAATTTGAACACGACTGTTAT 1232
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
385 nGlnSerLeuSerArgThyIleProProAspLysThyValIleGlnIle 401

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seq_name: A_Geneseq_36:R71035

seq_documentation_block:

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ID R71035 standard; Protein; 337 AA.
AC R71035;
DE 11-OCT-1995 (first entry)
DE Human IFN-gamma accessory factor-1.
KW Interferon-gamma; AF-1; tumour.
OS Homo sapiens.
PN W09505847-A.
PD 02-MAR-1995.
PF 22-AUG-1994; D09438.
PR 20-AUG-1993; US-110119.
PA (UTNE-) UNIV NEW JERSEY.
PI Cook JR, Donnelly RJ, Emanuel S, Kotenko S, Mariano TM;
PI Pestka S, Schwartz B, Soh J;
DR N-PSDB; 084697.
PT Suppressing tumours in mammals with accessory factor 1 (AF-1) -
PT for interferon gamma, specifically induction of class I HLA
PS antigens, including use of AF-1 DNA in gene therapy
PS Disclosure; Fig 21a; 114p; English.
CC The sequence is that of human interferon-gamma accessory factor-1.
CC Incorporation of AF-1 into immune and tumour cells re-establishes
CC normal function with elimination of malignant cells.
SQ Sequence 337 AA;

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alignment_scores:

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Quality: 155.50 Length: 300
Ratio: 1.030 Gaps: 14
Percent Similarity: 50.333 Percent Identity: 22.333

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alignment_block:

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US-09-240-675-1 x R71035
Align seg 1/1 to: R71035 from: 1 to: 337

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60 GTCGCTGCGCGGCGCCATNGGCTGTTGCCGAGCGGAGGAGGA. 107
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9 LeuLeuLeuLeuGlnValPheAlaAlaAlaAlaAlaAlaProProAs 25
108 .....AAAATCTAAATCTCTCAAAAGTAGAGCTGACATCATAG 150
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25 ProLeuSerGlnLeuProAlaProGlnHisProLysIleArgLeuThyA 42

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151 ATGACAACTTATCTGAGGTG.....AACAGAGC 182
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42 snlgluglnvalleusertrpgluprovalalaleuserasnserthr 58
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59 ArgProvalaltryglnvalglinpheLysylThrAspserLys... 73
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233 GATGATTAATGGATAAATGTCT.....GGGTGC 264
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74 .....TriphethrAlaaspIleMetSerIleGlyValasnCysT 87
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265 AGAATATTACTAGTACCAATGCACTTTCTTCA..... 299
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87 hrcInIlethrAlaIthrGlucysAspPheThrAlaAlaSerProserAla 103
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300 .....CTCAAGCTGATGTTATGAGAATTAATTCGTATAG 340
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104 GlyPheProMetLaspPheasnVal.....ThrLeuArgLeuAr 116
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341 AGCAGAAAAAGAAAAACT...TCTTCATGCTATAGAGTTCACATTTA 387
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116 glalgluleuglyalaleuHisSerAlaIleThrValIleMetProIlePheG 133
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388 CACCAATTCGCAAAAGCTCAGATGGCTCCGAGAGTACATTAGAA... 434
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133 lnhIstYrArgasnValThrValGlyProProGlu...AsnIleGluVal 148
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165 eAlaAspThrSerThrAlaPhe.....PheCysTyrTyrValH 178
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226 alGlyHisLeuSerAsnIleSerCysTyrGluThrMetAlaAspAlaSer 242
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744 .....CAAAATCAGACT 756
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259 uSerValleuAlaGlyAlaCysPhePheLeuValleuLysTyrArgGlyL 276
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757 ATGTTCTTAATGGGATTATACATATGCAACATGACCTTCAAGTTCAG 806
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276 euIleLysTyrTrpPheHisThrProProSerIleProLeuGlnIleGlu 292
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351 GlyAlaProIysGlnSerGlyAsnThrProValIleGlnAspTyrProle 367
      |||||||
1127 GATTATGAAATATATTTTTTGGGAAAAACTTCAAATGCTGAGAGAAAAA 1176
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367 uileTyrgLulleIlePheThrPrluSnThrSerAsnAlaGluArgLysI 384
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1177 TTATCGAGAAAAAAACGTGATGTACAGTTCCTAATTGAAACCACTGACT 1226
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1227 GATATGTGTGTGAAGCCAGACACACACCATGGATGAAAGCTGAATAA 1276
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401 ValTyrCyseValLysAlaArgAlaHisThrMetAspLulysLeuAsnLys 417
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1277 AACCACTGGTTTTAGAGAGCGCTGTATGTGAGAAACAAACCAAGGAATA 1326
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417 sSerSerValrPheSerAspAlaValLysGluLysThrLysProLysAsnT 434
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434 hrSerLys 436

seq_name: /cgn2_6/ptodate/L/1aa/5A.COMB.pep:US-08-328-256-10

seq_documentation_block:
Sequence 10, Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RAYOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
FAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

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US-08-328-256-10

alignment scores: Quality: 2313.00 Length: 436
Ratio: 5.305 Gaps: 0
Percent similarity: 100.000 Percent identity: 100.000

alignment block:
US-09-240-675-1 x US-08-328-256-10

Align seg 1/1 to: US-08-328-256-10 from: 1 to: 557

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1 MethectValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
77 CCATGGGTGTGTCCGAGCGCGAGGTGGAATAATCTAAATCTCTCTC 126
17 yProtrValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerPro 34
127 AAAAAGTGAAGGTGACATCATAGATGACACTTATCTGAGTGAAC 176
34 InLysValGluValAspIleLeuAspAsnPhelLeuArgTrpAsn 50
177 AGGAGCGATGAGTCTGCGGGAATGTGACTTTTTCATTCGATTATCAA 226
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlu 67
227 AACTGGGATGATTAATGATTAATTTGCTGGGTGAGATATATCTA 276
67 sthGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleH 84
277 GTACCAAAATGCACTTTTCTCTCACTCAAGCTGAATGTTATGAGAA 326
84 erThrLysCysAsnPheserSerLeuLysLeuAsnValTyrGluIle 100
327 AAATGGCTATPAGAGCAGAAAAGAAAACACTTCTCATGTATGAGGT 376
101 LysLeuAlaGlyIleArgAlaGlyLysGlnAsnThrSerSerTyrGlu 117
377 TGACTCATTTACACCATTTCCGAAAGCTCAGATTGGTCTCCAGAA 426
117 LasperherhtrproPheArgLysAlaGlnIleGlyProProGluVal 134
427 ATTGGAAGCTGAGATAGGAGCATATGATACATCTCTCTGGAACA 476
134 AsLeuGluAlaGluAspLysAlaIleValIleHIsIleSerProGly 150
477 AAAGTACTGTATGTGGCTTTGATGATGTTAACTTTACATTAAGCT 526
151 LysAspSerValMetTrpAlaLeuAspLysLeuSerPheTrpTyrSer 167
527 ACTATCTGGAAGAACTCTCAGGTGTGAGAAAGATGGAATTAATTT 576
167 uLeuIleTrpLysAsnSerSerGlyValGluGlnArgLysLeuAsn 184
577 ATTCGACGATTAATTAATTAATCTCCACAGAGACTACTATTGTCTA 626
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627 AAAGTTAAGCAGACTACTAGCTAGCGAGAAATGTTGTTCTATAGCC 676
201 LysValLysAlaAlaLeuLeuThrSerTrpLysIleGlyValTyrSer 217
677 AGTACATTTATTAAGACACAGTGAAGAAAGATACCTCCACAGAA 726
217 oValHIsCysIleLysThrThrValGluAsnGluLeuProProGlu 234
727 ATATGAGTGAAGTGTCCAAATGAGAACTATGTTCTTAATGGATAT 776
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877 AAAATGTCAAAACATCCAGTGTCTTTCTCTCAAAACGTTTCCAAA 926
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317 erTrpSerGluGluIleLysPheAspTrpGluIleGlnAlaPheLeu 334
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334 roProValPheAsnIleArgSerLeuSerAspSerPheHIsIleTyr 350
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401 ValTyrCysValLysAlaArgAlaHIsThrMetAspLysLysLeu 417
1277 AAGCAGTGTTTTGTAGCGGTGATGTGAGAAAACCAAGGAATA 1326
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434 HsSerLys 436

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seq.name: /cgn2.6/ptodata/1/aa/5A.COMB.pep:US-08-471-454-2

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seq.documentatation block:
: Sequence 2, Application US/08471454
: Patent No. 5731169
: GENERAL INFORMATION:
: APPLICANT: MOGENSEN, Knud E.
: APPLICANT: UZE, Gilles
: APPLICANT: LOTFALLA, Georges
: TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
: TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
: TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NIXON & VANDERHAYE P. C.
: STREET: 1100 NORTH GLEBE ROAD
: CITY: ARLINGTON
: STATE: VIRGINIA
: COUNTRY: U.S.A.
: ZIP: 22201-4714
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS

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seq_name: /cgn2_6/ptodata/1/laa/5b_COMP.pep:US-08-466-974-2

seq_documentation_block:

Sequence 2, Application US/08466974
Patent No. 5861258

GENERAL INFORMATION:

APPLICANT: MOGESEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LOTFALLA, Georges
TITLE OF INVENTION: GPCR FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,974
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEPHONE: (703) 816-4100

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEPHONE: (703) 816-4100

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: proteind

US-08-466-974-2

Alignment scores:

Quality: 2313.00 Length: 436
Ratio: 5.305 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

Alignment block:

US-09-240-675-1 x US-08-466-974-2

Align seg 1/1 to: US-08-466-974-2 from: 1 to: 557

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17 yProtrValLeuSerAlaAlaAlaAlaAlaAlaAlaAlaAla 34
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67 sThrGlyMetAspAsnTrpIleValSerIleValGlnAsnIleTrp 84
277 GTACCAAAATGCACTTTCTTCACATCAAGCTGAAGTTATTA 326
84 eThrIleValSerPheSerIleValSerIleValSerIleVal 100
327 AAATGCTATATAGACAGCAAAAGCAAACTTCTATGATGAT 376
101 LysLeuArgIleArgAlaGluValGlnValSerTrpTyrGluVal 117
377 TGACATTTTACATTCATTCGCAAGCTGATGCTGCTGCTGCT 426
117 LysPhePheTrpPhePheArgLysAlaGlnIleValProPheGluVal 134
427 ATTTAGAGCTGATAGATAGCAATGATGATGATGATGATGAT 476
134 sLeuGluValGluValSerValAlaIleValIleValIleVal 150
477 AAAGATGATGATGATGATGATGATGATGATGATGATGAT 526
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527 ACTTATCTGGAAGAACTCTGCTGCTGCTGCTGCTGCTGCT 576
167 uLeuIleTrpLysAsnSerSerGlyValGluValGluValGlu 184
577 ATTCAGACATTAATTAATTAATTAATTAATTAATTAATTA 626
184 ySerArgHisIleValIleValIleValIleValIleValIle 200
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201 LysValIleValAlaAlaLeuLeuTrpSerTrpLysIleGlyVal 217
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284 LuAsnValIleThrThrGlnCysValPheProGlnAsnValPhe 300
927 GGAATTAACCTTCTGCGGAGCAAGATGATGATGATGATG 976
301 GlyIleValIleValIleValIleValIleValIleValIle 317
977 TTGCTGTAAGAGATTAAGTGAATGATGATGATGATGATG 1026
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seq_name: /cgn2_6/prodata/1/lae/5B_COMB.pep:US-08-471-453-2
seq_documentation_block:
: Sequence 2, Application US/08471453
: Patent No. 5886153
: GENERAL INFORMATION:
: APPLICANT: MOGENSEN, Knud E.
: APPLICANT: UZE, Gilles
: APPLICANT: LUTFALLA, Georges
: APPLICANT: GRESSER, Ion
: TITLE OF INVENTION: cDNA FRAGMENT CODING FOR THE GENE FOR
: TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
: NUMBER OF SEQUENCES: 2
: PREPARATION OF THE CORRESPONDING PROTEIN
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NIXON & VANDERBYE P.C.
: STREET: 1100 NORTH GLEBE ROAD
: CITY: ARLINGTON
: STATE: VIRGINIA
: COUNTRY: U.S.A.
: ZIP: 22201-4714
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/471.453
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/900,642
: FILING DATE: 15-JUN-1992
: APPLICATION NUMBER: FR 89/13770
: FILING DATE: 20-OCT-1989
: ATTORNEY/AGENT INFORMATION:
: NAME: BYRNE, THOMAS E.
: REGISTRATION NUMBER: 32,205
: REFERENCE/DOCKET NUMBER: 960-7
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 816-4000
: TELEFAX: (703) 816-4100
: TELER: 200797 NIXN DR
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 557 amino acids
: TYPE: amino acid
: STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-453-2
Alignment scores:
Quality: 2313.00 Length: 436
Ratio: 5.305 Gaps: 0
Percent similarity: 100.000 Percent identity: 100.000
Alignment block:
US-09-240-675-1 x US-08-471-453-2
Align seg 1/1 to: US-08-471-453-2 from: 1 to: 557
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1 METETVALVALLLEULGILALATHRTHLEUVALLLEUVALALVALGI 17
77 CCCATGGGTGTTGCCGAGCCGAGTGAAGAAAAATCTAAATCTCTC 126
17 PPTOTRVALLEUSERALALALAGLYGLYASNLEULYSSEPTG 34
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51 ARGSEKSPGLUSERVALGILYASNVALTHRPHSEKSPHSPYRGLNLY 67
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201 LYSVALYSALALALALALALALALALALALALALALALALAL 217
677 AGTACATGTATTAAGACACAGTGAAGTGAAGTGAAGTGAAGTGA 726
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234 snllgluValSerValGlnasnGlnasnTyrValLeuLysTrpAspTyr 250
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1177 TTATGAGAAAAAACTGATGTATACACTTCTTATTTGAACCACTGACT 1226
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1277 AAGCACTGTTTATGAGCTGTATGTGTGAGAAACAAACAGGAAATA 1326
417 sSerSerValPheSerAspAlaValLysGlnLysTrpLysProGlyAsnT 434
1327 CCTCTTAAA 1334
434 hserLys 436

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seq_name: /cgn2_6/ptodate/1/laa/5b.comb.pep:us-08-307-588-4

seq_documentation_block:
 : Sequence 4, Application US/08307588
 : Patent No. 5919453
 : GENERAL INFORMATION:
 : APPLICANT: BENOTT, Patricia
 : APPLICANT: MEYER, Francois
 : APPLICANT: MAGUIRE, Deborah
 : APPLICANT: PLAVEC, Ivan
 : APPLICANT: TOYER, Michael G
 : TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
 : TITLE OF INVENTION: RECEPTOR WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
 : NUMBER OF INVENTIONS: 4
 : NUMBER OF SEQUENCES: 4
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Foley & Lardner
 : STREET: 3000 K Street, N.W., Suite 500
 : CITY: Washington
 : STATE: D.C.
 : ZIP: 20007

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAKI, Bernard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 117283/117/GUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-588-4

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alignment_scores:
 Quality: 2313.00 Length: 436
 Ratio: 5.305 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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Align seq 1/1 to: US-08-307-588-4 from: 1 to: 557

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67 sThylGlyMetAspAsnIleLysLeuSerLysGlnAsnIleThrS 84
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117 lAspSerPheThrProPheArgLysAlaGlnIleLysProProGlnVal 134
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134 lSerGlnAlaGlnLysLysAlaIleValIleHisIleSerProGlyThr 150

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477 AAGATAGTGTATGTGGCTTGGATGGTTAAGCTTACATATAGCT 526
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1277 AAGCAGGTGTTTATGACGCTGTATGTGAAAACAAACAGGAAATA 1326
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1327 CCTCTAAA 1334
434 InSerLys 436

seq_name: /cgn2_6/pidodata/1/laa/5A_COMB.pep:US-08-328-256-11
seq_documentation_block:
: Sequence 11, Application US/08328256
: Patent No. 5643749
: GENERAL INFORMATION:
: APPLICANT: REVEL, Michel
: APPLICANT: ABRAMOVICH, Carolina
: APPLICANT: RATOVSNIK, Edward
: TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin, Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/328,256
: FILING DATE: 24-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 107378
: FILING DATE: 24-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.
: REGISTRATION NUMBER: REVEL-13
: REFERENCE/DOCKET NUMBER: 25,618
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 434 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-328-256-11
Alignment scores:
Quality: 2265.00 Length: 427
Ratio: 5.304 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
Alignment block:
US-09-240-675-1 x US-08-328-256-11
Align seq 1/1 to: US-08-328-256-11 from: 1 to: 434
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seq_documentation_block:
Sequence 3, Application PC/TUS9414277
GENERAL INFORMATION:
APPLICANT: Aguet, Michel
APPLICANT: Bohml, Ruth
APPLICANT: Hemml, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid

TOPOLOGY: linear
PCT-US94-14277-3

Alignment scores:
Quality: 490.50 Length: 202
Ratio: 3.337 Gaps: 1
Percent Similarity: 72.772 Percent Identity: 48.515

Alignment block:
US-09-240-675-1 x PCT-US94-14277-3

Align seg 1/1 to: PCT-US94-14277-3 from: 1 to: 202

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705 AATGAA 710
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seq_name: /cgr2_6/prodata/1/aa/PCTUS_COMB.dep.PCT-US94-14277-4

seq_documentation_block:

Sequence 4, Application PC/TUS9414277

GENERAL INFORMATION:

APPLICANT: Aguet, Michel

APPLICANT: Bohnl, Ruth

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APPLICANT: Hemml, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SBO ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-4

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Alignment scores:
Quality: 466.50 Length: 208
Ratio: 3.049 Gaps: 3
Percent Similarity: 73.558 Percent Identity: 44.712

Alignment block:
US-09-240-675-1 x PCT-US94-14277-4

Align seg 1/1 to: PCT-US94-14277-4 from: 1 to: 200

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193 LysThrArgProGlySerPheSer 200

seq_name: /cgn2_6/ptodata/1/laa/5B_COMB.pep:us-08-683-743-4

seq documentation block:
: Sequence 4, Application US/08683743
: Patent No. 5843697
:
: GENERAL INFORMATION:
: APPLICANT: Pestka, Sidney
: APPLICANT: Kotenko, Serguei
: TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
: TITLE OF INVENTION: CHAIN
: NUMBER OF SEQUENCES: 25
: CORRESPONDENCE ADDRESS:
: ADDRESS: David A. Jackson, Esq.
: STREET: 411 Hackensack Ave, Continental Plaza, 4th
: CITY: Florio
: STATE: Hackensack
: COUNTRY: USA
: ZIP: 07601
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy/disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/683,743
: FILING DATE: 17-JUL-1996
: CLASSIFICATION: 435
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Jackson Esq., David A.
: REGISTRATION NUMBER: 26,742
: REFERENCE/DOCKET NUMBER: 601-1-050
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-487-5800
: TELEFAX: 201-343-1684
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 325 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEetical: NO
: FRAGMENT TYPE: NO
: US-08-683-743-4

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  Ratio: 1.693      Gaps: 8
  Percent Similarity: 60.268      Percent Identity: 29.911

alignment_block:
US-09-240-675-1 x US-08-683-743-4

Align seg 1/1 to: US-08-683-743-4 from: 1 to: 325

81 TGGGTGTTGTCGACAGCCGACGAGTGAAGAAATCTTAATCT..... 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   3 TrpSerLeuGlySerTrpLeuGlyCysLeuValSerAlaLeu 19
123 .....CCGCAAAAAGTAGAGGTCCACATCATAGTACACT 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   19 yMetValProProGluAsnValArgMetAsnSerValAsnPheLysA 36
160 TTATCTGAGTGAAGACAGACGATGAGTCTGTGCGGAATGACTTT 209
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   36 snIleLeuGlnTrpGluSerProAlaPheAlaLysGlnPheLeuThrPhe 52
210 TCAATTCGATTACAAAACCTGGATGATTAATTGGATAAATTGTCTGG 259
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   53 ThrAlaGlnTyr.....LeuSerTyrArgGlnPheGlnAspLys 65
260 GGTGTCGATATTACTAGTACCAATGCACATTTCTTCTGACACACTGA 309
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   65 sCysMetAsnThrThrLeuThrGlnCysAspPheSer.....LeuS 80
310 ATGTTATGAGAAATTAATTGCGTATAGAGCAGAA...AAAGAAAC 356
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   80 erLysTyrClyAspHisThrLeuAlaGlnValAlaGlnPheAlaAspGln 96
357 ACTTCTCATGTTATGATGAGTTGACTCATTTACCACTTCCGAAACTCA 406
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   97 HisSerAspTrpValAsnIle...ThrPheCysProValAspAspThrI 112
407 GATTGCTCTCCAGAGACATATTGAACT...GAAGTAAGCAATAG 453
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   112 eIleGlyProProGlyMetGlnValGlnValLeuAlaAspSerLeuHisM 129
454 TGATACACATCTCTCTGAGACAAAAGATAGTGT...ATGGGGCTTGG 500
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   129 eArgPheLeuAlaProLysIleGlnAsnGlnTyrGlnThrThrPheMet 145
501 GATGGTTA...AGTTACATATAGCTTACTTATCTGAAAACTC 544
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   146 LysAsnValTyrAsnSerTrpThrTyrAsnValGlnTyrTrpLysAsnG 162
545 TTCAGGTGAGAAAGAGATTGAAATTTATTTCCAGACATAAAATTT 594
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   162 yThrAspLysPheGlnIleThrProGlnTyrAspPheGlnValLeuA 179
595 ATAACTCTCACAGACACTACTTATTTCTAAAGATAAGACACACTA 644
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   179 yGAsnLeuGlnProTrpThrTyrCysValGlnValAlaGlnPheLeu 195
645 CTTACGTCATGAAAATGTTGCTCTATAGTCCAGTACATTGTATTAAG 694
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   196 ProAspArgAsnLysAlaGlnTyrPheSerGlnProValCysGlnGlnTh 212
695 CACAGTGAAGAAATGACACTGCT 716
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   212 ThrHisAspGlnThrValPro 219

seq_name: /cgn2_6/ptodata/1/laa/PC/US_COMB.pep:PCF-US94-14277-2

seq documentation block:
: Sequence 2, Application PC/US9414277
: GENERAL INFORMATION:
: APPLICANT: Aguet, Michel

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STREET: 1401 EASTLAKE AVENUE EABL
CITY: Seattle
STATE: WA
COUNTRY: USA


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|||||
327 MetSerLeuLeuGlyLysSerSerAspValSerSerLeuAsnAsp..... 341
1064 CCATATCTATATGCGTGCCTCCAAACAGCTCTGGAACACGCCCTGTGATCC 1113
342 .....ProGlnProSerGlyAsnLeuArgProProG 352
1114 AGCATATCCACTGATTTATGAATT..... 1139
352 InGlnGluGluValLysHisLeuGlyTyrAlaSerHisLeuMetGlu 368
1140 ATTTTGGAAACACTTCAATGCGAGAGAAAAATTATCGAGAAAA 1189
369 IlePheCysAspSerGluIuAsnThrGluGlyThrSerPheThrGlnGlu 385
1190 AACTGATGT.....ACAATTCCTAATTGAACCACTGACTGTATAT 1232
385 ngIuSerLeuSerArgThrIleProProAspLysThrValIleGluTyr 401

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OM of: US-09-240-675-1 to: PIR_63: * out_format : pfs
 Date: Jun 1, 2000 5:46 PM

About: Results were produced by the Gencore software, version 4.5,
 Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODE=frame+dp2 model -DEV=alp
 -O=/cgn21/USFTO.spool/US09240675/runat.30052000.165118.2984/app-query.fasta.1
 -DB=PIR_63 -QFMT=fastan -SUFFIX=modif.rpr -GAPOP=12.000
 -GAPEXT=4.000 -MINMATCH=0.100 -LOOP=0.000 -LOOPEXT=0.000
 -OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
 -DUPOP=6.000 -DELEX=7.000 -START=1 -MATRIX=blomsu62
 -TRAN=human40.cdi -LIST=45 -DOCALLIGN=200 -THR.SCORE=pct
 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09240675 -NCPU=6 -ICPU=3 -NO_XLPRY -WAIT
 -THREADS=1

Search information block:

Query: US-09-240-675-1
 Query length: 1343
 Database: PIR_63:
 Database sequences: 168808
 Database length: 58629743
 Search time (sec): 70.990000

Sequence	Score	Seq Len	Doc Len	Documentation
PIR2:A32694	2313.00	3450.13	6.3e-184	557 Interferon alpha/beta receptor
PIR2:S37387	1507.00	2230.45	4.1e-117	560 Interferon alpha receptor type
PIR2:A45283	1069.00	1578.08	8.6e-81	590 Interferon alpha/beta receptor
PIR2:G01418	233.50	341.31	1.4e-11	273 cytokine receptor family II, m
PIR2:A47003	228.50	332.33	3.8e-11	325 cytokine receptor family class
PIR2:J06311	221.50	331.29	1.5e-10	342 Interferon receptor class II cy
PIR2:AA9947	203.00	294.19	5.0e-09	339 Interferon gamma receptor beta
PIR2:118500	155.50	223.36	4.3e-05	337 Interferon gamma receptor acces
PIR2:T13822	129.00	171.56	0.0081	1375 frazzled gene protein - fruit
PIR2:T13823	129.00	170.64	0.0082	1526 frazzled gene protein, log 1sc
PIR2:150600	127.50	168.90	0.0109	1443 neogenin - chicken (fragment)
PIR2:A36080	127.00	168.53	0.0119	1383 insulin receptor precursor - h
PIR2:A31555	124.50	173.95	0.0168	489 Interferon gamma receptor precu
PIR2:S42167	123.50	162.90	0.0233	981 190K protein - human
PIR2:S31604	118.00	158.15	0.0634	1451 receptor-tyrosine kinase-B
PIR2:S49015	118.00	157.94	0.0636	1005 Interleukin-10 receptor - mouse
PIR2:AA9667	117.50	154.11	0.0731	1427 tumor suppressor - African cl
PIR2:T19121	117.50	153.19	0.0741	1585 probable protein-tyrosine-phos
PIR2:A48721	117.00	158.27	0.0749	817 titin, muscle - chicken (fragme
PIR2:A41517	111.00	153.72	0.0800	1372 insulin receptor precursor - m
PIR2:S45618	116.00	149.31	0.1011	1912 protein-tyrosine-phosphatase 0
PIR2:T16040	115.50	157.94	0.0970	658 hypothetical protein F12A10.4 -
PIR2:AA4037	115.00	150.25	0.1181	1450 165K myofibrillar M-band struc
PIR1:138344	113.00	124.56	0.1715	26926 titin, cardiac muscle - human
PIR1:0C4166	113.50	152.41	0.1475	880 protein-tyrosine kinase (EC 2.7
PIR2:BA9502	113.00	146.33	0.1754	1615 protein-tyrosine-phosphatase 0
PIR2:S46216	113.00	145.54	0.1774	1767 leukocyte antigen-related prot
PIR2:T77934	113.00	133.65	0.2109	6831 hypothetical protein ZK617.1a
PIR2:S57242	113.00	133.64	0.2109	6839 vitchin - Caenorhabditis eleg
PIR2:T27935	111.50	133.23	0.2121	7160 Down syndrome cell adhesion p
PIR2:700851	109.00	152.30	0.3165	416 hypothetical protein T20F10.4 -
PIR2:158164	109.50	143.30	0.3908	1028 B6-1 protein - rat
PIR2:700348	108.50	137.61	0.4264	2033 hybrid receptor ScfLA precurs
PIR2:178843	108.00	136.85	0.4311	2215 IL11 protein - mouse
PIR1:1NH0R	108.00	143.18	0.4280	991 receptor protein-tyrosine kinas
PIR2:S51603	107.50	140.26	0.4465	1382 insulin receptor precursor - h
PIR2:156215	107.00	146.43	0.4835	578 interleukin-10 receptor - human

PIR2:AA4147 + 107.00 140.85 0.5244 1091 calcium channel protein
 PIR2:S47489 + 106.50 141.81 0.5627 898 receptor tyrosine kinase
 PIR2:AA4100 + 106.00 136.88 0.6580 1447 tumor suppressor protein
 PIR1:AA0091 + 105.50 140.52 0.6791 878 interleukin-3 receptor b

seq_name: PIR2:A32694

seq_documentation_block:

Interferon alpha/beta receptor precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 22-Jun-1990 #sequence, revision 22-Jun-1990 #text_change 22-Oct-1999
 C:Accession: A32694; S17112
 R:Oze, G.; Lufalla, G.; Gresser, I.
 Cell 60, 225-234, 1990
 A:Title: Genetic transfer of a functional human interferon alpha receptor into mo
 A:Reference number: A32694; MID:90124632
 A:Accession: A32694
 A:Molecule type: mRNA
 A:Residues: 1-557 <OZE>
 A:Cross-references: GB:J03171; NID:q184645; PIDN:AAA52730.1; PID:q306914
 R:Lufalla, G.
 Submitted to the EMBL Data Library, July 1991
 A:Description: The structure of the human interferon alpha/beta receptor gene.
 A:Reference number: S17112
 A:Accession: S17112
 A:Molecule type: DNA
 A:Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUT>
 A:Cross-references: EMBL:X60459; NID:q32671
 C:Genetics:
 A:Gene: GDB:IFNAR1; IFNAR; IFNC
 A:Cross-references: GDB:120078; OMIM:107450
 A:Map position: 21q22.1-21q22.1
 A:Intons: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
 C:Keywords: cytokine receptor; glycoprotein; transmembrane protein
 F.1-21/Domain: transmembrane status predicted <TRN2>
 F.37/45/Domain: transmembrane status predicted <TRN2>
 F.50/58, 81, 88, 110, 172, 254, 313, 314, 376, 416, 433, 507, 518, 537/Binding site: carbohydrate

alignment_scores:

Quality: 2313.00 Length: 436
 Ratio: 5.305 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

align_block:
 US-09-240-675-1 x A32694

Align seg 1/1 to: A32694 from: 1 to: 557

27 ATGATGTCCTCTCTCGGCGGAGACCTTAGTGTCTGCGCGGG 76
 1 Metcervallaleuenglyalathrthleuvalleuvalalvalgl 17
 77 CCATGGGTGTTCGCGACCGCAGGTGAAAAATCTAAATCTCTTC 126
 17 YPOTRPVallleuseralalalacglylsasnlleuylserpro 34
 127 AAAAGAGAGCGTCACATCATGAGACACTTATCTGAGGTGAC 176
 34 Inlysalgluvalalpilelleaspaspasnhelleuagtrpasp 50
 177 AGAGGAGTACGTCGCGGATGTGACTTTTCATGATGATGAAAA 226
 51 Argseraspjuseralglglsanvalthrpheserphespyglndly 67
 227 AACTGGAGTGAATATGATATAAATGTCTGGGTGTCAGAAATACAA 276
 67 strnglymetaspasntripileylserserglycslndsllethrs 84
 277 GTACAAAGGCACTTCTCCTACCTAACCTGAATTTTGAAGAAAT 326
 84 ethrlyscysasnpheserleuylsleuasnvaltryglndly 100

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327 AAATGCGTATAGAGCAGAGAAAAGAACTCTTCATGATGAGT 376
101 Lysleuagllleuaglaellulysellunthrserttrpygluac 117
377 TGACTCATTTACACATTTGCGAAAGCTCAGATGGTCTCCAGAGTAC 426
117 lnsperpethrprophedargylsalallleghlproprogluvalh 134
427 ATTGAGACCTGAGATAGGCAATAGATACATCTCTCTGAGACA 476
134 lseuclulagllunsplysalallleghlserprogluylth 150
477 AAGATAGTATGATGGCTTGGATGGTTAAGCTTACATATAGCT 526
151 LysaspservalmettrpalauehspglyleuSerPherthtyserie 167
527 ACTTATCTGGAAGAACTCTTCAGCTGATAGAGAAAGATGAAATATT 576
167 uleuiletrplysasnserSerGlyalglugluargilegluaslllet 184
577 ATTCGAGATATAAATTTTAACTCTCAGCAGAGACTCTATTTGCTTA 626
184 ysertrghslusylletrLysleuSerProglunthrtthtyrCysleu 200
627 AAGTTAAAGCAGACACTTACGTCATGAGAAATGGTGTATAGTCC 676
201 Lysvallyalalaleuenuhrsertrpyslllecllyaltrsertr 217
677 AGTACATTTGATTAAGACACACACTTGAATGAATGAACTCCACAGAAA 726
217 ovalhscyslllelysthrthvalglunsgluleuproprogluA 234
727 ATTTAAGCTGCTGCCAAACACACACATCTCTTAAAGGATTTT 776
234 snllelualservalglunsglunsnryvalleuylstrpasytr 250
777 ACATATGCAACATGACCTTCAAGTCAAGTGGCTCCAGCCCTTTTAA 826
251 Thrtyralasnmetthrphelglunlntprleuhsalshelueuyl 267
827 AAGCAATCTCGAAGACCATTTGATTAAGGAAACAAATACCTGACTGG 876
267 sargasnprogllyasnhsleuylrlystrpysglulleproaspcysg 284
877 AAAATGCAAACTACCCAGCTGTCTCTTCCAAAAGCTTCCAAAA 926
284 lunsbnvallysthrthglncysvalphetproglunsnvalphelglu 300
927 GGAATTTACCTCTCCGCGTACAGCATGTGATGAAATACACATCTT 976
301 Glyiletyrleuenuargvalglunlaserapgllyasnbnphserph 317
977 TTGGCTGAGAGATTAAGTTGATGATGAAATACAGCTTCTTCCTTC 1026
317 etrpserglglullellyspheasprthglulleglunlaphelenu 334
1027 CTCAGCTTACATAGATCCCTTGTGATTCATCCATATCTATATC 1076
334 roprovalpheasnllleatrgserleuSerphelhsllletryle 350
1077 GGTGCTCCAAAACAGTCTGGAACACGCTGTGATCCAGGATATTCAC 1126
351 Glyalafrolysglnsergllyasnthtrprovalilleglunsplyrprole 367
1127 GATTATGAATTAATTTTGGGAAAAACATTCATTCGAGAGAAAA 1176
367 uilletyrghullellephetrglunsnthrsasnallagluargyls 384
1177 TTATCGAGAAAAAATGATGATTCATCTCTATTTGAACACCTACT 1226
384 lelleglulyslysthrasphalthrvalproasnleuylsproleuht 400
1227 GTATATTTGTGTGAAGCAGACACACACATGATGATGAAAAAGCTGAATA 1276

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401 ValtyrCysvallysalalargalalehlsrmetasprglulysleuasnly 417
1277 AAGCAGGCTTTTGTAGCAGCTGTATGTGAGAAAACAAACCGGAAATA 1326
417 sserSerValpheserasnpralalvalCysglulyslthlysthrproglunsn 434
1327 CCTCTAAA 1334
434 hrserlys 436
seq_name: pl12:527387

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seq_documentation_block:
  Interferon alpha receptor type 1 precursor - bovine
  C:Species: Bos primigenius taurus (cattle)
  C:Date: 13-Jan-1995 #sequence, revision 13-Jan-1995 #text, change 05-Nov-1999
  C:Accession: S27387, S33770
  R:Mouchel-Viehl, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
  FEBS Lett. 313, 255-259, 1992
  A:Title: Specific antiviral activities of the human alpha interferons are determined
  A:Reference number: S27387, MIMD:93076908
  A:Accession: S27387
  A:Status: preliminary; nucleic acid sequence not shown
  A:Molecule type: mRNA
  A:Residues: 1-560 <MOL>
  A:Cross-references: EMBL:X68443; NID:9431; PIRN:CAA48484.1; PID:9432
  R:Lum, J.K.; Langer, J.A.
  Blochim. Biophys. Acta 1173, 314-319, 1993
  A:Title: Cloning and characterization of a bovine alpha interferon receptor.
  A:Reference number: S33770, MIMD:93305725
  A:Accession: S33770
  A:Status: preliminary; nucleic acid sequence not shown
  A:Molecule type: mRNA
  A:Residues: 1-421, V, 423-560 <LINK>
  A:Cross-references: EMBL:L06320; NID:9163187; PIRN:AAA02571.1; PID:9163188
  A:Experimental source: lung
  A:Keywords: antiviral; cytokine receptor; transmembrane protein
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  F:25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>

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alignment_scores:
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alignment_block:
  US-09-240-675-1 x S27387

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1 MetleuAlaleuLenglyAlalThrthreuleuValala..GlyAr 16
80 ATGGGCTGTGCGCGACGCGCGAGTGAAGAAAATATAATCTCTCAAA 129
|||||
16 gtrpvalleuproalalasergllyglunlasnleuys..Proglua 32
130 AAGTAGAGTCACATCATATGACACAACTTATTCCTGAGGTGAGAG 179
|||||
32 snvalglullehsllelleaspaapnphelenuylstrpsnser 48
180 AGCGATGATCTGTGGGAGATGATGCTTTTCATTCGATTCAGAAAAAC 229
|||||
49 SerSerGlnSerVallylsasnvalthrpheserAlalasnpryglulle 65
230 TGGGATGATTAATTTGATTAATTTGCTGGGTGTCAGATATATAGTA 279
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65 uelgthrarnpanttrpyslyleuSerGlycyslnhsllethrsert 82

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280 CCAATGCACTTTCTTCACCAAGCTG...AATGTTATGAAAGAAAT 326
82 hLysCysaspSerSerValGluLeuGluValPheIleuLysIle 98
327 AATTCGCGATATAGACAGAAAA...GAAACACTCTTCAAGTATGA 373
99 GluLeuArgIleArgIleGluGluGluGluGluGluGluGluGlu 115
374 GGTGACGATATATACACATTCGCAAGCTGAGATGGTCCGCAAG 423
115 uValGluProPheValProPheLeuGluLeuGluGluGluGluGlu 132
424 TACATTAAGCTGAAAGATGCAATGCAATGATACACTCT...CCT 470
132 AHisLeuGluValGluValGluValGluValGluValGluValGlu 148
471 GGAACAAAGATAGTGTATGAGGCTTGAAGTGAAGTGAAGTGAAG 520
149 GlyThrLysAspSerIleLeuThrPalaMetLysAspSerSerPhe 165
521 TAGCTTACTATCTGAAAAAAGCTTCAAGCTGAGTGAAGAAAGAT 570
165 rSerValValIleThrLysAspSerSerSerLeuGluGluGluGlu 182
571 AATTTATCCAGACATAAATTTATTAAGCTCTCACACAGACTCTAT 620
182 hValIleProGluValLysIleLysIleLysIleLysIleLysIle 198
621 TGTCTAAAGTAAAGCACTACTTACCTATGCAATGAAATGCTGTGA 670
199 CysLeuLysValLysIleLeuLeuLeuLeuLeuLeuLeuLeuLeu 215
671 TAGTCCAGTACATGTTATTAAGACCAAGCTGAAAAAGTACCTCAC 720
215 rSerProValIleLysCysIleAsnThrThrGluArgIleLysVal 232
721 CAGAAATATAGAGCACTGTCGCAAAACAGAACATATCTTTAAAG 770
232 rGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 248
771 GATTATACATATGCAACATGACCTTCAAGTCAAGTGGCTCCAGCCT 820
249 AspTyrProTyrGluAsnAlaThrPheGluGluGluGluGluGlu 265
821 TTTTAAAGGAATCTGGAACCACTTGTATTAATGGAACCAATACCTG 870
265 rPheLysIleProGluGluGluGluGluGluGluGluGluGluGlu 282
871 ACTGGAATATGCAAACTACCAAGCTGCTTCCCAAAAGCTTTTC 920
282 rSerGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 298
921 CAAAAAGAAATTTACCTCTCCGCGTACAAAGCTGATGAAATACAC 970
299 SerArgGlyIleTyrTyrValArgValArgAlaSerAsnGlyAsn 315
971 ATCTTTTGGTGTGAAGGATTAAGTTGAACTGAATACAAAGCTTCC 1020
315 rSerPheThrPheSerGluGluGluGluGluGluGluGluGluGlu 332
1021 TACTTCCGCAAGCTTTTAACTAGTACCTTACCT...GATCATCTCA 1067
332 rPheProProValIleSerValLysSerValThrAspAspSerLeu 1348
1068 ATCTATATCGGTCTCCAAACAGTCTGGAACAGCTGATGATCAGGA 1117
349 ValSerValGlyAlaSerGluGluGluGluGluGluGluGluGlu 365
1118 TTATCAGCTGATTTATGAATATTTTGGAAAAAAGCTTCAATGCTG 1167
365 uTyrProLeuIleTyrGluValIlePheThrPheGluGluGluGlu 382
1168 AGAGAAAAATATATGAGAAAAAAAGTGAATGTTACAGTTCCTAA 1217

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382 uValGluValLeuGluLysArgThrAsnPheIlePheProAspLeuLys 398
1218 CCAGTACGATATATGTTGGAAGCCGAGACACACACAGATGATGAAA 1267
399 ProLeuThrValTyrCysValLysAlaArgAlaLeuIleGluAsnAsp 415
1268 GCTGATATAAGCAAGTGTATGAGCTGATGATGAGAAACAAAC 1317
415 rArgAsnLysGlySerSerPheSerAspThrValCysLysIleThrLys 432
1318 CAGCAATATCTCTTAA 1334
432 rGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu
seq_name: p1r2:A45283
seq_documentation_block:
Interferon alpha/beta receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Mar-1993 #sequence revision 18-Nov-1994 #text change 05-Nov-1999
C:Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429
R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992.
A:Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in
A:Reference number: A45283; M01D:92262522
A:Accession: A45283
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-590 <UZE>
A:Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1; PID:g194112
A:Note: sequence extracted from NCBI backbone (NCBIN:102354; NCBIPI:102357)
R:Lutfalla, G.; Uze, G.
Gene 148, 343-346, 1994.
A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: hL
A:Reference number: I48423; M01D:95047447
A:Accession: I48423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
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A:Accession: I48424
A:Status: preliminary; translated from GB/EMBL/DBJ
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A:Residues: 127-224 <RE2>
A:Cross-references: EMBL:006238; NID:g497104; PIDN:AA01749.1; PID:g755811
A:Accession: I48425
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
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A:Accession: I48426
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 265-375 <RB4>
A:Cross-references: EMBL:006240; NID:g497108; PIDN:AAA65005.1; PID:g510262
A:Accession: I48427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 397-424 <RE5>
A:Cross-references: EMBL:006241; NID:g497110; PIDN:AAA65006.1; PID:g755812
A:Accession: I48428
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 426-445 <RE6>
A:Cross-references: EMBL:006242; NID:g497112; PIDN:AAA65007.1; PID:g755813
A:Accession: I48429
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 473-590 <RE7>
A:Cross-references: EMBL:006244; NID:g497114; PIDN:AAA65008.1; PID:g510265
C:Genetic:
A:Gene: IFNAR

```

A: Introns: 177/3: 331/1
 C: Keywords: cytokine receptor; transmembrane protein

Alignment scores:
 Quality: 1069.00 Length: 436
 Ratio: 3.230 Gaps: 4
 Percent Similarity: 75.917 Percent Identity: 48.624

Alignment block:
 US-09-240-675-1 x AA5283

Align seg 1/1 to: AA5283 from: 1 to: 590

```

30 ATGGTCGCTCTCTGGCGCGACGACCTAGCTCTGCGCGCGCCGCCC 79
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 MetLeuAlaValAlaGlyAlaAlaLeuValLeuValAlaGlyAlaLys 17
80 ATGGGCTGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
17 CTPValLeuProSerAlaGlyGlyGlnLeuLysProProGln 34
130 AAGTAGAGCGCATCATGATGATGATGATGATGATGATGATGATGAT 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
34 snleAspValIleIleIleAspAsnIleIleLysIleLysIleSer 50
180 AGCGAGAGCTGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 229
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
51 HleGlyLysSerMetGlySerValIlePheSerAlaGlyIleIle 67
230 TGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 279
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
67 sAspGlnAlaLysIleLysIleValIleProGlnCysGlnHisIle 84
280 CCAATGCACTTTCTTCACTCACTCACTCACTCACTCACTCACTCA 329
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
84 hIysCysGlnPheSerLeuLeuAspIleAsnValIleIleLysIle 100
101 PheArgValArgAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 117
377 TGACTCATTCACCATTCGCAAGCTGATGATGATGATGATGATGAT 426
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
117 LAspProPheIleProPheIleIleIleIleIleIleIleIleIle 134
427 ATTAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 476
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
134 rGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 150
477 AAGATAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 526
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
151 GlnAspGlnAsnMetIleIleGlnGlnGlnGlnGlnGlnGlnGln 167
527 ACTATGCGGAAAGCTTCAGCTGATGATGATGATGATGATGATGAT 576
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
167 eArgIleIlePheIleLysSerSerAspLysIleIleAsnSerIle 184
577 ATTCAGACATGATGATGATGATGATGATGATGATGATGATGATGAT 626
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
184 yIleIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 200
627 AAGTTAAGCAGACATCTAGCTGATGATGATGATGATGATGATGAT 676
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
201 GlnValLysAlaIleIleIleIleIleIleIleIleIleIleIle 217
677 AGTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 726
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
217 rValGlnCysIleSerIleIleIleIleIleIleIleIleIleIle 234
727 ATATAGAGTCACTGATGATGATGATGATGATGATGATGATGATGAT 776
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
234 snLeuGlnValAspAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 250

```

```

777 .. ACATATGCAACATGACCTTTCAAGTTCAGTGGCTCCAGGCTTTT 823
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
251 IleAlaSerAlaAspValLeuPheArgAlaGlnIleIleProGlyIle 267
824 AAAAAGAACTCTGGAACCTTTGTATTAATGGAACAAATACCTGACT 873
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
267 rLysSerSerSerGlySerHisSerAspLysIleIleProIleProHis 284
874 GTGAATATGTAACAACTACCGAGTGTCTTCTCTCAAAAGCTTTCCA 923
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
284 yAlaAsnValGlnIleIleIleIleIleIleIleIleIleIleIle 300
924 AAGGAATTTACCTTCCGCGTACCAAGCATCTGATGATGATGATGAT 973
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
301 ThrGlyIleIlePheIleLeuHisValGlnAlaSerGlnGlnHisIle 317
974 TTTTGTCTGAGAGATGATGATGATGATGATGATGATGATGATGAT 1023
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
317 rPheIlePheIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 334
1024 TTCTCCAGCTTTTACATTCATGATGATGATGATGATGATGATGAT 1073
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
334 rProProValIleIleIleIleIleIleIleIleIleIleIleIle 350
1074 ATCGGTCCTCCAAACAGCTGGAACAGCGCTGATCCAGATATTC 1123
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
351 ValAsnCysGlnAspSerIleCysAsp.....G1 360
1124 ACTGATTTATGAAATTTTGGGAAACACTTCAATGCTGAGAGA 1173
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
360 yLeuAsnIleGlnIleIleIleIleIleIleIleIleIleIleIle 377
1174 AATATTCGAGAAAACAGCTGATGATGATGATGATGATGATGATGAT 1223
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
377 eMetGlnLysAspGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 393
1224 ACTGATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1273
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
394 ThrValIleCysValGlnAlaIleVal...LeuPheArgAlaLeuLeu 409
1274 TAAACAGCTGTTTATGATGATGATGATGATGATGATGATGATGAT 1323
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
409 nLysIleIleIleIleIleIleIleIleIleIleIleIleIleIle 426
1324 ATACCTCT 1331
426 ePheSer 428
seq_name: pir2:G01418

```

seq_documentation_block:
 cytokine receptor family II, member 4 - human
 C: Species: Homo sapiens (man)
 C: Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
 C: Accession: G01418
 R: Unifaila, G
 submitted to the EMBL Data Library, April 1994
 A: Reference number: G06935
 A: Accession: G01418
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 A: Residues: 1-273 <LUD>
 A: Cross-references: EMBL: U08988; NID: 9571295; PID: 9571296
 C: Genes:
 A: Gene: GDB: CRFB4; CRF2-4
 A: Cross-references: GDB: 138168; OMTM: 123889
 A: Map position: 21q22.1-21q22.2
 A: Introns: 17/1, 58/2, 111/1, 166/3, 216/1

alignment_scores: Quality: 233.50 Length: 224

Ratio: 1.704
Percent Similarity: 61.161 Percent Identity: 29.911

Alignment block:
US-09-240-675-1 x G01418

Align seg 1/1 to: G01418 from: 1 to: 273

```

81 TGGGTGTTGTCGCCAGCCGCGAGTGGAAAAATCTAAATCT..... 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
3 TrpserLeuGlySerTrpLeuGlyGlyCysLeuValSerAlaLeuG1 19
123 ..... CCTCAAAAGTAGAGGTGACATCATATGACAACT 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
19 yMeValProProGluAsnValArgMetAsnSerValAsnRheYSA 36
160 TTATCTGAGGTGGACAGAGCATGAGTCTGTGGGATGTGACTTTT 209
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
36 snlleuGlnTrpGluSerProAlaRheAlaYsglyAsnLeuTrpHe 52
210 TCATTCGATTATCAAAAACTGGAGTGAATATTGGATAAATGCTGG 259
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
53 ThrAlaGlnTrp..... LeuSerTrpArgIleRheGlnAspLy 65
260 GTGCAGAAATTTACTAGTACCAATGCAATTTTCTCAGTCAAGTGA 309
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
65 sCyMetAsnTrpThrLeuThrGluCysAspRheSer..... LeuS 80
310 ATGTTATGAGAAATTAATTGCGTATTAAGCAGAA... AAAGAAAC 356
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
80 eTrpYsTrpGlyAspRheThrLeuArgValAlaGlnRheAlaAspGlu 96
357 ACTTCTCAAGTATGAGAGTGTGACTATTACACCAATTTGCGAAAGTCA 406
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
97 HisSerAspTrpValAsnIle... ThrRheCysProValAspAspTrpI1 112
407 GATTGGTCCGCGAGAGTACATTTAGAAAGCGAAGATTAAGGCATAGTGA 456
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
112 eIleGlyProProGluMetGlnValGluValLeuAspRheLeuIsm 129
457 TACAC... ATCTCTCTGGAACAAAGATAGTGT... ATGTGGGCTTGG 500
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
129 eTrpRheLeuAlaRProGlyAlleGluAsnGlnTrpGluTrpTrpMet 145
501 GATGGTTA... ACCTTACATAGCTTACTTATCTGAAAAATC 544
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
146 LyAsnValIlyAsnSerTrpTrpIlyAsnValGlnTrpRlyAsnG1 162
545 TTCAGGTGTAGAAAGATGAAATTAATTATTCAGACATTAATTT 594
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
162 yThrAspGluLysRheGlnIleThrProGlnIlyAspRheGlnValLeuA 179
595 ATAAACTCTCAGCAGACTACTATTGTCTAAAGTTAAAGCAGACTA 644
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
179 rGAsnLeuGlnProTrpTrpTrpIlyTrpCysValGlnValAlaGlnRheLeu 195
645 CTTACGTCATGAGAAATTTGGTGTCTATAGTCCAGTACATGTATTAAGAC 694
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
196 ProAspTrpAsnIlyAsnIlyGlnIlyTrpSerGluProValCysGlnGlnTrh 212
695 CACAGTTGAAATGAGACTACT 716
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
212 yThrHisAspGluTrpValPro 219

```

seq_name: p1r2:A47003

seq_documentation_block:

Cytochrome receptor family class II protein CR2-4 precursor - human

C:Species: Homo sapiens (man)

C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1997

C:Accession: A47003

R:Infitalia, G: Gardiner, K: Use, G.

Genomic: 16, 366-373, 1993

A:Title: A new member of the cytochrome receptor gene family maps on chromosome 21 a
A:Reference number: A47003; MID:93300510
A:Accession: A47003
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1325 (LUT)
A:Cross-references: GB:Z17227; MID:9393378; PID:9393379
C:Genetics:
A:Map position: 21q
C:Keywords: transmembrane protein

alignment_scores:

Quality: 228.50 Length: 224
Ratio: 1.693 Gaps: 8
Percent Similarity: 60.268 Percent Identity: 29.911

alignment_block:
US-09-240-675-1 x A47003

Align seg 1/1 to: A47003 from: 1 to: 325

```

81 TGGGTGTTGTCGCCAGCCGCGAGTGGAAAAATCTAAATCT..... 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
3 TrpserLeuGlySerTrpLeuGlyGlyCysLeuValSerAlaLeuG1 19
123 ..... CCTCAAAAGTAGAGGTGACATCATATGACAACT 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
19 yMeValProProGluAsnValArgMetAsnSerValAsnRheYSA 36
160 TTATCTGAGGTGGACAGAGCATGAGTCTGTGGGATGTGACTTTT 209
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
36 snlleuGlnTrpGluSerProAlaRheAlaYsglyAsnLeuTrpHe 52
210 TCATTCGATTATCAAAAACTGGAGTGAATATTGGATAAATGCTGG 259
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
53 ThrAlaGlnTrp..... LeuSerTrpArgIleRheGlnAspLy 65
260 GTGCAGAAATTTACTAGTACCAATGCAATTTTCTCAGTCAAGTGA 309
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
65 sCyMetAsnTrpThrLeuThrGluCysAspRheSer..... LeuS 80
310 ATGTTATGAGAAATTAATTGCGTATTAAGCAGAA... AAAGAAAC 356
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
80 eTrpYsTrpGlyAspRheThrLeuArgValAlaGlnRheAlaAspGlu 96
357 ACTTCTCAAGTATGAGAGTGTGACTATTACACCAATTTGCGAAAGTCA 406
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
97 HisSerAspTrpValAsnIle... ThrRheCysProValAspAspTrpI1 112
407 GATTGGTCCGCGAGAGTACATTTAGAAAGCGAAGATTAAGGCATAGTGA 453
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
112 eIleGlyProProGluMetGlnValGluValLeuAspRheLeuIsm 129
454 TGAATACATCTCTCTGGAACAAAGATAGTGT... ATGTGGGCTTGG 500
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
129 eTrpRheLeuAlaRProGlyAlleGluAsnGlnTrpGluTrpTrpMet 145
501 GATGGTTA... ACCTTACATAGCTTACTTATCTGAAAAATC 544
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
146 LyAsnValIlyAsnSerTrpTrpIlyAsnValGlnTrpRlyAsnG1 162
545 TTCAGGTGTAGAAAGATGAAATTAATTATTCAGACATTAATTT 594
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
162 yThrAspGluLysRheGlnIleThrProGlnIlyAspRheGlnValLeuA 179
595 ATAAACTCTCAGCAGACTACTATTGTCTAAAGTTAAAGCAGACTA 644
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
179 rGAsnLeuGlnProTrpTrpTrpIlyTrpCysValGlnValAlaGlnRheLeu 195
645 CTTACGTCATGAGAAATTTGGTGTCTATAGTCCAGTACATGTATTAAGAC 694
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
196 ProAspTrpAsnIlyAsnIlyGlnIlyTrpSerGluProValCysGlnGlnTrh 212

```

695 CACAGTGAATAAGACTACT 716
 212 rthrlhlsaspqlurthralpro 219

seq_name: p1r2:JC6311

seq_documentation_block:

Interferon receptor class II cytokine receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: J06311

R:Gibbs, V.C.; Pennica, D.

Gene 186, 97-101, 1997

A:Title: CRF-4: isolation of cDNA clones encoding the human and mouse proteins.

A:Reference number: J06311

A:Accession: J06311

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-349 <GIB>

A:Cross-references: GB:U53696

alignment_scores:

Quality	Ratio	Length	Gaps
221.50	1.582	228	10
Percent Similarity: 61.404	Percent Identity: 28.070		

alignment_block:

US-09-240-675-1 x JC6311

Align seg 1/1 to: JC6311 from: 1 to: 349

```

72 GTGGCCCATGGGTGTTCGCCGACCCGAGTGAATAATCTAATC 121
   |||||
9  LeuGlyGlyPheLeuLeuValProAlaLeuGly...MetIleProPr 23
122 TCCTCAAAAGTAGAGTCGACATCATAGTACCACTTATCCGAGT 171
   |||||
23 OProGluValArgMetLysSerValAsnIleLeuGlnT 40
172 GGAACAGAGCGATGAGTCGTGCGGAATGACCTTTTCATCGATT 221
   |||||
40 IProIValProAlaPheProLysThrAsnLeuThrPheThrAlaGlnTyr 56
222 CAA...AAACTGGATGATTAATTCGATTAATTCGCGGTGCA 265
   |||||
57 GluSerTyrArgSerPheGlnAspHis...CysIy 67
266 GAATATTTACTAGTACCAATGCACTTTCTTCACCAAGCTGAGTGT 315
   |||||
67 SarThrAlaSerThrGlnCysAspPheSer...HisLeuSerLysT 82
316 ATGAGCAAAATTAATGCGTATAGAGCAAA...AAAGAAAACACTTCT 362
   |||||
82 YrGlyAspPyrThrValArgValArgAlaGlnLeuAlaAspGlnHisSer 98
363 TCATGATGATGAGTGTGACTATTACCACTTTTCGAAAAGCTCAGATT 412
   |||||
99 GluTrpValAsnVal...ThrPheCysProValGlnAspThrIleIleG 114
413 TCCTCCAGAGTACATTAGAACCTGAAGCAATAGTATGATCACA 462
   |||||
114 YProProGluMetGlnIleGlnSerLeuAlaGlnSerLeuGlnLeuArg 131
463 TCCTCT...CTGGAACAAGATAGTACTGTTATG 491
   |||||
131 HeSerAlaProGlnIleGlnAsnGlnProGlnThr... 142
492 TGGGCTTGGATGATGTTA...ACCTTACATATAGCTTACTATCTG 355
   |||||
143 TrpThrLeuLysAsnIleTyrAspSerTyrPalaTyrValGlnTyrTr 159

```

seq_name: p1r2:A49947

seq_documentation_block:

Interferon gamma receptor beta subunit - mouse

N:Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor; ty

C:Species: Mus musculus (house mouse)

C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C:Accession: A49947

R:Hemmi, S.; Bohm, R.; Stark, G.; Di Marco, F.; Aguet, M.

Cell 76, 803-810, 1994.

A:Title: A novel member of the interferon receptor family complements functionality

A:Reference number: A49947; MUID:9417081

A:Accession: A49947

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-332 <HEMM>

A:Cross-references: GB:S69336; NID:9545841; PIDN:AA830165.1; PID:9545842

A:Experimental source: early B-cell line Y16

A:Note: sequence extracted from NCBI backbone (NCBI:145654, NCBI:145656)

C:Keywords: cytokine receptor

alignment_scores:

Quality	Ratio	Length	Gaps
203.00	1.471	229	13
Percent Similarity: 60.262	Percent Identity: 30.131		

alignment_block:

US-09-240-675-1 x A49947

Align seg 1/1 to: A49947 from: 1 to: 332

```

87 TTGTCGCGAGCGCGAGTGA...AAAAATCTAATAATCTCC 124
   |||||
16 LeuGlyAlaAlaLysSerProAspSerPheSerGlnLeuAlaLysPr 32
125 TCATAAATAGAGTGCACATCATAGTACAACTTTATCTCGAGGGA 174
   |||||
32 OLeuAsnProAlaGlnLeuHisLeuTyrAsnAspGlnGlnIleLeuThrPr 49
175 ACAGAGGAGTGAAGTCT...GTGCGGAATGAGTCT 206
   |||||
49 LuroSerProSerSerAsnAspProAlaGlyProValValTyrGlnValGlu 65
207 TTTTCATTCGATTATCAAAAACTGGGATGAT...AATTCGATTAAT 253
   |||||
66 TyrSerPhe...IleAspGlySerThrPheAspGly 76
254 G...TCGGGTGTCGAATATATACAGTACCAAAATGCAACTTTCT 297
   |||||
76 LLeuGlnProAsnGlnCysThrAspIleThrGlnThrLysCysAspLeuThr 93
298 CA...CTCAAGCTGAATGTTATGAA...GAATTAATATTCGCT 335
   |||||
93 YrGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeuGly 109
336 ATTAGAGCAGAAAAAGAAAC...ACTTCTTCATGATGATGAGTTGACTC 382

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110 VALATPAllySAr9eLysnLeuThrSerLysTrpValGlyLeuGlyP 126
383 ATTTACACCATTTTCGCAAGCTCAGATTGGTCTCCAGAA...GTACATT 429
126 oPhEgInHsTrGlyAsnValThrValGlyProProlYsAsnIleSerY 143
430 TGAACCTGAAATGAAGCAATGATACATCTCTCTGGAACAAA 479
143 aLThrProGlyLysGlySerLeuValIleHisPheSerProPheAsp 159
480 GATAGGTATATGGGCTTGGATTGATTAGCTTACATATAGCTTACT 529
160 .....ValPheHisGlyAlaThrPheGlnTrpLeuValH 171
530 TATCTGAAAAACTCTTCAGGTGTAGAGAAAGATTGAAATATTATT 579
171 sTrYTrpGlyLysSerGlnThrGlnGlnGlnValGlyGlyProPhe 188
580 CCAGACATATAATTAT.....AACTCTCAGCAGAGCTACTTATTGT 623
188 ySerHisSerIleValLeuGlyAsnLeuLysProTrpAlaGlyValTr 204
624 CTAAAGTTAAAGCAGACACTA...CTTACGTCTAGGAAATT..... 662
205 LeuGlnThrGlnAlaGlnLeuIleLeuLysAsnLysLysIleArgPro 221
663 :GGTGTATAGTCCAGTACTGATTGATTAAGACCA 698
221 sGlyLeuLeuSerAsnValSerCysHisGlnThr 233

```

seq_name: p1r2:138500

seq_documentation_block:

Interferon gamma receptor accessory factor-1 precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 05-Nov-1999
 C:Accession: I38500; I38501
 R:Sch, J.; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S.
 Cell 76, 793-802, 1994
 A:Title: Identification and sequence of an accessory factor required for activation of
 A:Reference number: A49946; MIMD:94170380
 A:Accession: I38500
 A:Molecule type: mRNA
 A:Residues: 1-337 <RES>
 A:Cross-references: EMBL:U05875; NID:9463549; PIDN:AA16955.1; PID:9463550
 A:Experimental source: clone pK1
 A:Accession: I38501
 A:Molecule type: mRNA
 A:Residues: 1-63, Q, 65-337 <RES>
 A:Cross-references: EMBL:U05877; NID:9463551; PIDN:AA16956.1; PID:9463552
 A:Experimental source: clone pJ53
 C:Genetics:
 A:Map position: 21
 C:Keywords: cytokine receptor

alignment_scores:
 Quality: 155.50 Length: 300
 Ratio: 1.030 Gaps: 14
 Percent Similarity: 50.333 Percent Identity: 22.333

alignment_block:
 US-09-240-675-1 x I38500

Align seg 1/1 to: I38500 from: 1 to: 337

```

60 GTGCTGTCGCGCGGCGCCATGGGTGTGTCGCGAGCGCGAGGTGA...107
9 LeuLeuLeuLeuGlyValAlaPheAlaAlaAlaAlaAlaAlaProPhe 25
108 .....AAAAATCTAAATATCTCCCAAAAGTAAGGTGCATCATG 150

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25 ProlSerGlnLeuProAlaProGlnHisProLysIleArgLeuTrp 42
151 ATGACAACTTTATCTGAGGTGG.....AACGAGAC 182
42 snAlaGlnValLeuSerTrpGlyProValAlaLeuSerHisSerThr 58
183 GATGAGTCTGCGGGAATGTGACTTTTCATTCAGTATTAACAATAAG 232
59 ArgProValValTrpArgValGlnPheLysTrpThrAspSerLys... 73
233 GATGATTAATTGCAATAATTGCT.....GGGTGTC 264
74 .....TrpPheThrAlaAspIleMetSerIleGlyValaLysCys 87
265 AGAATATTACTGTACCAATGCAATCTTTCTCA..... 299
87 hGlnIleThrAlaThrGlnCysAspPheThrAlaAlaSerProSerAla 103
300 .....CTCAAGCTGAATGTTATGAGAAATTAATTAATTCGCTAAG 340
104 GlyPheProMetAspPheAsnVal.....ThrLeuAlaGlyLeuTr 116
341 AGCAGAAAAAGAAAAACT...TCTTCATGTATGAGGTGACTCATTTA 387
116 GAlaGlnLeuGlyAlaLeuHisSerAlaTrpAlaThrMetProTrpPhe 133
388 CACCAATTCGCAAGCTCAGATTGGTCTCCAGAAAGTACATTAGAA... 434
133 InHsTrpArgAsnValThrValGlyProGln...AsnIleGlnVal 148
435 .....GCTGAAGATAGCAATAGTATACATCATCTCTCGAACA 478
149 ThrProGlyGlnGlySerLeuIleLeuArgPheSerSerProPheAsp 165
479 AGATAGTGTATAGTGCGCTTGAGTGTGATGCTTACATATAGCTTAC 528
165 eAlaAspHisSerThrAlaPhe.....PheCysTrpTrpValH 178
529 TTATCTGAAAAACTCTTCAGCTGTAGAGAAAGATTGAAATATTATT 578
178 sTrYTrpGln.....LysGlyGlyIleGlnGlnValLysGlyProPhe 192
579 TCCAGACATATAATTAT.....AACTCTCAGCAGAGCTACTTATTG 622
193 ArgSerHisSerIleSerLeuAspAsnLeuLysProSerHisValTrpC 209
623 TCTAAAGTTAAGCAGCACTACTTACGCTA.....TGCAAA 660
209 sLeuGlnValGlnAlaGlnLeuLeuTrpAsnLysSerAsnIlePheArg 226
661 TTGGTGTCTAATGTCAGTACTTGTATTAAGCCACAGTTGAAATGAA 710
226 aLglnHisLeuSerAsnIleSerCysTrpGlnThrMetAlaAspAlaSer 242
711 CTACCTCCACCAAGAAATATAGAGTCAGTCTC..... 743
243 ThrGlnLeuGlnGlnValIleLeuIleSerValGlyThrPheSerLeu 259
744 .....CAAATCCAGACT 756
259 uSerValLeuAlaGlyAlaCysPhePheLeuValLeuLysTrpArgGly 276
757 ATGTCTTAATAGGATTATACATATCCAAACAGACCTTCAGTTCAG 806
276 euIleLysTrpTrpPheHisThrProProSerIleProlLeuGlnIle 292

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seq_name: p1r2:113822

seq_documentation_block:

frizzled gene protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T13822

R:Kolodziej, P.A.; Timpe, L.; Mitchell, K.J.; Goodman, C.S.; Fried, S.; Jan, L.Y.; Jan, Cell 87, 197-204, 1996
A:Title: Frazzled encodes a Drosophila member of the DCC immunoglobulin subfamily and is
A:Reference number: 217780
A:Accession: J13822
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1375 <COL>
A:Cross-references: EMBL:U71001; NID:91621114; PIR:91621115; PIR:AA047314.1
C:Genetics:
A:Gene: frazzled
A:Map position: 2
C:Function:
A:Description: may function in vivo as a receptor or component of a receptor mediating N

Alignment scores:
Quality: 129.00 Length: 622
Ratio: 0.542 Gaps: 22
Percent Similarity: 38.264 Percent Identity: 16.399

Alignment block:
US-09-240-675-1 x J13822

Align seg 1/1 to: J13822 from: 1 to: 1375

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147 GYGLYLYSPROLEUSPSEGLYLEUGLALARGLEUPROSERGLNP 463
125 TCAAAAGTAGAGTCGACATCATAGTACCACTTATC...CTGAGGT 171
463 GARGAPLEVALAGLILEVALYSSERARGPHEVALTHLEUSERT 480
172 GG..... 173
480 rpaValGluProLeuGlnAsnAlaGlyAspValValTyrThrValTyr 496
174 .....AACAGAGCGATGAGTCGTGGGAAATGCTTTTCAT 214
497 TYLYSMETASNSERGLARGLUGLILYSMETVALTHLYSSEHN 513
215 CGATTTCAAAACCTGGATGATATGATAAATGCTGGGTG 264
513 SARPARGLINCIVALASNILEGINSERLEUPROGLYARGTHYR 530
265 AGAATATTACTAGTACCAATGCACTTTCTCA..... 299
530 InPheArgValGluAlaAsnThrAsnPhelGlyAlaSerSerAla 546
300 ..CTGAGCTGATCTTTATGAAGAATAATGCGT..... 335
547 PROLEUGLVALSERTHRGLEUPROGLIVALASNILEAGLYPROPOAR 563
336 .....ATAAGAGCAGAAAAGAAAACACTTTCATG 369
563 GAAPRHEGLUGLYTURLARGSERHISLYSGILLETYVALLYSTRP 580
370 ATGAG..... 374
580 LUGLUPROTHRVALTHRASNGLYGLILEULYSTYRARGVALTYR 596
374 ..... 374
597 SERGLUASNPSERGYLAASPLEUTYRHLASPSERTHRALALUGL 613
375 .....GTGACACTTAA 387
613 VALVALLEUTHRGILEUARGPROHISTHRASPRTYVALILESERVAL 630
388 CACCATTTCCGAAAGCTCAGATTGCT..... 413
630 ALPROPEASNPARGSNGLYMETGLYAPRSERSEALAGLILEARGVAL 646
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663 VALTHRSERSESERSETHRVALHISITRGLUPROPROALGLUG 680
481 ATAGCTATGTGGCTTGATGTTAACTTACTTAACTTACTT 530
680 LUASPARGASNGLYGLINLETHRGLYTURLYSILEARGVALYLS... 695
531 ATCTGAAAACACTCTGAGGTAGACAAAGATGGAATATTATTTC 580
696 ..PHELYSAPRALPROGLINVALYLSERTHRPROALASNILE..Ar 710
581 CAGACATAAATTTATAAATCTCCACGAGACACTATTGCTTAAAG 630
710 GTYRHEGLILEUSERTASNLEUASPARGASNALAGLUTYRGLINVALYSI 727
631 TTAAGCAGCACTACT.....ACGTCATGGAAAT 662
727 LEALALEMETHRVALASNGLYSERGLYPROPHETHRGLUTRPSNARG 743
663 GGTGCTATAGTCCAGTACATTGTTAAAGACACAGTGAATGAACT 712
744 Ala.....AsnThrLeuGluAsnAspLe 751
713 ACCT..... 716
751 USPRLUTHRGINVALPROGLYSPROILETHRILESETHLENSIPROG 768
717 .....CCACCGAATAATAGAACTC 737
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785 LYSILE.....ArgAsnTyrValLeuGLYTRPGLYARGGLYILEPROAS 799
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771 .....GATTA 776
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777 ..ACATATGCAAAACATGACCTTTCAGTTCAGTGGCTCCAGCCCTTTTA 824
866 LEHMETSESESESERILEVALVALTYRTRIPLEASPTHMETLEU 882
825 AAAAGGAAT..... 833
883 ASNLYASASNGLNHISVALTHRASPASNARGHISTYRTHRVALSERTYRGL 899
834 .....CCTGGAACCATTTGTATAATGGAACAAATACCTGCTGAA 879
899 YLIEHRTGLYSERASNARGLYARGTYR.....HISA 910
880 ARGTCAAAACCTACCCAGTGTCTTCTCCAAAGCTTTCCAAAAGGA 929
910 SNTHRTHRSPLEUASNCYSMETILE..AsnAspLeuArgProAsnThr 925
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771 .....GATTAT..... 776
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776 ..... 776
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776 ..... 776
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1093 psermetSerValLeuasnSerThrTyrGlnasnValproValThrPro 1110
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neogenin - chicken (fragment)

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C:Species: Gallus gallus (chicken)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
C:Accession: 150600
R:Veiometer, J.; Kayem, J.F.; Roman, J.M.; Dreyer, W.J.
J. Cell Biol. 127, 2009-2020, 1994
A:Title: Neogenin, an avian cell surface protein expressed during terminal neuronal
A:Reference number: A55193; MUID:95105243
A:Accession: 150600
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1443 <VIE>
A:Cross-references: EMBL:U07644; NID:9641965; PID:9641966

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  137 GGTGACATCATAGACACATTATC...CTGAGGTGACAGC... 179
  432 lAlaThrLeuValSerThrArgPheIleArgLeuThrTrpArgThrPro 449
  180 ..ACGATGAGTCTGTCGGGAATGATGCTTTTCATTCATGATTAACAAA 227
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  466 GluGly.....IleasnArgGluArgValGluasn...Thrse 477
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  477 rArgProGlyGluThrGlnValMetIleGlnasnLeuMetProGluThr 494
  328 AATGCGATATAGACAGAAAAGAAAACCTTTCATGATGATGAGGT 377
  494 alTyrValPheArgValValAlaGlnasnLysHisGlyHisGlyGlu... 509
  378 GACTCATTTACACCATTTCCGAAAGCTCAGATTGCTCTCCAGAAATGAC 427
  510 ..SerSerAlaProleuLysValAlaThr.....GlnProGluValG 523
  428 TTAGAACCTGAGATAGGCAATAGCATAGTACATCTCTCCGAGACAA 477
  523 nleuProGlyProAlaProasnIleArgAlaTyrAlaGlySerProThrS 540
  478 AAGATAGCTATGCGGCTTG.....GAGGTTTAAGCTT 515
  540 erValThrValThrTrpIleuThrProleuSerGlyasnGlyGlnIleGln 556
  516 ACATATAGCTTACTTATCTGGAAGAACTCTCAGGTGTAGAGAAAGAT 565
  557 AsnTyrLysleuTyrTyrMetGlnLysGlyGlnAspSerGluGlnAsp 573
  566 TGAATAATTTATTCACAGACATTAATTTATTAACCTGCACCAAGACTA 615
  573 lAspValAlaGlyLeuSerTyrThrIleThrGlyLeuLysLysTyrTrp 590
  616 CTATATGCTAAAGTTAAAGCAGACACTTACCTATGAGAAATAGT 665
  590 lutySerPheArgValValAla.....TyrasnLysHisGlyProGly 604
  666 GCTATATGTCAGTACATTGTATTAAGACACAGTTGAAATGAACATACC 715

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605 ValSerThrGlnAspValValAlaGlnThrLeuSerAspValProSerAl 621
716 TCACACAGAAATATATAGAGTGTGTCACAAAT...CAGACTATGTC 762
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763 TTAATGGGATTTATCATATGCAAAACGACCTTCAAGTTCAGTGGCTC 812
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646 ...GlyThrHisSerGlyGlnIleThrG1 654
849 TATATATGAAACAAATATACCTGCTGCAAAATGCAAACTACCACT 897
654 YTyLysIleAlaGlyArgValSerArgLysSerAspValThrG1us 671
898 GTGCTCTTCCCAAAACGTTTCCAA...AAGGAAT... 932
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933 ...TACCTTCCTCCGCTACAGCATCTGTAATACACA... 971
688 ThrGluThrAsnPheArgIleAlaIleMetThrValAsnGlyThrGlyPr 704
972 ...TCCTTTGGCTGAGAGATTAAGTTGATGATCAATACAGCTT 1017
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721 erArgValProGlnValProSerSerLeuHisValArgProIleValThr 737
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seq_name: p1r2:A36080
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Insulin receptor precursor rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 18-Jun-1999
C.Accession: A36080
R.Goldstein, B.J., Dudley, A.L.
MOL. Endocrinol. 4, 235-244, 1990
A.Title: The rat insulin receptor: primary structure and conservation of tissue-specific
A.Reference number: A36080; M0ID:90331337
A.Accession: A36080
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-1383 <GOL>
A.Cross-references: GB:M2016; NID:9204953; PIDN:AA41441.1; PID:9204954
C.Keywords: ATP; autophosphorylation; hormone receptor; phosphoprotein; transmembrane pr
F:1022-1298/Domain: protein kinase homology <KIN>
F:1030-1038/Region: protein kinase ATP-binding motif

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  Percent Similarity: 41.561
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583 ... 583
600 CTCACACAGAGCTACTTATGCTAAAGTAAAGCAAGCACTACTTAC 649
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617 LThrAspAlaThrAsnProSerValProLeuAspProIleSerValSer 633
741 GTCAAAATCAGAACTATGCTTAAAGG...GATATTAACA 781
634 AsnSerSerSerGlnIleLeuLysTrpLysProProSerProAs 650
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650 nGlyAsnIleThr... 654

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 Interferon_gamma_receptor_precursor human
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 CDate: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Jul-1999
 CAccession: A31555
 RAgnet, M.; Dembic, Z.; Merlin, G.
 Cell 55, 273-280, 1988
 ATitle: Molecular cloning and expression of the human interferon gamma receptor.
 AReference number: A31555; MIM:89003065
 A.Molecule type: mRNA
 A.Residues: 1-489 <AGD>
 A.Cross-references: GB:J03143; NID:G184650; PIDN:AA52721.1; PID:G306915
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 A:Gene: GDB:IFNGR1, IFNGR
 A:Cross-references: GDB:120688; OMIM:107470
 A:Map position: 6q23-6q24
 C:Superfamily: Interferon gamma receptor

C:Keywords: cytokine receptor; transmembrane protein

alignment_scores: quality: 124.50 length: 351
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 Percent Similarity: 53.276 Percent Identity: 22.222

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 180 AGCATGAGTGTGTCGGAATGTG... ACTTTTCATTCGATTAACAAA 226
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 113 rAlaLysSerGlnuPheAlaValAlaCYsArgspLysLLeGlyProP 130
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 130 rOlyLysLeuAspLLeArgLysGlnuLysGlnLLeMetLLeAspLLe 145
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 518 AATAGCTTACTTATCTGAAAACCTCTCAGGTGTAGAGAAAGATG 567
 147 sProSerValPheVal..... AsnOlyAspGlnuGlnuValAla 160
 568 AATATTTTATTCAGACATAAATTTTAAACCTCAGACAGACTACT 617
 160 sp..... TYrAspProGlnuThr 166
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seq_documentation_block:

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190K protein - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C:Accession: S42167
R:Vikmeier, U.; Obermann, W.; Weber, K.; Fuerst, D.O.
J. Cell. Sci. 106, 319-330, 1993
A:Title: The globular head domain of titin extends into the center of the sarcomeric M
A:Reference number: S42166; MUID: 9409565
A:Accession: S42167
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1451 <VIN>
A:Cross-references: EMBL:X69090; NID:9407098; PIDN:CAA48933.1; PID:9407099
C:Superfamily: skelamin

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alignment_scores:

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Quality: 123.50 Length: 460
Ratio: 0.588 Gaps: 21
Percent Similarity: 45.652 Percent Identity: 19.783

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alignment_block:

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US-09-240-675-1 x S42167
Align seg 1/1 to: S42167 from: 1 to: 1451

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153 GACAACTTATCTGAGCGAAGACGAGCATGCTCTGGCAAT.. 200
388 AAPTyrIleIleIleSerTyrPysGlnProAlaValAspGlyLysSer 404
201 ..GTGACTTTTCATTGATATCAAAAGAACTGGATGATATGGA 246
404 oIleLeuGlyTyrPheIleAspLysGluValGlyThrAspSerTTP 420
247 TAAATTTGCTGCTGCTGAGAAATATTACTAGTACCAATGCAACTTTCT 296
421 .....SerGlnCysAsnAspThr 426
297 TCACCAAGCTGATGTTTATGAGAAATTAATG..... 332
427 ProValLysPheAlaArgPheProValThrGlyLeuIleGluGlyArgSe 443

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333 .....CGATAGAGCAGAAAGAAAGAAACACTTTTCATG... 368
443 rTyrIlePhePheValArgAlaValAsnLysMetGlyIleGlyPheProS 460
369 .....TATAGCTTGACTATTTCACCACTTTCGCAAGCTCAG 407
460 eArgValSerGluValAlaAlaLeuAspProAlaGluLysAlaArg 476
408 ATTGGTCTCCAGAGACTATAGAGCTGAGATAGCAATAGTGAT 457
477 LeuLysSerPro.....LeuSerThrLeuAspTyrThrValIleVal 490
458 ACACATCTCTCGAGCAAAAGATAGTGTATGCGCGCTTGAGATG 507
490 lThrGluGluGluProSerGlyIleValProGlyProThrAspL 507
508 TTAGCTTTTACA.....TATAGCTTACTTATCTGAAA... 539
507 eSerValThrGluAlaThrArgSerTyrValValLeuSerTyrPysPro 523
540 .....ACTCTTCAGCTGATAGCAAGAGATTGAAATATTTA 577
524 ProGlyGlnArgGlyHisGluGlyIleMetTyrPheValGluLysCysG 540
578 TTCC..... 581
540 uAlaGlyThrGluAsnTyrPglArgValAsnThrGluLeuProValLys 557
582 .....AGACATTAATTTATTAACCTTCACACGAGACTATATGTGCA 626
557 eProAlaPheAlaLeuPheAspLeuAlaGluGlyLysSerTyrCysPhe 573
627 AAGTTTAAAGCAGCACTACTACGTACGAGAAATGTGTCTAATAGTC 676
574 ArgValArgCys.....SerAsnSerAlaGlyValGlyGluThr 586
677 ACTCATGTGTAAAGACACAGTT..... 701
586 oSerGluAlaThrGluValThrValValGlyAspLysLeuAspIleProL 603
702 .....GAAATGACACTACCTCCACGAGAAATATAGATGAGTCCAA 746
603 yAlaProGlyLysIleIleProSerArgAsnThrAspThrSerVal... 618
747 AATCAGAACTATGTTCTTAATGGAT..... 773
619 .....ValValSerTyrPglGluLysSerLysAspAlaLysGluLe 631
774 .....TATTCATATGCAACATGATGCTTCACATGAGGCGTCC 813
631 uValGlyTyrTyrIleGluAlaAsnValAlaGlySerGlyLysTyrPgl 648
814 AGCCCTTTTAAAGAAATCCT...GGAACCACTTGTATTAATGGA 860
648 rCys.....AsnAsnAspProValLysThrHisArgPhe... 659
861 CAATACCTGAGCTGAAATGTAATAACTACCAAGTGCTCTTCTCA 910
660 .....ThrCysHisGlyLeuValThrGlyLysSer... 669
911 AAGCTTTTCCAAAGAAATTTACCTTCCTCCGCTACAGCATGTGATG 960
670 .....TyrIlePheAlaValArgAlaValAsnA 679
961 GAAATACACATCTTTTGTCTGAGAGATTAAGTTGATACAGATA 1010
679 lAlaGlyLeuSerGlyTyrSerGlnAspSerGlu...AlaIleGluVal 694
1011 CAAGCTTCTACTCTCA.....GTCTTAACATTAG 1045
695 LysAlaAlaIleAlaProSerProCysAspIleThrCysLeuG 711
1046 ATCCCTTAGATCATTCATATCTATATCGGTCGTCACAAAGAGTCTG 1095

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455 yThrArgGlnTyrValSerValAsnValThrThrSnglnAlaAlaProS 472
1102 GCGCTGTATCCAG..... 1115
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472 erProValThrAsnValLysLysGlyLysIleAlaLysAsnSerIleSer 488
1116 .....GATATCCA.....CTGATTATGA 1135
||| ||| ||| ||| |||
489 LeuSerTTPGlnGlnProAspArgProAsnglyIleIleLeuGlnTyrGln 505
1136 AATTATTTTGGAAAAACACTTCAATGCTGAGAGAAAAATTATCGAG. 1184
||| :::::||||| :::::|||||
505 uIleLysTyrPheGlnLysAspGlnGlnThrSerTyrThrIleIleLysS 522
1185 ..AAAAAACTGATGTACAGTTCTTAATTGAAACCACTGACTATAT 1232
|||:::||||| :::::||||| :::::|||||
522 erLysGlnThrThrIleThrAlaGlnGlyLeuLysProAlaSerValTyr 538
1233 TGTGTGAAGCAGACACACAC 1256
::: |||||:::|||||
539 ValPheGlnIleArgAlaArgThr 546

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OM of: US-09-240-675-1 to: SwissProt_38.* out-format : pfs
Date: Jun 1, 2000 6:24 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

-MODEL-framed_n2p_model -DEV-rip
-O-cp2_1/USPRO_gpool/US09240675/runat_30052000_165119_3047/app-query.fasta.1
-DB-SwissProt_38 -QFMT-fastan -SUFFIX-modif.rsp -GAPOP-12.000
-GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000 -LOPEXT-0.000
-OGAPOP-4.000 -OGAPEXT-0.050 -YGAPOP-10.000 -YGAPEXT-0.500
-FCAPOP-6.000 -FCAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
-TRANS-human40 cdt -LIST-45 -DOCALLIGN-200 -THR_SCORE-pct
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NOM-ext -MINLEN-0
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-THREDS-1

Search information block:

Query: US-09-240-675-1
Query length: 1343
Database: SwissProt_38.*
Database sequences: 83857
Database length: 30454973
Search time (sec): 84.100000

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Sequence	Strd Orig	ZScore	Escore	len	Documentation
SwissProt_38:INRL_HUMAN	+ 2313.00	3405.81	7.4e-183	557	P17181 homo sapiens (human)
SwissProt_38:INRL_BOVIN	+ 1507.00	2214.75	1.6e-116	560	P04780 bos taurus (bovine)
SwissProt_38:INRL_SHEEP	+ 1503.00	2208.84	3.4e-116	560	P08589 ovis aries (sheep)
SwissProt_38:INRL_MOUSE	+ 1069.00	1567.06	1.8e-80	590	P08896 mus musculus (mouse)
SwissProt_38:CEFA_HUMAN	+ 228.50	330.47	2.5e-11	335	P08834 homo sapiens (human)
SwissProt_38:INSG_HUMAN	+ 155.50	222.27	2.6e-05	337	P18484 homo sapiens (human)
SwissProt_38:INSG_RAT	+ 127.00	167.38	0.0072	1383	P15127 rattus norvegicus (rat)
SwissProt_38:INSG_HUMAN	+ 124.50	173.10	0.0097	449	P15260 homo sapiens (human)
SwissProt_38:KMWI_HUMAN	+ 123.50	161.77	0.0140	1451	P52179 homo sapiens (human)
SwissProt_38:EPAS_RAT	+ 118.00	156.97	0.0374	1005	P54757 rattus norvegicus (rat)
SwissProt_38:INOR_MOUSE	+ 117.50	161.28	0.0376	575	P06177 mus musculus (mouse)
SwissProt_38:INSG_MOUSE	+ 117.00	152.67	0.0476	1372	P15308 mus musculus (mouse)
SwissProt_38:INSG_HUMAN	+ 116.00	148.19	0.0606	1912	P23468 homo sapiens (human)
SwissProt_38:INSG_CHICK	+ 115.00	149.22	0.0701	1450	P02173 gallus gallus (chick)
SwissProt_38:INSG_RAT	+ 113.50	151.32	0.0860	880	P55146 rattus norvegicus (rat)
SwissProt_38:DECC_MOUSE	+ 111.50	144.06	0.1360	1447	P54756 homo sapiens (human)
SwissProt_38:EPAS_HUMAN	+ 108.00	141.91	0.2503	1037	P54756 homo sapiens (human)
SwissProt_38:INOR_HUMAN	+ 107.00	148.46	0.2622	427	P15308 mus musculus (mouse)
SwissProt_38:INOR_HUMAN	+ 107.00	145.72	0.2753	1912	P23468 homo sapiens (human)
SwissProt_38:INSG_RAT	+ 107.00	139.97	0.3050	1091	P4290 rattus norvegicus (rat)
SwissProt_38:INSG_HUMAN	+ 107.00	135.83	0.3168	1382	P13652 homo sapiens (human)
SwissProt_38:DECC_HUMAN	+ 106.00	135.94	0.3858	1447	P43146 homo sapiens (human)
SwissProt_38:INSG_MOUSE	+ 105.50	139.72	0.3913	878	P26954 mus musculus (mouse)
SwissProt_38:INSG_HUMAN	+ 105.50	137.75	0.4053	1091	P54756 homo sapiens (human)
SwissProt_38:INSG_HUMAN	+ 104.50	140.80	0.4520	662	P42701 homo sapiens (human)
SwissProt_38:INSG_MOUSE	+ 104.00	137.32	0.5217	886	P26955 mus musculus (mouse)
SwissProt_38:NRG_DROME	+ 104.00	134.39	0.5497	1239	P20241 drosophila melanogaster
SwissProt_38:PEPE_HUMAN	+ 104.00	130.53	0.5888	1897	P10586 homo sapiens (human)
SwissProt_38:TCF2_TBOAC	+ 104.00	128.86	0.6065	2280	P09976 nicotiana tabacum (tobacco)
SwissProt_38:INSG_HUMAN	+ 103.50	136.36	0.5758	918	P40189 homo sapiens (human)
SwissProt_38:INSG_MOUSE	+ 102.50	140.81	0.6263	477	P15261 mus musculus (mouse)
SwissProt_38:TCF2_SPTOL	+ 102.50	127.26	0.7972	2131	P08873 spinacia oleracea (spinach)
SwissProt_38:TCF2_ARATH	+ 101.00	123.11	0.9750	2294	P56786 arabidopsis thaliana
SwissProt_38:CD45_HUMAN	+ 99.50	133.21	1.117	1304	P08875 homo sapiens (human)
SwissProt_38:CYR2_HAASIN	+ 99.50	133.66	1.122	897	P43211 haemophilus influenzae
SwissProt_38:INSG_HUMAN	+ 99.50	119.33	1.50	3135	P08837 plasmidium falciparum
SwissProt_38:INSG_MOUSE	+ 98.50	125.52	1.58	1345	P38800 saccharomyces cerevisiae
SwissProt_38:RRPO_TMY	+ 98.50	123.86	1.63	1615	P03586 tobaccum mosaic virus
SwissProt_38:CYAA_YEAST	+ 98.50	121.81	1.69	2026	P08678 saccharomyces cerevisiae
SwissProt_38:KTR7_YEAST	+ 98.00	133.43	1.49	517	P40504 saccharomyces cerevisiae

SwissProt_38:KTR7_YEAST	+ 97.50	137.44	1.50	306	P06242 saccharomyces cerevisiae
SwissProt_38:LEPR_MOUSE	+ 97.50	125.36	1.86	1162	P48356 mus musculus
SwissProt_38:INSG_CHICK	+ 97.50	124.66	1.89	1256	P17122 gallus gallus
SwissProt_38:CALC_CHICK	+ 97.50	116.41	2.19	3124	P13944 gallus gallus
seq_name: SwissProt_38:INRL_HUMAN					
seq_documentation_block:					
ID	INRL_HUMAN	STANDARD	PRT	557	AA
AC	P17181				
DT	01-AUG-1990	(Rel. 15, Created)			
DT	01-AUG-1990	(Rel. 15, Last sequence update)			
DT	15-FEB-2000	(Rel. 39, Last annotation update)			
DE	INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IN-ALPHA-REC).				
GN	IFNARI OR IFNAR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
CC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
LN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 90124632.				
RA	Uze G., Lutfalla G., Gresser I.,				
RT	"Genetic transfer of a functional human interferon alpha receptor				
RL	into mouse cells: cloning and expression of its cDNA."				
RL	Cell 60:225-234(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 92129376.				
RA	Lutfalla G., Gardiner K., Proudman D., Vieh E., Uze G.,				
RT	"The structure of the human interferon alpha/beta receptor gene."				
RL	J. Biol. Chem. 267:2802-2809(1992).				
RN	[3]				
RP	PHOSPHORYLATION BY TYR2.				
RX	MEDLINE; 95059042.				
RA	Cotnam J., Yan H., Domanski P., Handa R., Smalley D.,				
RT	Mullersman J., Witte M., Krishnan K., Krolewski J.,				
RL	"Direct binding to and tyrosine phosphorylation of the alpha subunit				
RL	of the type I interferon receptor by p135tyk2 tyrosine kinase."				
RL	Mol. Cell. Biol. 14:8133-8142(1994).				
CC	-1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE				
CC	I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS				
CC	INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA- AND BETA-				
CC	SUBUNITS THEMSELVES.				
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	-1- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND				
CC	EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.				
CC	-1- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.				
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.				
CC	-1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.				
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
DR	EMBL; J03171; AAA52730.1;				
DR	EMBL; X60459; CAA4292.1;				
DR	PIR; A32694; A32694.				
DR	PIR; S17112; S17112.				
DR	KIM; 107450;				
KW	Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;				
FT	Phosphorylation.				
FT	SIGNAL	1	27	POTENTIAL.	
FT	CHAIN	28	557	INTERFERON-ALPHA/BETA RECEPTOR ALPHA	
FT	DOMAIN	28	436	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	437	457	POTENTIAL.	
FT	DISULFID	458	557	CYTOPLASMIC (POTENTIAL).	
FT	DISULFID	79	87	BY SIMILARITY.	
FT	DISULFID	199	220	BY SIMILARITY.	

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FT MOD_RES 466 466 PHOSPHORYLATION (BY TYK2) (PROBABLE)
FT CARBOHYD 481 481 POTENTIAL.
FT CARBOHYD 50 50 POTENTIAL.
FT CARBOHYD 58 58 POTENTIAL.
FT CARBOHYD 81 81 POTENTIAL.
FT CARBOHYD 88 88 POTENTIAL.
FT CARBOHYD 110 110 POTENTIAL.
FT CARBOHYD 110 110 POTENTIAL.
FT CARBOHYD 172 172 POTENTIAL.
FT CARBOHYD 254 254 POTENTIAL.
FT CARBOHYD 313 313 POTENTIAL.
FT CARBOHYD 314 314 POTENTIAL.
FT CARBOHYD 376 376 POTENTIAL.
FT CARBOHYD 416 416 POTENTIAL.
FT CARBOHYD 433 433 POTENTIAL.
FT VARIANT 168 168 /L->V.
FT CONFLICT 17 17 G->A (IN REF 2)
SQ SEQUENCE 557 AA: 63525 MW: 0f674dcb1adeb73 CRC64:
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Quality: 2313.00 Length: 436
Ratio: 5.305 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1 x INRL_HUMAN

Align seg 1/1 to: INRL_HUMAN from: 1 to: 557

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1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAlaGly 17
77 CCCATGGGTGTTCGCGCGCAGCGAGGAGGAAAAATCTAAATCTCTC 126
17 YPPIOTRYValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
127 AAAAGTAGAGTCGACATCATAGATGACACTTATCTGAGGTGAGAC 176
34 LnlYValGluValAlaSerPheIleLeuAspAsnPheIleLeuArgTrpAsn 50
177 AGAGCCATGTCCTCTGCGCGCAGACCTTCTCTGCGCGG 226
51 ArgSerAspGlnSerValGlyAsnValThrPheSerPheAspTrpGlnGly 67
227 AACGGGATGATATGATGATGATGATGATGATGATGATGATGATGAT 276
67 sthGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleHis 84
277 GTACCAATGCACTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 326
84 ertHlyLysCysAsnPheSerSerLeuLysLeuAsnValIlyGluGluIle 100
327 AAATGGCTATAGAGCAGAAAAAGAAACCTCTCTCTCTCTCTCTCTCTCT 376
101 LysLeuArgIleArgGluAlaGluLysGluAsnThrSerSerTrpTrpGluVal 117
377 TGACATCATTTACACCATTTCCCAAGCTCAGATGGCTCTCTCTCTCTCT 426
117 LAspSerPheThrPhePheArgLysAlaGlnIleGlyProProGluValAla 134
427 ATTAGAGGTGAGAGATAGAGCAATGATGATGATGATGATGATGATGATG 476
134 LsLeuGluAlaGluAlaSerLysAlaIleValIleHisIleSerProGlyThr 150
477 AAAGTATGCTTATGCTGCTTGTGAGTGTGATGCTTATGATGATGATG 526
151 LysAspSerValMetTrpAlaLeuAspLysPheLysSerPheTrpLysSerLe 167
527 ACTATCTGCAAAAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 576
167 uLeuIleTrpLysAsnSerSerGlyValGluGluAlaGlyIleGluAsnIle 184
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577 ATTCAGACATATAAATTATTAACCTCTCACAGACACTTATGCTCTA 626
184 YSerTrpGlnLysIleLysIleLysLeuSerProGlnThrThrLysCysLeu 200
627 AAAGTAAAGCAGCAGCTACTTACGTCATGGAATTTGGTGTCTATAGTGC 676
201 LysValLysAlaAlaLeuLeuThrSerTrpLysIleGlyValLysSerTr 217
677 AGTACATTTGATTAAGACACAGCTTGAATAATGACTACTCCACAGCAAA 726
217 ValHisCysIleLysThrThrValGluAsnGluLeuProProGlnAla 234
727 ATATAAGTCACTGTCTCAAAATCAGAACTAGTCTTATGATGATGAT 776
234 snIleGluValSerValGluAsnGlnAsnThrValLeuLysTrpAspTrp 250
777 ACATATGCAAACTGACCTTTCAAGTTCAGTGTGCTCTCACGCTTTTAA 826
251 ThrTrpAlaAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeuLys 267
827 AAGCAATCTGGAACCACTTTGATTAATGGAACCAATACCTGACTGTG 876
267 sArgAsnProGlyAsnHisLeuTrpLysTrpLysGlnIleProAspCysG 284
877 AAATGTCAAAACCTACCCAGTGTCTCTCTCAAAACGTTTCCAAAAA 926
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301 GlyIleLysLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerP 317
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1027 CTCACGCTTTTACATTAATGATCCCTTATGATGATGATGATGATGATG 1076
334 rProValPheAsnIleArgSerLeuSerAspSerPheHisIleLysIle 350
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1127 GATTATGAAATTAATTTTGGGAAAACCTTCAATGCTGAGAGAAAAA 1176
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1177 TATTCGAAAAAAACAGTATGATGATGATGATGATGATGATGATGATG 1226
384 IeIleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
1227 GTATATGCTGTAAGCAGCAGACACACACATGATGATGATGATGATGAT 1276
401 ValLysCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnLys 417
1277 AACAGTGTGTTTATGAGCCTGATGATGATGATGATGATGATGATGATG 1326
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1327 CCTCTTAAA 1334
434 hSerLys 436
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ID INRL_BOVIN STANDARD: PRT: 560 AA.
AC Q04790:
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
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DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
 GN IFNARI OR IFNAR.
 OS Bos taurus (Bovine).
 CC Eukariota; Metazoa; Chordata; Vertebrata; Mammalia;
 CC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 CC Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LUNG.
 RX MEDLINE: 93076908.
 RA Mouchel-Viehl E., Lutfalla G., Mogenssen K.E., Uze G.;
 RT "Specific antiviral activities of the human alpha interferons are
 RT determined at the level of receptor (IFNAR) structure."
 RL FEBS Lett. 313:255-259(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93305725.
 RA Lin J.-K., Langer J.A.;
 RT "Cloning and characterization of a bovine alpha interferon receptor."
 RL Biochim. Biophys. Acta 1173:314-319(1993).
 CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 CC 1 IFNS TRIGGERS THIOSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
 CC SUBUNITS THEMSELVES.
 CC -1- SUBCELLULAR LOCATION: TYPE I. MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC
 DR EMBL: X68443; CAA48484.1;
 DR EMBL: L06320; AAA02571.1;
 DR PIR: S33770; S33770.
 DR PIR: S27387; S27387.
 DR PIR: PF00041; fn3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 560
 FT
 FT DOMAIN 25 437
 FT TRANSMEM 438 458
 FT DOMAIN 459 560
 FT DISULFID 76 84
 FT DISULFID 199 220
 FT CARBOHYD 47 47
 FT CARBOHYD 55 55
 FT CARBOHYD 85 85
 FT CARBOHYD 109 109
 FT CARBOHYD 172 172
 FT CARBOHYD 254 254
 FT CARBOHYD 313 313
 FT CARBOHYD 377 377
 FT CARBOHYD 434 434
 FT CONFLICT 422 422
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 Ratio: 3.987 Gaps: 6
 Percent Similarity: 86.105 Percent Identity: 64.920

alignment_block:

US-09-240-675-1 x INRI_BOVIN
 Align seq 1/1 to: INRI_BOVIN from: 1 to: 560

30 ATGGCTGCTCTCTCTGGCGCCGACACCTAGTCTGTCGCCGCGGCCCC 79
 1 MetLeuAlaLeuLeuGlyAlaThrThrLeuMetLeuValAla... GlyAla 16
 80 ATGGGTGTGTCGCCGCGCCGACGCGGAAAAAATGTAATCTGCTCAAA 129
 16 GTTPValLeuProAlaAlaSerGlyGluAlaLysLeuLys... ProGlu 32
 130 AAGTAGAGTCGACATCATGACATGACAACTTATCTGAGGCGAACAG 179
 32 snValGluIleHisIleLeuLysPaspaspPhePheLeuLysTrpSer 48
 180 ACCGATGCTCTGCGGAATGTCATTTTCATTCGATTATCAAAAAAC 229
 49 SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGluIle 65
 230 TGGGAGGATATGATGATAAATGTGCGGTGTCAGAAATATCTACTA 279
 65 uGlyThrAspAsnTrpLysLysSerGlyCysGlnHisIleTrpSer 82
 280 CCAATGCACTTCTCTCACTCAAGTCG...AATGTTATGAGAATTT 326
 82 hTrpCysAspPheSerSerValGluLeuGluAsnValPheGluLysIle 98
 327 AATTCGCTATPAGACGAAAAA...GAAACACTTCTTCATGTATGA 373
 99 GluLeuAlaGlyLeuAlaGluGluGlyAsnTrpSerThrTrpTyrGly 115
 374 GGTGACATCTTACACATTTCCGAAAGCTCAATTTGCTCTCAAGAG 423
 115 ValGluProPheValProPheLeuGluAlaGluIleLeuProPhe 132
 424 TACATTGAGCTGAGATPAGCAATGAGATGATGATGATGATGATGAT 470
 132 AlHisLeuGluAlaGluAspLysAlaIleIleLeuSerIleSerPro 148
 471 GGAACAAAAGATGATGATGATGATGATGATGATGATGATGATGAT 520
 149 GlyThrLysAspSerIleMetTrpAlaMetAspTrpSerSerPheArg 165
 521 TAGCTTACTTCTGGAAGAACTTCAAGCTGATGAGAAAGATGATA 570
 165 SerValValIleTrpLysAsnSerSerSerLeuGluGluTrpThrIle 182
 571 ATATTATCCAGACATATAATTAATACTCTCAGCAGACACTTAT 620
 182 hValTrpProGluAspLysIleTyrLysLeuSerProGluIleThrTyr 198
 621 TGCTAAAGTAAAGCAGCAGCTACTTACGTCGAAATTTGCTGCTA 670
 199 CysLeuLysValLysAlaGluLeuArgLeuGlnSerLysValGlyCys 215
 671 TAGCCGCTCATGTATTAAGACACAGCTGAAATGAACTACTCTCAC 720
 215 rSerProValTyrCysIleAsnThrTrpGluArgLysValProSer 232
 721 CAGAAATATAGAGTACGCTGCAAAATCAGAACTGTCTTAATG 770
 232 rGluLysIleGlnIleAsnAlaAspAsnIleTyrValLeuLysTrp 248
 771 GATTATCATATGCAAAAGACCTTCAAGTCAAGCTGCGCTCAAGCTT 820
 249 AspTyrProTyrGluAsnAlaThrPheGlnAlaGluTrpLeuTrpAla 265
 821 TTAAAGGAATCCGGAACCAATTTGTAATGAAACAAATACCTG 870
 265 ePheLysLysIleProLysHisSerAspLysTrpLysGlnIleTrp 282
 871 ACTGTGAAATGTCAAAATACCACTAGTGTCTTCTCAAAAGCTTTC 920
 282 snCysGluAsnValIleThrHisCysValAlaPheProArgGluValSer 298
 921 CAAAGGAATTTACTCTTCCGCGTACAAAGCATCTGATGAAATACAC 970


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299 SerAsgGlyIleTyrValArgValArgAlaSerAsnGlyAsnGlyTh 315
971 ACTTTTGGTGAAGATAGTTGATGCTGAAATACAGCTTCC 1020
315 rterPheTTPSerGluGluGluPheAsnThrGluMetLysThrIleI 332
1021 TACTTCCCTCAGCTTTTACATTAGATCCCTAGT...GATTCATTCCAT 1067
332 lPheProProValIleSerValIleSerValThrAspSerLeuHis 348
1068 ACTATATGGGTGCTCCAAACAGTGTGGAACACCCCTGTATCCAGA 1117
349 ValSerValGlyAlaSerGluGluSerGluAsnMetSerValAsnGlu 365
1118 TATTCACGATTTATGATTAATTTTGGGAAACACATCAATGCTG 1167
365 uTyrProLeuIleTyrGluValIlePheThrGluAsnThrSerAsnAla 382
1168 AGAGAAATATTCAGAGAAATACGATGTTACGTTCTTAATTGAA 1217
382 lndrGysValLeuGluLysArgThrAspHeIlePheProAspLeuLys 398
1218 CCCTGACGTATATGTGTGGAAGCCAGACACACCATGATGATAA 1267
399 ProLeuThrValTyrCysValLysAlaArgAlaLeuIleGluAsnAsp 415
1268 GCGATTAATAAGAGATGTTTGTGACGCTGATGATGAGAAACAAAC 1317
415 gaGAsnLysGlySerSerSerAspThrValCysGluLysThrLysP 432
1318 CAGAAATACCTCTAAA 1334
432 rGlyAsnThrSerLys 437
seq_name: SwissProt_38:INRL_SHEEP
seq_documentation_block:
ID INRL_SHEEP STANDARD: PRT: 560 AA:
AC Q28589: Q95206:
DT 01-NOV-1997 (Rel. 35, created)
DT 01-NOV-1997 (Rel. 35, last sequence update)
DT 15-FEB-2000 (Rel. 35, last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
DE (INTERFERON ALPHA/BETA RECEPTOR-1)
GN IFNAR1 OR IFNAR
OS Ovis aries (Sheep)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Caprinae; Ovis
OC [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM;
RX MEDLINE: 98006426.
RA Han C.-S., Machuga N., Klemann S.W., Roberts R.M.,
RA Molecular cloning of ovine and bovine type I interferon receptor
RA subunit from uteri, and endometrial expression of messenger
RA ribonucleic acid for ovine receptors during the estrous cycle and
RA pregnancy.
RL Endocrinology 138:4757-4767(1997).
-1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I INRS TRIGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

```

```

CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
CC CONCEPTUS AT DAY 15 OF PREGNANCY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X95939; CAA6183.1; -
DR EMBL: U65978; AAB84231.1; -
DR PDB: PF00041; fn3.1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 560
FT FT INTERFERON-ALPHA/BETA RECEPTOR ALPHA
FT FT CHAIN.
FT FT DOMAIN 25 437
FT FT TRANSEM 438 458
FT FT DOMAIN 459 560
FT FT DISULFID 76 84
FT FT DISULFID 199 220
FT FT CARBOHYD 47 47
FT FT CARBOHYD 55 55
FT FT CARBOHYD 85 85
FT FT CARBOHYD 108 108
FT FT CARBOHYD 109 109
FT FT CARBOHYD 172 172
FT FT CARBOHYD 222 222
FT FT CARBOHYD 285 285
FT FT CARBOHYD 313 313
FT FT CARBOHYD 359 359
FT FT CARBOHYD 377 377
FT FT CARBOHYD 434 434
FT FT CONFLICT 352 352
FT FT CONFLICT 522 522
FT FT SEQUENCE 560 AA: 63918 MW: E7198A1905D4805C CRC64;
align_scores:
Quality: 1503.00 Length: 439
Ratio: 3.997 Gaps: 6
Percent Similarity: 85.649 Percent Identity: 64.465
alignment_block:
US-09-240-675-1 x INRL_SHEEP
Align: seg 1/1 to: INRL_SHEEP from: 1 to: 560
30 ATGGTGCTCTCTGCGGCGGAGACCCAGTGTGCTGCGCGTGGCC 79
1 MetLeuSerLeuLeuGlyAlaThrThrLeuMetLeuValAla...GlyAr 16
80 ATGGGTGTTCGCGACGCCGAGGTGGAATAATCTTAATCTCTCAA 129
16 gTPValLeuProAlaIleSerGlyValAlaSerLeuLysSer...GluA 32
130 AACTAGATGCGATCATGATGACAACTTATCTGAGTGAACAG 179
32 snValGluLeuHisIleLeuAspAspAspPheHeuLeuLysTrpAsnSer 48
180 AGCGAGATCTGTGCGGATGTGACTTTTATTCATATCAAAAAC 229
49 SerSerGluSerValArgAsnValThrPheSerAlaAspTyrGluIleLe 65
230 TGGAGATGATATGATATAATGTGTGCGGTGATATATTAAGTA 279
65 uGlyThrAspAsnThrLysLeuProGlySerGlnHisIleThrSerS 82
280 CAAAGCAACTTTCTTCATCAAGCTG...AATGTTATGAGAAAT 326

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82  erlyscysanpReserSerValGluLeuLysaspAlaIhegluIlystle 98
327  AATTCGCGTATAGACGAGAAAA...GAAACACTCTTCATGGTATCA 373
      ::::::::::::::::::::::::::::
99  GluLeuArGluIleArgAlaGluGluGluGluLysAsnThrSerThrTyrGcl 115
374  GGTTGGACTCATATACCAATTCGGCAAACTGAGANTGGTCTCCAGAG 423
      ::::::::::::::::::::::::::::::
115  uValGluProPheValProPheLeuLysAlaGlnIleGlyProProAspY 132
424  TACATTAGAACCTGGAAGATAAGGCAATATGATGATACACTCT...CCT 470
      ::::::::::::::::::::::::::::::
132  aHisLeuGluAlaGluLysAspLysAlaIleIleLeuSerIleSerProPro 148
471  GGAACAAAGATAGTGTATATGCGGCTTGGATGGTGTATTAACATACA 520
149  GLyThrGluAspSerIleMetThrAlaLeuAspArgSerSerPheArgTy 165
521  TACTTACTTATATCGGAAAAACCTTCACAGTGTAGAGAAAGAGATTGAA 570
165  rSerValValIleTyrLysAsnSerSerSerLeuGluGluArgThrGluT 182
571  ATATTATATTCACACACATATAAATTATTAACCTGCACACAGACTATAT 620
182  hrValTyrProGluAspLysIleTyrLysLeuSerProGluIleThrTyr 198
621  TGCTCTAAAGTTAAACACACTACTTACTTACGTATGAGAAAATGGTGCTCA 670
199  CyLeuLysValLysAlaGluLeuArGluLeuArgLeuInsErArgValGlyCysTy 215
671  TACTCCAGTACATGTGTATTAAGACCCACAGCTGAAATGAATCACTCCAC 720
215  rSerProValTyrCysAlaGlnThrThrGluArgHisLysValProSerP 232
721  CAAAAAATATAGAGACAGTGCCTCAAAATCAGACATATGTTCTTAATGG 770
232  roGluAsnValGlnIleAsnValAspAsnGlnAlaTyrValLeuLysTyrP 248
771  GATTATACATATGCAAAACATGACCTTCACAGTTCAGTGGCTCCAGCGCTT 820
249  AspTyrProTyrGluSerThrThrPheGlnAlaGlnTyrPheLysAlaPhe 265
821  TTTTAAAGATACCTCGGAACCATTTGTATTAATGGAACCAATACCTG 870
265  eleuLysLysIleProGlyLysHisSerAsnLysTyrLysGlnIleProA 282
871  ACTGTGAAATGTCAAACTATCCAGTGTGTCTTCCTCAAACTTTTC 920
282  snGlyGluAsnValThrThrHisCysValPheProArgAspIlePhe 298
921  CAAAAAGATTTTACCCTTCCTCCGCGTACAGATCTGATGAGAAATACAC 970
299  SerMetGlyIleTyrTyrAlaPheValArgAlaSerAsnGlyLysGlyTh 315
971  ATCTTTTGGCTGGAAGAGATTAAGTTGATACTGAATAACAGCTTCC 1020
315  rSerPheThrPserGlnGluLysGluPheAsnThrGluValLysProIleI 332
1021  TACTCTCTCAGCTTTTAACTATTAAGTCCCTTACT...GATTCATTCAT 1066
332  IePheProProValIleSerMetLysSerIleThrAspAspSerLeuHis 348
1068  ATCTAATCGCTCTCCAAACAGTGTGGAACAGCGCTGATACACAGA 1114
349  ValSerValSerLysSerGluLysSerGluLysAsnMetSerValAsnGlnLe 365
1118  TTAATCACTGATTATGAAATATATTTTGGAAAAACACTCAATGCTG 1167
365  uTyrProLeuValTyrGluValIlePheThrPgluLysnThrSerAsnAlaG 382
1168  AGGCAAAATATATCGGAAAAAACCTGATGTACAGTCTCAATTGTAAA 1217
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[illegible]

	seq_documentation_block	STANDARD;	PRT;	590 AA.
ID	INRL_MOUSE			
AC	P3386;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-FEB-2000 (Rel. 39, Last annotation update)			
DE	INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).			
GN	IFNAR1 OR IFNAR OR IFNR.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
CC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 92262522.			
RA	Use G. Lutfalla G. Bandu M.T. Proudhon D. Mogensen K.E.			
RT	"behavior of a cloned murine Interferon alpha/beta receptor expressed			
RT	In homospesific or heterospecific background."			
RL	Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).			
CC	- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE			
CC	I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS			
CC	INCLUDING JAKS, TYK2, STAT PROTEINS AND IN-R ALPHA-AND BETA-			
CC	SUBUNITS THEMSELVES.			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; M89641; AAA37890.1;			
DR	PIR; A45283; A45283.			
DR	MGI; MGI:107658; IFNR.			
KW	Receptor; Transmembrane; Glycoprotein; Signal.			
FT	CHAIN	1	26	
FT	SIGNAL	27	590	
FT	DOMAIN	27	426	
FT	TRANSMEM	430	449	
FT	DOMAIN	450	590	
FT	DISEULEID	78	86	
FT	DISEULEID	199	220	
FT	CARBOHYD	43	43	
FT	CARBOHYD	109	109	
FT	CARBOHYD	181	181	
FT	CARBOHYD	214	214	
FT	CARBOHYD	314	314	
FT	CARBOHYD	370	370	
FT	CARBOHYD	409	409	
FT	CARBOHYD	413	413	
FT	SEQUENCE	590 AA;	65776 MW;	7ECDDFF37018U53A CRC64;

alignment_scores:

Quality: 1069.00 Length: 436

Ratio: 3.230 Gaps: 4

Percent Similarity: 75.917 Percent Identity: 48.624

alignment_block:

US-09-240-675-1 x INRL_MOUSE

Align seg 1/1 to: INRL_MOUSE from: 1 to: 590

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30 ATGCTCTCTCTCTGCGGCGCAGCACCCTAGCTGTCTGCGCGCGCC 79
   |||.....|.....|.....|.....|.....|.....|.....|
1 MetleuAlaValIglYAlaAlaLeuValLeuValAlaIglYAlaPr 17
80 ATGGGTGTTCGCCAGCCGCGAGGTGGAAAAATCTAAATCTCTCAA 129
   |||.....|.....|.....|.....|.....|.....|.....|
17 OTTPValLeuProSerAlaAlaIglYglYAlaLeuLeuProProGluA 34
130 AAGTAGAGTGCACATCATAGATGACACTTATCTCAGGTGGAACAG 179
   |||.....|.....|.....|.....|.....|.....|.....|
34 snlleAspValTyrIleIleAspAsnTyrThrLeuIlyStrSerSer 50
180 AGCGATGATGTCTGCGGAGATGACCTTTTCATTCATACAAAAAC 229
   |||.....|.....|.....|.....|.....|.....|.....|
51 HisIglYSerMetGlySerValThrPheSerAlaIglYAlaGlyThly 67
230 TGGGATGATGAATGATGAATATGTCGGGTGCAGAAATATCTACTA 279
   |||.....|.....|.....|.....|.....|.....|.....|
67 sAspGluAlaIlyStrPheIlyValProIglYsGlnIHisThrThrT 84
280 CCAATGCAACTTTCTTCACTCAAGCTGAATGTTATGAGAATTAAT 329
   |||.....|.....|.....|.....|.....|.....|.....|
84 hrIysCysGluPheSerLeuLeuAspThrAsnValTyrIleYstrGln 100
330 TTGGGTATAGACGAGAAAAAGAAAC...ACTTCTCATGGTATGAGT 376
   |||.....|.....|.....|.....|.....|.....|.....|
101 PheArgValAlaGluIglYAlaIglYsAsnSerThrSerItrAsnGluVa 117
377 TGACATCATTCACCATTCGCAAGCTCAGATTCGTCCTCCAGAGTAC 426
   |||.....|.....|.....|.....|.....|.....|.....|
117 AspProPheIleProPheTyrThrAlaHisMetSerProProGluValA 134
427 ATTAGAAGCTGAGATAGAGCAATAGATGATACATCTCTCTGAGACA 476
   |||.....|.....|.....|.....|.....|.....|.....|
134 rglLeuGluAlaIglYsAspIlyAlaIleLeuValHisIleSerProProGly 150
477 AAAGTATGTTATGTGGCTTGGATGGTTAACTTACATTAATGCTT 526
   |||.....|.....|.....|.....|.....|.....|.....|
151 GlnAspGlyAsnMetItrPalaLeuGluIlyProSerPheSerTyrThrI 167
527 ACTTATCGAGAAACTCTGTCAGTGTAGAGAAAGATGGAATTAAT 576
   |||.....|.....|.....|.....|.....|.....|.....|
167 eArgIleItrPalaIlySerSerSerAspIlyStrIleAsnSerThrT 184
577 ATTCAGACATTAATTAATTAACCTCTCAGAGACTATTAATGTCTA 626
   |||.....|.....|.....|.....|.....|.....|.....|
184 YTYValIglYIlyStrIleProGluLeuLeuProGluThrThryCysLeu 200
627 AAAGTTAAAGCGACACTTACGTCATGAGAAATGGGTGTATAGTCC 676
   |||.....|.....|.....|.....|.....|.....|.....|
201 GluValIlyAlaIleHisProSerLeuIlyStrHisSerAspIlySerTh 217
677 AGTACATGTATTAAGACCAAGTGAATAATTAACCTCCACAGGAA 726
   |||.....|.....|.....|.....|.....|.....|.....|
217 YValIglYsIleSerThrThyValAlaAsnIlyMetProValProGlyA 234
727 ATATGAAGTCAAGTCTCAAAATCAGAACTATGTTTAAATGAGATAT 776
   |||.....|.....|.....|.....|.....|.....|.....|
234 srlLeuGluValAspIlyAsnIglYsSerTyrValLeuIlyStrAspTyr 250
777 ...ACATATGCAAACTGACCTTTCAGATTCAGTCTCCAGCCCTTTT 823
   |||.....|.....|.....|.....|.....|.....|.....|
251 IleAlaSerAlaAspValLeuPheArgAlaIglYThrLeuProGluIlyYrse 267

```

```

824 AAAAGAAATCCGGAACCACTTTGTATTAATGGAACAAATCACTGACT 873
   |||.....|.....|.....|.....|.....|.....|.....|
267 rIySerSerSerGlySerHisSerAspIlyStrPlyStrProIleProThrC 284
874 GTGAAAATGTCAAACTACCACTGTGTCTTCTTCTCAAAAGCTTTTCAA 923
   |||.....|.....|.....|.....|.....|.....|.....|
284 YsAlaAsnValIglYThrThrHisCysValPheSerGlnAspThrValTyr 300
924 AAGGAATTTACTTCTCCGCGTACAGACATCTGAGAGGAATTAACATC 973
   |||.....|.....|.....|.....|.....|.....|.....|
301 ThrGlyThrPhePheLeuHisValGlnAlaSerGluIlyAsnIleThrSe 317
974 TTTTGTCTGAGAGAGATAAAGTTGATGATGAAATTAACAGTTTCTTAC 1023
   |||.....|.....|.....|.....|.....|.....|.....|
317 rPheItrPseGluIglYsPheIleAspSerGlnIlyStrHisIleLeuPro 334
1024 TTCTCCAGCTTTTAACATTAATCCCTTAGTATTCATTCATTCATAT 1073
   |||.....|.....|.....|.....|.....|.....|.....|
334 roProProValIleThrValThrAlaMetSerAspThrLeuLeuValTyr 350
1074 ATGGGTCTCCAAAACAGTCTGGAACACCCCTGTATTCAGATTAATCC 1123
   |||.....|.....|.....|.....|.....|.....|.....|
351 ValAsnCysGlnAspSerThrCysAsp.....Gt 360
1124 ACTGATTATGAATTAATTTTGGGAAACACTTCAAATGCTGAGAGAA 1173
   |||.....|.....|.....|.....|.....|.....|.....|
360 YLeuAsnTyrGluIleIlePheItrPalaIlyAsnThrSerAsnThrIlyS 377
1174 AAATTAACGAGAAAAAACTGATGTTACAGTCTTAATTTGAACACCTG 1223
   |||.....|.....|.....|.....|.....|.....|.....|
377 erMetGluIlyAspGlyProGluPheThrLeuIlyAsnGlnProLeu 393
1224 ACTGATATATGTGTGAAGCCAGACACACACATGATGATGAAGCTGAA 1273
   |||.....|.....|.....|.....|.....|.....|.....|
394 ThrValIlyCysValGlnAlaAlaArgVal...LeuPheArgAlaLeuLeuAs 409
1274 TAAAGCAGATGTTTGTAGTACGCTGATGTGAGAAACAAACAGGAA 1323
   |||.....|.....|.....|.....|.....|.....|.....|
409 nIyThrSerAsnPheSerGluIlyLeuCysGluIlyThrArgProIlyS 426
1324 ATACCTCT 1331
   |||.....|.....|.....|.....|.....|.....|.....|
426 erPheSer 428
seq_name: SwissProt_38-CRF4_HUMAN
seq_documentation_block:
ID   CRF4_HUMAN          STANDARD;   PRT;   325 AA.
AC   008334
DT   01-FEB-1995 (Rel. 31, Created)
DI   01-FEB-1995 (Rel. 31, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.
GN   CRF4
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=FETAL BRAIN;
RX   MEDLINE: 93300510.
RA   Iutfalga G., Gardiner K., Uze G.,
RT   *A new member of the cytokine receptor gene family maps on chromosome
RT   21 at less than 35 kb from IFNAR *.
RL   Genomics 16:366-373(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE: 96054036.
RA   Iutfalga G., McInnis M.G., Antonarakis S.E., Uze G.,
RT   *Structure of the human CRF4 gene: comparison with its IFNAR
RT   neighbor *.
RL   J. Mol. Evol. 41:338-344(1995).

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CC
CC -1- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM:
CC -1- SUBCELLULAR LOCATION: TYPE I, MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC or send an email to license@isdb-sib.ch).
CC -----

DR	EMBL; Z17227; CAJ78933.1;	-
DR	EMBL; U08988; AA68672.1;	+
DR	PIR; A47003; A47003.	
DR	HSSP; P13726; IDAN.	
DR	MIM; 123889;	
KM	Receptor; Transmembrane; Glycoprotein; Signal.	
FT	SIGNAL	1..19
FT	CHAIN	20..325
FT	DOMAIN	20..220
FT	TRANSHEM	221..249
FT	DOMAIN	230..325
FT	DISULEID	66..74
FT	DISULEID	188..209
FT	CARBOHYD	49..68
FT	CARBOHYD	102..102
FT	CARBOHYD	161..161
FT	CARBOHYD	124..124
FT	CONFLICT	269
FT	CONFLICT	274
SO	SEQUENCE	325 AA; 37011 MM; 66706C79F8514B3 CRC64; MISSING (IN REF. 2). FLAGDP -> VERME (IN REF. 2).

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alignment_scores:      Quality: 228.50      Length: 224
                       Ratio: 1.693      Gaps: 8
Percent Similarity: 60.268      Percent Identity: 29.911
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alignment_block:
US-09-240-675-1 x CRF4_HUMAN
Align seg 1/1 to: CRF4_HUMAN

Align seg 1/1 to: CRF4_HUMAN from: 1 to: 325

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81 TGGGTGTTGTCGCGAGCGCGAGTGGAAAAAATATAAACT... 122
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
3 TrpSerLeuGlySerTTrpLeuGlyGlyCysLeuLeuValSerAlaLeuG1 19
123 ..... CCTCAAAAAGTAGAGTGTCGACATCATGATGACAACT 159
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
19 YMetValProProGlnuSnValArgMetAlaSnSerValAlaSnPheYsa 36
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
160 TTATCCTAGAGGTGCAGACACGACGACGATGTCGTGGGAAATGTGACTTT 209
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
36 snIleLeuGlnTrpGlnSerProAlaPheAlaIlyscGlyAlaLeuThrPhe 52
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
210 TCATTCGATTCATCAAAAACCTGGAGTCGAAATTCGATTAATAATTCCTGG 259
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
53 ThrAlaGlnIlyr ..... LeuSerTyrArgIleGlnSply 65
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
260 GTGCAGAAATTTACTAGTACCAAAATCAACTTTCTTCACAGCTGA 309
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
65 sCyMetAlaSnThrThrLeuThrGlnGlyAspPheSerSer ..... LeuS 80
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
310 ATGTTTTCAGAGAAATTAATTCGCGTAAAGAGCAGAA ..... AAAGAAAC 356
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
80 eTrpIlyTrpGlyAspHisThrLeuThrValArgAlaGlnPheAlaAspGlu 96
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
357 ACCTTCCTCAGGATGATGAGGTGACTACTTTTACACCAATTCGCAAACTCA 406
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
97 HisSerSpirValAlaSnIle ..... ThrPheCysProValAlaAspSphTr 1122

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[illegible]

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seq.name: SwissProt_38:INGS_HUMAN
seq.documentation_block:
ID      INGS_HUMAN      STANDARD:      PRT:      337 AA.
AC      P36484.
DT      01-OCT-1994 (Rel. 30, Created)
DT      01-OCT-1994 (Rel. 30, Last sequence update)
DT      01-NOV-1997 (Rel. 35, Last annotation update)
DE      INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA
DE      RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).
GN      IFNGR2 OR IFNGCT1
OS      Homo sapiens (Human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominoidea; Homo.
(1)
RA      SEQUENCE FROM N.A.
RX      TISSUE-LUNG.FIBROBLAST.
RX      MEDLINE: 94170380.
RA      Soh J., Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R.,
RA      Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.,
RT      Identification and sequence of an accessory factor required for
RT      activation of the human interferon gamma receptor.
RL      Cell.76:193-802(1994)
CC      1- FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR
CC      SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF
CC      THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO
CC      INTERACT WITH GAF, JAK1, AND/OR JAK2.
CC      1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC      1- SIMILARITY: CONTAINS 2 FIBROBLAST-TYPE III-LIKE DOMAINS.
CC      1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed, usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
DR      EMBL: D05875; AAA16955.1;
DR      EMBL: D05877; AAA16956.1;
DR      PFM: PFM0041; fn3.1.
DR      Receptor: Transmembrane; Glycoprotein; Signal; Repeat.

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60 GTGCTGTCCGCCGGCGGCCCATGGGTGTTCGCCGACGCCAGGTGA... 107
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9 LeuleuleuleuleuglyValPheIleAlaIleAlaIleAlaProIols 25

108 ..... AAAATCTAAATCTCCTCAAAAAGTAGAGTGCATCATNG 150
      :::::||||| :::::||||| :::::||||| :::::|||||
25 ProlenSerLeInnProAlaProGlnHisProLysIleAglLeuTYA 42

151 ATGACACTTAATCTCGTAGGTG..... AACAGAAC 182
      :::::||||| ||| ||| ||| ||| ||| ||| |||
42 snlaagluInvalIleuSerTrpIguProValAlaIleuSerInserrThr 58

183 GATGAGTCTGTGGGAAATGTGACTTTTCATTGATTACAAAAAATCG 232
      ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
59 ArgProValValTYArgValGlnPheLysTYrHisPserLys.... 73

233 GATGATTAATGGATAAATGTCT..... GGSTGTC 264
      ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
74 ..... TrpPheThrAlaAspIleMetSerIleGlyValAsnCysT 87

265 AGAATATTACTAGTACCAATGCAACTTTTCTCA..... 299
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
87 hrgIleThrAlaIlehrgLucyAsnPheThrAlaIleSerProserAla 103

300 ..... CTCACGTGAATTTTATGAGAATTAATTCGCTATAG 340
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
104 GlyPhePrometAspPheInsVal..... ThrLeuArgLeuTr 116

341 AGCAAAAGAAAGAAACACT... TCCTCATGCTATGAGTGTGACTCATTA 387
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
116 galagluLeuGlyAlaIleuHisSerAlaIleThrAlaIleMetProIphg 133

388..CACCATTTTGCAAAAGCTCAGATTGTCTCTCCAGAACTACATTAGAA... 434
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
133 InHIsTYrArgInsValThrValIGlyProIogu... AsnIleGlyVal 148

435 ..... GCGAAGATAGAAGCATATGAGTATGACATCTCTCGGACAAA 478
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
149 ThrProGlyGlnGlySerLeuIleIleArgPheSerSerProPheAspII 165

479 AGATAGCTTATGTGGGCTTGCGATGAGCTTAAAGCTTACATATAGCTTAC 528
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
165 enlaAspTrnSerThrAlaPhe..... PlecSYTYrTYrValH 178

529 TTATCTGGAAAAACCTTGACGCTAGAGAAAGAAAGATGAAATATTATT 578
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
178 IsTYrTrpIou... LysGlyGlyIleGlnIleValLysGlyProPhe 192
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seq documentation block:
ID INSR_RAT STANDARD: PRT: 1383.AA.
AC P15127: P97681:
AD 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INSULIN RECEPTOR PRECURSOR (EC 2.7.1.12) (IR).
GN INSR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RX MEDLINE: 90231337.
RX GOLDSTEIN B.J., DUDLEY A.L.;
RA Goldstein B.J., Dudley A.L.;
RT "The rat insulin receptor: primary structure and conservation of
RT tissue-specific alternative messenger RNA splicing."
RL Mol. Endocrinol. 4:235-244(1990).
RN [2]
RP PARTIAL SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Liu Y., Tam J.W.O.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS RECEPTOR BINDS INSULIN AND HAS A TYROSINE-PROTEIN
CC KINASE ACTIVITY
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- ENZYME REGULATION: AUTOPHOSPHORYLATION ACTIVATES THE KINASE
CC ACTIVITY.
CC -1- SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE
CC BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-
CC BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINASE DOMAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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CC entities requires a license agreement (see http://www.isb-sdb.ch/announce/
CC or send an email to license@sdb.ch).
CC
CC EMBL: M29014; AAA41441.1;

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DR	EMBL	AF005776	AAB61414.1	
DR	EMBL	AF005777	AAB61415.1	
DR	EMBL	U80653	AAB58746.1	
DR	EMBL	U80652	AAB38968.1	
DR	EMBL	U80631	AAB38968.1	JOINED.
DR	EMBL	U80630	AAB38967.1	
DR	EMBL	U80629	AAB38967.1	JOINED.
DR	PIR	A36080	A36080.	
DR	HSSP	P06213	11RK.	
DR	PRINTS	PRO0014	ENTPEP11.	
DR	PRINTS	PRO0109	TYRKINSE	
DR	PROSITE	PS00107	PROTEIN_KINASE_ATP_1	
DR	PROSITE	PS00109	RECEPTOR_TYR_KIN_1	
DR	PROSITE	PS00239	RECEPTOR_TYR_KIN_11	
DR	PROSITE	PS50011	PROTEIN_KINASE_DOM_1	
DR	PFAM	PF00041	fn3_1	
DR	PFAM	PF00069	phkinase_1	
DR	PFAM	PF00757	Furin-like_1	
DR	PFAM	PF01030	Recep_L_domain_1	
DR	Transferrase		tyrosine-protein kinase; Receptor; Transmembrane; Glycoprotein; ATP-binding; Phosphorylation; Signal; Repeat.	
KM	GLYCOP	Signal	1	
FT	CHAIN	27	760	
FT	PROPEP	761	763	
FT	CHAIN	764	1383	
FT	DOMAIN	764	957	
FT	TRANSMEM	958	978	
FT	DOMAIN	979	1383	
FT	DOMAIN	619	848	
FT	DOMAIN	849	949	
FT	DOMAIN	1024	1298	
FT	NP_BIND	1030	1038	
FT	BINDING	1058	1058	
FT	ACT_SITE	1160	1160	
FT	MOD_RES	1190	1190	
FT	ACT_SITE	1000	1000	
FT	DISULF	461	494	
FT	DISULF	550	550	
FT	CARBOHYD	42	42	
FT	CARBOHYD	51	51	
FT	CARBOHYD	104	104	
FT	CARBOHYD	137	137	
FT	CARBOHYD	241	241	
FT	CARBOHYD	281	281	
FT	CARBOHYD	321	321	
FT	CARBOHYD	363	363	
FT	CARBOHYD	423	423	
FT	CARBOHYD	444	444	
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FT	CARBOHYD	770	770	
FT	CARBOHYD	783	783	
FT	CARBOHYD	921	921	
FT	CARBOHYD	934	934	
FT	CONFLICT	1119	1119	
FT	SEQUENCE	1383	AA: 16756 MW: 489195656902A944A CRC64;	

[illegible]

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US-09-240-675-1 x INSR_RAT
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472 SerGlyThrGlyArgGlnGluArg.AsnAspIleAlaLeuLysThrA 488

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175  AACAGAGCATGATAGCTGTGCGGAAAGTGCATTTTCATCGATTAACAA 2244
176  ..... 111 111
488  stcglaspnlmlaserCysgluasgluleuleuylsPheSerPheIle 5046
225  AAAACTGGGATGGATTAAT ..... 2424
505  ArgThrSerPheAspLysIleLeuLeuArgTrpLupIrrProTrp 5211
243  ..... TCGATAAATTGCTGGGT 2611
531  oAspPheArgAspLeuLeuGlYpHeMetLeuPheTrYlYsGluaIleProT 5388
262  GTCCAGAAATTTACT ..... AGTACCAAAATGCAACTTTTCTCA 2399
538  yTGluaValThrLcUpheAspGlyGluaInaspAlaCys ..... 5506
300  CTCAGCTGMAATGTTTATGMAAAATTAATTGCTATAGAAGCAGCAAAA 3494
550  ..... 5506
330  ACAAACACTTCTTATGATGGTATGAGGTACATTTACACCACTTTGCA 3999
551  ... GlySerAsnSerTrpThrValValAsp ..... 5599
400  AAGCTCAGATTGCTCTCCAGAAAGTACATTTAGAACTGAAGTAAAGCA 4499
350  ..... IleAspTrpProGln ..... ArgSerAsnSpProLys 5700
450  ATAGATATACACATCTCTCTCGAACAAAGATAGTATGAGGCGCTT 4999
571  SerGlnThrProSerHisProLys ..... TrpLeuIle 5811
500  GGATGGTTTAAGCTTTACATATAGTACTTACTTCTGGAAAACTCTTCAG 5499
581  Lafgely ..... 5883
550  GTGTGAAGAAGAAAGTAAAAATTTATTTCAGACATAAAAATTTTAAA 5599
583  ..... 5883
600  CTCACACAGAGACTTACTTATTTGTCTAAAGTTAAAGCAGCACTACTTAC 6449
584  LeuLysProTrpThrGlnThrValAlaIlePheValLysThrLeuValThrPh 6000
650  GTCACTGCAA ..... ATGGGTCTATAGTCAGTACATTGTATTA 6900
600  eSerAspLupArgThrTrpGlyAlaLysSerAspIleIleTrpValG 6171
691  AGACACAGATGAAATGAATGACTACTCCACGCAAGAAATTTAAATGTCAT 7400
617  InThrAspAlaThrAsnProSerValProLeuAspProIleSerValSer 6333
741  GTCCAAATCGAACTATGTTCTTAAATG ..... GATTATACATA 7811
634  AsnSerSerSerGlnIleIleLeuLysTrpLysProProSerAspProAs 6500
782  TGCAAACATGACCTTCAAGTCAAGTCAAGTGCCTCAGCCCTTTTAAAAAGA 8311
650  nglYAsnIleThr ..... 6544
832  ATCTGGAACACATTTGTATATAATG ..... AAACAATACCTGACGTGAA 8788
655  ... HisTrpLeuValTrpTrpGlnArgGlnAlaGlnLysSerGln 6688
879  AATGTCAAAACTACCCAGGTGTCTTCTCCAAAACGTTTCCAAAAGAG 9288
669  LeuPheGlnLeuLeuAspTrpCysLeu ..... LysGln 6788
929  AATTATACCTT ..... CTCCGGGTACAGCAT 9544
678  yLeuLysLeuProSerArgThrTrpSerProProPheGlnSerAspAs 6954

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565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000


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34 snvalthrileugserlyrlnmetasnprollevaltyrtrpqlutyr 50
180 AGCGAGAGTCGTGGGAGATGTG...ACCTTTTCATTCGATTATACAAA 226
51 .....Glnilemetproglvalprovalphervaleglvalylsas 65
227 AACGGGATGATTAATGGATTAATGTCTGGGTGCAGAAATTTACTA 276
65 ntyrlyvalylsasnserserlyrtrpilleaspilacyslleasnsleserh 82
277 GTACCAATGCACTTTCTCTCAAGCAGCATGTTTGAAGAAAT 326
82 tshstrlyrlyrlnleaseraspilvalglyaspseroserserleu 98
327 AAATGGGTATAGACA...GAAAGAAAACCTCTTCATG 367
99 Trpvalargvalylsalargvalglylnlysglu.....Serlaly 113
368 GTATGAGTTCATCTATTACACATTTGCCAAAGCTCAGATTGGCTC 417
113 talalyserserlyrlnlealvalcysargaspilyllylleglyprop 130
418 CAGAGATCATTTAGAGCTGAGATAGCAATAGCATCATCTCT 467
130 rplysleuaspilarglyserlyrlnlysglnilemetlleaspile... 145
468 CTGGAACAAAAGATAGTGTATGTGGCTTGGATGTTTACCTTAC 517
146 .....Pheh1 147
518 ATATAGCTTACTTCTGGAACAACTCTCAGGTGAGAGAAAGATG 567
147 sproservalphelyal.....Asnrglyaspilunclunvala 160
568 AAAATATTATTCAGACATAAATTTATAACCTCACCCAGACACT 617
160 sp.....Tyraspptoglthrthr 166
618 TATGTGTAAAGTTAAAGCAGCACTACTTACGTGAGAAATTTGGTGT 667
167 Cystylleargvalyltyrasval.TyrvalArgmetasnly.....S 181
668 CTATAGCCAGTAC..ATGTATAAAGACCAAGTGAAGAAAGTAC 714
181 ergtulleuglyrlyrlnlethrlyrlnlysgluaspascysargp 197
715 CTCACACAGAAATATAGAGTCAAGTCCAAATCAGAACTAGTTC 762
198 lileuglyserlyrlnlealaleprovalseraserleuasnserlyrly 214
763 .....TAAATGGATTTACATATAGCAAAACATGACCTTCAAGTCA 805
214 svalseralagluclyvalleuhsval.....TrpG 225
806 GTGGCTCAGCCCTTTTAAAGGAATCCTGGAACCAT 846
225 lvalalthrlyrlnlyserlyrlnlysgluvalcysllyrtrillep 241
847 TGTATATGGAACAAATACCTGACGTGAATATGCAAACTACCCAG 896
242 Serlileyserserleutrp.....lleprova 251
897 TGTGTCTTCTCAAAAGCTTTCCAAAAGAAATTTACCTTCGCCGT 946
251 lvalalaleuvalleuvalleuvalleuvalleuvalleuvalleuval 268
947 ACAAGCATCTGATGGAATATACACATCTTTGGTCTGAGAGATAAGT 996
268 he.....Tyrilleyserserleuasnprolleuvalyllyr 280
997 TGTATATGAAATATACAGCTTCTCTACTCTCCAGCTTTTACATTA 1046
281 lileleuvalprolyserleuvalleuvalvalargseralthrleugl 297

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1047 T 1047
297 u 297
seq_name: SwissProt_38:MYO1_HUMAN
seq_documentation_lock:
ID MYO1_HUMAN STANDARD PRT: 1451 AA.
AC P52179;
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE MYOHEXIN 1 (190 KD TITIN-ASSOCIATED PROTEIN) (190 KD CONNECTIN-
DE ASSOCIATED PROTEIN).
GN MYO1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SKELETAL MUSCLE;
RX MEDLINE: 94095665.
RA Vinkeleer U., Obermann W., Weber K., Fuerst D.O.;
RT "The globular head domain of titin extends into the center of the
RT sarcomeric M band. cDNA cloning, epitope mapping and immunoelectron
RT microscopy of two titin-associated proteins."
RL J. Cell Sci. 106:319-330(1993).
CC - FUNCTION: MAJOR COMPONENT OF THE VERTEBRATE MYOFIBRILLAR M BAND.
CC BINDS MYOSIN, TITIN, AND LIGHT MEROMYOSIN. THIS BINDING IS DOSE
CC DEPENDENT.
CC - SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC - SIMILARITY: CONTAINS 7 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: X69090; CAA48833.1;
DR MIM: 603508;
DR PFM: PFM0041; fn3, 5.
DR PFM: PFM0047; 19; 3.
DR PRINTS: PR00014; FNTYPEIII.
KW Immunoglobulin domain, Muscle protein, Thick filament, Repeat.
FT DOMAIN 46 81 1
FT REPEAT 46 51 1
FT REPEAT 52 57 2
FT REPEAT 58 63 3
FT REPEAT 64 69 4
FT REPEAT 70 75 5
FT REPEAT 76 81 6
FT REPEAT 156 289 6
FT DOMAIN 290 384 6
FT DOMAIN 385 511 6
FT DOMAIN 512 612 6
FT DOMAIN 613 711 6
FT DOMAIN 712 816 6
FT DOMAIN 817 917 6
FT DOMAIN 918 1023 6
FT DOMAIN 1024 1137 6
FT DOMAIN 1138 1239 6
FT DOMAIN 1240 1352 6
FT DOMAIN 1353 1451 6
FT SEQUENCE 1451 AA; 162452 MW; 352933FE6CSFFD10 CRC64;

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alignment_scores:
Quality: 123.50
Ratio: 0.588

Length: 460
Gaps: 21

RA		Lasemann D., Steck A.J.	"Expression and developmental regulation of Eph-1, a neuronal
RT		Eph-like receptor tyrosine kinase in brain."	
RL		Neuroscience 63:163-178(1994).	
CC	-1-	FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO	
CC	-1-	EPHRIN-A1, -A2, -A3, -A4 AND -A5.	
CC	-1-	CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP +	
CC	-1-	PROTEIN TYROSINE PHOSPHATE.	
CC	-1-	SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	
CC	-1-	ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY	
CC	-1-	ALTERNATIVE SPLICING.	
CC	-1-	TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS	
CC	-1-	SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.	
CC	-1-	SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC	
CC	-1-	DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.	
CC	-1-	SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.	
CC	-1-	This Swiss-Prot entry is copyright. It is produced through a collaboration	
CC	-1-	between the Swiss Institute of Bioinformatics and the EMBL Outstation -	
CC	-1-	the European Bioinformatics Institute. There are no restrictions on its	
CC	-1-	use by non-profit institutions as long as its content is in no way	
CC	-1-	modified and this statement is not removed. Usage by and for commercial	
CC	-1-	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	-1-	or send an email to license@sib-ch.ch).	
DR		EMBL; X76889; CA53537.1; -	
DR		HSSP; P00523; 2PTR.	
DR		PRINTS; PR00014; FNTYPEP11.	
DR		PRINTS; PR00109; TYRKINASE.	
DR		PROSITE; PS00107; PROTEIN_KINASE_TYR_1.	
DR		PROSITE; PS00109; PROTEIN_KINASE_TYR_1.	
DR		PROSITE; PS50011; PROTEIN_KINASE_DOM_1.	
DR		PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.	
DR		PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.	
DR		PROSITE; PS01186; BGF_2; UNKNOWN_1.	
DR		Pfam; PF00041; fcs; 2.	
DR		Pfam; PF00069; pkinase; 1.	
DR		Pfam; PF01404; Eph_Lbd; 1.	
KW		Transferase; tyrosine-protein kinase; ATP-binding; phosphorylation;	
KM		Receptor; transmembrane; glycoprotein; signal; alternative splicing.	
FT		SIGNAL	1 ?
FT		CHAIN	? 1005
FT		DOMAIN	? 575
FT		TRANSMEM	576 596
FT		DOMAIN	597 1005
FT		DOMAIN	677 938
FT		NP_BIND	703 691
FT		BINDING	709 709
FT		ACT_SITE	802 802
FT		CARBOHYD	266 266
FT		CARBOHYD	301 301
FT		CARBOHYD	371 371
FT		CARBOHYD	425 425
FT		CARBOHYD	438 438
FT		CARBOHYD	463 463
FT		VASPLIC	10 20
FT		VASPLIC	306 358
FT		VASPLIC	358 470
FT		VASPLIC	597 621
FT		VARSPLIC	170 170
FT		CONFLICT	566 566
FT		CONFLICT	578 578
FT		CONFLICT	669 669
FT		CONFLICT	708 708
FT		CONFLICT	979 979
FO		SEQUENCE	1005 AA; 111007 MW; 1ABDA2C99693C574 CRC64;

Alignment scores:		Quality: 118.00	Length: 458
Percent Similarity:	Ratio: 0.602	Gaps: 21	Percent Identity: 20.087
Alignment block: US-09-240-675-1 x EPA5_RAT			
Align seg 1/1	to: EPA5_RAT	from: 1	to: 1005
105	GGAAAAATCTAAATATCTCTCAAAAAGTAGGCTGCATCAATA.....	144
165	GLYARGSNHILIELYASPSHSGILTYLRIELYSILHSPHILHIALI	181
150	GATGACACACTT.....	170	ATCTGAGTGGA
181	AASPDLERHERHTRIGLLEUASRLGLYASPARGLALWELYSLEUA	198
175	ACAGAGCGAGAGAGCTGTGGGAATGGAGT.....	215	TTTTCATTC
198	SNPHGLIVALALASPALGLYPROLEUSERLYSGLYPHETYLEU	214
216	GATTATCAAAAAGCTGGGATGATAATTCGATTAATAATTCGTGGGTCA	265
215	ALAPHESINASPVALGY.....	222	ALACYSII
266	GAATTTACTATGAC.....	300	AAATGCACCTTTCTTCAC
223	EALAEULVALSERVALALRYVALITYTYLYSLYSPROSERVALVALA	240
301	TCAAGCTCAATGTTATGAGAAATTAATTCGCTHNAAGCAGAAAAA	356
240	RGHISLEALVALPHENPROSP.....	251	THLLETHGLY
351	GAACAACCTTCTATGATAGAGATTGACATTCATTACACATTTCGCA	400
252	ALASPSPSERSGILNLEUGLVALISERGLYSECYVALHSHLISE	266
401	AGCTCAGATTGTGCTCCAGAAAGTACATTTGAAGCTGAAGANNAAGCAA	455
268	IVALTHNASPARSPROPLYSMETHLYSCYSERLALGLYGLYTRPL	285
451	TAGTGATACATCTCTCTGGACCAAAAGATAGTGTATGTGGGCTTGG	500
285	EVAL.....	239	PROLIEGLYSGYMECYs
501	GATGGTTTACGTTTACATATAGCTTACTTATCTGGAACAACTTCACG	550
294	286	LYSALAGI
551	TGTAGAGAAAGATGTAATAATAT.....	597
296	UTYGLGILLYASNSGLYTHRCYSGILVALCYVALPROGLYRPHENHEL	313
598	AACSTCAGCAGACACTATTAATGCTTAAAGTTAAACAGACACTACTT	647
313	YSLASERPROHLISSEGLNTHRCYSEERYSCYSPROPRO.....	326
648	ACGTCATGGAATATGGTGTCTATAGTCCAGTACAT.....	683
327	336	HLISERTYTHHISGLIULALASERTH
684	719
336	TSERCYSVALCYSGILYASPRYTRPHEALGRLGELUSERASPRPROTOR	353
720	740	CSAGAAATATAGAAAGTCAGI
353	HYMETALACYSTHARGLPROFROSERALALPROALRYGSHALILIESERAN	369
741	GTCGAAATAGACACTATGTTCTTAATGCG.....	770

```

370 ValAsnGluThrSerValPheLeuGluThrPheProAlaAspThrG1 386
771 .....GATTATACATATGCAAAACATGACCTTTCAGTTCAGTGC 810
386 yGlyGlyLysAspValSerTyrThrLeuGlyLysGlySAsn...S 402
811 TCCAGCCCTTTTAAAGAAATCTCGAAGAACATTTGTATTAATGAAGA 860
402 eRh1AlaGlyValCysGluGlyCysGlyGlyHisValArg... 415
861 CAAATACCTGACTGTGAATGCAAAACTACCAGTGTCTTCCCA 910
416 .....TyrLeuProG1 419
911 AAACCTTTTCCAAAAGAAATTTACTTCCGCGTACAGACATGATG 960
419 nGlnIleGlyLeuLysAsnThrSerValMetMetAlaAspProLeuAlaH 436
961 GAAATACACATCTTTTGGTGTGAAGATAAAGTTGATACGTAAATA 1010
436 1stHisAspTyrThrPhe.....GluIle 443
1011 CAAGCTTTCCTACTCCCTCAGCTTACATTAGATCCCTAGTATTC 1060
444 GluAla.....ValAsnGlyValSerAspLeuSerProG1 455
1061 ATTCATATCATATATCGGT.....CTCCAAAACAGTCTGGAACA 1101
455 yThrAlaGlyLysValSerValAsnValThrThrAsnGlnAlaAlaProS 472
1102 CGCCTGTGATCCAG..... 1115
472 eProValThrAsnValLysGlyLysIleAlaLysAsnSerIleSer 488
1116 .....GATTATCA.....CTGATTATGA 1135
489 LeuSerTyrPheGlnIleProAspArgProAsnGlyIleIleLeuGluTyrG1 505
1136 AATTATTTTGGGAAACACATTCATATGCTGAGAGAAAATATGAG. 1184
505 ulleLysTyrPheGlnIleLysAspGlnIleThrSerTyrThrIleIleLys 522
1185 .....AAAAAATGATGTTACAGTTCCTAATTTGAACACTGATGATAT 1232
522 eLysGluThrThrThrIleThrAlaGluGlyLeuLysProAlaSerValTyr 538
1233 TGTGTGAAGCCAGACACACACC 1256
539 ValPheGlnIleLysArgAlaArgThr 546
seq_name: SwissProt.38:IIOR_MOUSE
seq_documentation_block:
ID IIOR_MOUSE STANDARD. PRF: 575 AA.
AC 061727;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R)
GN IL10RA OR IL10R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NM [1]
RP SEQUENCE FROM N.A. FL: TISSUE-HEMATOPOIETIC;
RX MEDLINE: 94068585.
RA HO A.S.-T., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;
RT Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).
CC -1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

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CC entities requires a license agreement (see http://www.isb.ch/announce/
CC or send an email to license@isb.slb.ch).
DR EMBL: L12120; AAA16156.1;
DR MGD: MGI:96538; IL10RA.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1
FT CHAIN 17
FT DOMAIN 17 241 INTERLEUKIN-10 RECEPTOR.
FT TRANSMEM 242 262 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 263 575 POTENTIAL.
FT DISULFID 204 225 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 50 50 POTENTIAL.
FT CARBOHYD 66 66 POTENTIAL.
FT CARBOHYD 113 113 POTENTIAL.
FT CARBOHYD 182 182 POTENTIAL.
FT CARBOHYD 238 238 POTENTIAL.
SQ SEQUENCE 575 AA; 64248 MW; 820B9CD576F686B7 CRC64;

alignment_scores:
Quality: 117.50 Length: 389
Ratio: 0.691 Gaps: 16
Percent Similarity: 43.702 Percent Identity: 20.308

alignment_block:
us-09-240-675-1 x IIOR_MOUSE
Align seg 1/1 to: IIOR_MOUSE from: 1 to: 575
63 CTCGTGCGCGGCGCCATGCGGTGTCGCCAGCCGAGGTGGAAGAA 112
|||||
9 LeuValAlrThrIleSerSerLeuSerLeuGlnIleAlaTyrGlyThrG1 25
|||||
113 TCTAATATCTCTCAAAAAGTAGAGGTGACATCATAGATCAACACTTA 162
|||||
25 uLeuProSerProSerTyrValThrPheGlnAlaArgPheGlnHisI 42
|||||
163 TCCGTAGGTG.....AACAGAGCGATGACTGTGCGGAGAT 200
|||||
42 IeLeuHisTyrLysProIleProAsnGlnSerGlnSerThrTyrGly 58
|||||
201 GTGACTTTTCATTCGATTATCAAAAACGTGGATGATTAATGGATMA 250
|||||
59 ValAlaIleu.....LysGlnTyrGlyLysSerThrTyrPAsnAs 71
|||||
251 ATGTCGTGGGTGCAATATTAATAGTACCAACCAATTTCTTCTAC 300
|||||
71 PheHisIleCysArgLysAlaGlnAlaLeuSerCysAspLeuThrP 88
|||||
301 TCAACCTAATGTTATGACAA.....ATTAATTCGGATAGA 341
|||||
88 heRh1LeuAspLeuLysThrHisArgSerTyrGlyTyrArgAlaArgValArg 104
|||||
342 GCA.....GAAAGAAACACCTTTCATAGTATGAGTGTGCTCA...TT 385
|||||
105 AlaValAspAsnSerGlnTyrSerAsnThrPheThrThrGluThrArgPh 121
|||||
386 TACACCATTTGCAAAACCTCAGATTGTCCTCCAGAACTACATTAGAG 435
|||||
121 eRh1..... 122
436 CTGAAGATAGAGCATAGTATACATCTCTCTGGAACAAAGATGT 485
|||||
123 ..ValAspGluValIleLeu.....ThrValAspSer 132
|||||
486 GTT...ANGTGGCTTGGATGATTAGCTTTACATATACTACTAT 532

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RP RP SEQUENCE FROM N.A.
RA MEDLINE: 90094325.
RX Flores-Riveros J.R., Sibley E., Kastelic T., Lane M.D.:
RT "Substrate phosphorylation catalyzed by the insulin receptor tyrosine
RT kinase: kinetic correlation to autophosphorylation of specific sites
RT in the beta subunit."
RL J. Biol. Chem. 264:21557-21572(1989).
RN (2)
RP SEQUENCE OF 1-33 FROM N.A.
RX MEDLINE: 90099338.
RT Sibley E., Kastelic T., Kelly T.J., Lane M.D.:
RL "Characterization of the mouse insulin receptor gene promoter."
RL Proc. Natl. Acad. Sci. U.S.A. 86:9732-9736(1989).
CC -1 FUNCTION: THIS RECEPTOR BINDS INSULIN AND HAS A TYROSINE-PROTEIN
CC KINASE ACTIVITY.
CC -1 CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1 ENZYME REGULATION: AUTOPHOSPHORYLATION ACTIVATES THE KINASE
CC ACTIVITY.
CC -1 SUBUNIT: Tetramer of 2 alpha and 2 beta chains linked by disulfide
CC BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-
CC BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINASE DOMAIN.
CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1 SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -1 SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb.slb.ch).
CC -----
CC EMBL: J05149; AAA39318.1;
DR EMBL: M28869; AAA39319.1;
DR PIR: A34157; A34157.
DR HSRP: P06213; IIRK.
DR MGD: MG1:96575; INSR.
DR PRINTS: PR00014; ENTPEIIT.
DR PRINTS: PR00109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
DR PFAM: PF00041; fn3_1.
DR PFAM: PF00069; pkinase_1.
DR PFAM: PF00757; pkinase-like_1.
DR PFAM: PF01030; Recep_L_domain_1.
KM Transferrin: Tyrosine-protein kinase: Receptor; Transmembrane;
KW Glycoprotein; ATP-binding; Phosphorylation; Signal; Repeat.
FT SIGNAL. 1 27
FT CHAIN 28 743
FT PROPEP 750 752
FT CHAIN 753 1372
FT DOMAIN 753 946
FT TRANSMEM 947 967
FT DOMAIN 968 1372
FT DOMAIN 1372 937
FT DOMAIN 938 938
FT DOMAIN 1013 1286
FT NP_BIND 1019 1027
FT BINDING 1047 1047
FT ACT_SITE 1149 1149
FT MOD_RES 1179 1179
FT ACT_SITE 989 989
FT DISULFID 462 495
FT CARBOHYD 551 551
FT CARBOHYD 43 43
FT CARBOHYD 52 52
FT CARBOHYD 105 105
FT CARBOHYD 138 138
FT POTENTIAL.
FT POTENTIAL.
FT POTENTIAL.
FT POTENTIAL.
FT INTERCHAIN (BY SIMILARITY).

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588 LeuLysProThrPThrGlnTyrAlaIlePheValIleLysThrLeuValThrPhe 601
650 GTCATCGGAA.....ATTGGTGTATAGTCACATCATGTATATA 690
    ||| ||| ||| ||| |||
601 eSerSpeliuNgaGlyThrTyrGlyAlaIleLysSerAspIleLeuTyrValG 618
    :||| :||| :||| :||| :|||
691 AACACACAGTTGAAATGATGACTACCTCCACAGAAATAATGAAAGTCACT 740
    :||| :||| :||| :||| :|||
618 InThAspAlaThrAsnProSerValProLeuAspProIleSerValSer 634
    :||| :||| :||| :||| :|||
741 GTCCAAATCAGACTAATGTTCTTAAAG.....GATATACATA 781
    :||| :||| :||| :||| :|||
635 AnSerSerSerGlnIleLeuLysThrLysProProSerAspProAs 651
    :||| :||| :||| :||| :|||
782 TCCAAACATGACCTTTCAGATTCACTGGCTCCACGCTTTTAAAGCA 831
    :||| :||| :||| :||| :|||
651 polyAsnIleThr..... 655
    :||| :||| :||| :||| :|||
832 ATCTCGAAACCATTTGTATATAATGG...AACAAATACCTGACTGTGAA 878
    :||| :||| :||| :||| :|||
656 .....HisTyrLeuValTyrTrpGluArgGlnIleGluAspSerGln 669
    :||| :||| :||| :||| :|||
879 AATGTCAAACATCACCCAGTGTCTCTTCTCCAAACGTTTCCAAAGAAG 928
    :||| :||| :||| :||| :|||
670 LeuPheGlnLeuAspTyrCysLeu.....LysGln 679
    :||| :||| :||| :||| :|||
929 AATTATACCTT.....CTCCGCGTACACAGAT 954
    :||| :||| :||| :||| :|||
679 yLeuLysLeuProSerArgThrTyrSerProProPheGlnSerAspAsp 696
    :||| :||| :||| :||| :|||
955 CTGATGGAATATACACATCTTTTGGTGTGAAGATA..... 992
    :||| :||| :||| :||| :|||
696 eGlnLysHisAsnGlnSerGlnTyrAspAspSerAlaSerGlnCysGly 712
    :||| :||| :||| :||| :|||
993 .....AACTTGATATCTGAATATACACGTTTCCATCTCCATCCAGT 1033
    :||| :||| :||| :||| :|||
713 SerCysProLysThrAspSerGlnIleLeuLysGlnLeuGlnSerSe 729
    :||| :||| :||| :||| :|||
1034 CTTTACATAGTACGCTTAGTATGATTCATTCATCTATATCGGTGTC 1083
    :||| :||| :||| :||| :|||
729 rPheArg...LysThrPheGlnAspTyrLeuHisAsnValAlaPheValP 745
    :||| :||| :||| :||| :|||
1084 CAACACAGTCT.....GGAAC..... 1100
    :||| :||| :||| :||| :|||
745 rGlnProSerArgLysArgArgSerLeuGlnValAlaGlnValThr 761
    :||| :||| :||| :||| :|||
1101 .....ACGCTGTATGCCAGATATATCCACGATTTATGAATATATT 1144
    :||| :||| :||| :||| :|||
762 AlaThrThrLeuThrLeuProAspPheProAsnValSerSerThrIleVal 778
    :||| :||| :||| :||| :|||
1145 TTGGAAACACTTCATATGTCGAGAGAAATTAATCGAGAA..... 1187
    :||| :||| :||| :||| :|||
778 L.....ProThrSerGlnGlnHisArgProPheGlnLysValValA 793
    :||| :||| :||| :||| :|||
1188...AAACATGATGTACAGTCTCTAATTTGAACACATGACTGATATTT 1235
    :||| :||| :||| :||| :|||
793 snuYsgLysSerLeuValIleSerGlnLeuArgHisPheThrGlnTyrArg 809
    :||| :||| :||| :||| :|||
1236 GTGAAGCCAGACACACACACATGATGAAACCTGAATTAAGACGCT 1285
    :||| :||| :||| :||| :|||
810 IleGlnLeuGlnAlaLysAsnGlnAspSerProAspGlnArgCysSerVa 826
    :||| :||| :||| :||| :|||
1286 TTTTAGGACGGCTGTGTGAGAAACAAACCA 1319
    :||| :||| :||| :||| :|||
826 L...AlaAlaTyrValSerAlaArgThrMetPro 836
    :||| :||| :||| :||| :|||
seq_name: SwissProt_38: PTPD_HUMAN
seq documentation_block:
ID: PTPD_HUMAN STANDARD: PRT: 1912 AA: ---
AC: P23468:
DT: 01-NOV-1991 (Rel. 20, Created)
Dr: 01-OCT-1996 (Rel. 34, Last sequence update)

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535 ertphtpProPomgSer.....Asphttle 544
1125 CTGATTATGAAATATTTTGGGAAACACTTCAGAGAGAGAA 1174
545 AlaSerThraGluLeuValTyrIysAspGlyGlnHisGlyGlnGlnGln 561
1175 AATT...ATCGAGAAAAAACTGAGTGTACAGTCTCTAATTTGAAACAC 1221
561 glierHrIleGluProGlyThrSerTyrAlaGluGlnGlyLeuProA 578
1222 TGACTGTATAT..... 1232
578 snSerLeuTyrTyrPheArgLeuAlaAlaArgSerProGlnGlyLeuGly 594
1233 .....TGCTGAAAGCCAGACACACACCATGATGAAAGCTGAATA 1276
595 AlaSerThraGluLeuSerAlaArgThrMetGlnSerTyr.....Pr 609
1277 AAGCAGTGTATTTAGTACGCTGTATGTAGGAAACAAACAGGAAATA 1326
609 oSerAlaProProGlnAspIleSerTyr.....ThrSerProSerTyr 624
1327 CCTCT 1331
624 hrSer 625
seq_name: SwissProt_38:MPSF_CHICK
seq_documentation_block:
ID MPSF_CHICK STANDARD; PRT: 1450 AA.
AC 002173.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE M-PROTEIN, STRIATED MUSCLE.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP TISSUE-EMBRIONIC PECTORALIS MUSCLE.
RX MEDLINE: 93015907.
RA Tanaka T., Masaki T., Imanura M., Kasuya Y., Sakurai T.,
RA Noguchi J., Tanagisawa M.
RT "Complete primary structure and tissue expression of chicken
RT pectoralis M-protein."
RL J. Biol. Chem. 267:20302-20310(1992).
CC -1- FUNCTION: IS A STRUCTURAL CONSTITUENT OF MYOFIBRILLAR M-BAND IN
CC STRIATED MUSCLE.
CC -1- TISSUE SPECIFICITY: IS EXPRESSED IN PECTORALIS AND CARDIAC MUSCLE.
CC -1- DEVELOPMENTAL STAGE: CAN BE DETECTED BY DAY 10-13 IN OVO, THE
CC CONTENT IS GRADUALLY INCREASED THROUGHOUT THE OVO DEVELOPMENT AND
CC REACHED ITS PEAK AFTER HATCHING.
CC -1- SIMILARITY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to: license@sdb.ch).
CC EMBL: D11474; BA02033.1;
DR PIR: A44027; A44027.
DR HSSP: P56276; 1TLK.
DR PFAM: PF00041; fn3. 5.
DR PFAM: PF00047; 197. 3.
DR PRINTS: PRO0014; PRTYPE11.
KW Muscle protein; Repeat; Immunoglobulin domain.
FT DOMAIN 143 238 19-LIKE C2-TYPE DOMAIN.

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FT DOMAIN 266 364 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 368 464 FIBRONECTIN TYPE-III.
FT DOMAIN 496 592 FIBRONECTIN TYPE-III.
FT DOMAIN 597 693 FIBRONECTIN TYPE-III.
FT DOMAIN 696 794 FIBRONECTIN TYPE-III.
FT DOMAIN 797 898 FIBRONECTIN TYPE-III.
FT DOMAIN 899 990 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 1002 1095 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 1126 1205 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 1225 1312 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 1333 1427 IG-LIKE C2-TYPE DOMAIN.
SQ SEQUENCE 1450 AA; 163400 MW; E313C7D39F6C67 CAC64;

Alignment scores:
Quality: 115.00 Length: 425
Ratio: 0.618 Gaps: 26
Percent Similarity: 43.765 Percent Identity: 21.647

Alignment_block:
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Align seg 1/1 to: MPSF_CHICK from: 1 to: 1450

87 TGTCCGCGAGCCGCGAGTGGAATAATCTAAATCTCCCAAAAGTAGA 136
366 LeuIleAlaGlyAlaProGly.....AlaProMetAspVally 378
137 GGC...GACATCATGATGACACACTTATCTCGAGAGACAGAGAGC 183
378 scyHisAspAlaAsnAspAlaProValIleValIleThrTyrProProA 395
184 ARGAGCTGTGCGGAAT.....GTGACTTTTTCATTCGATTATCAAAA 227
395 snThrThrSerGlnAsnProValIleGlyTyrPheValAspIysCysGln 411
228 ACTGGATGATTAATGATGATAAATGCTGGGTGCAGAAATATCTAG 277
412 ValGlyLeuGlnAsnTyrAl..... 418
278 TACCAATCAACTTTTCTTCACTCAAGCTGATGTTATGAAGAATA 327
419 ..GlnCysAsnAspAlaProValIleCysIysTyrProValThrG 434
328 AATG.....CGRTAAGACAGAGAAAAAGAA 353
434 ILeuTyrGluGlyArgSerTyrIlePheArgValArgAla..... 447
354 AACACTTCTCATGTATGAGGTGACATTTTACACCTTTGGCAAGC 403
448 .....ValAsnSerAlaGlyIleSerArgProse 457
404 TCGATTGCTCCCGAGAGTACATTAGACCTGAAGT.....AAGG 447
457 ArgValSerGluProValAlaAlaLeuAspProValAspLeuArgT 474
448 CATATGATATACATCTCTCTGA.....ACAAAGT 482
474 hTrIlnThrValHisValAspGluGlyArgIleValIleSerTyrAsp 490
483 AGGTATATGGCTTGGATGT..... 506
491 Asp.....LeuGluGlyAspIleGlnIleProGlyProProh 503
507 .....TAACTTCAATTAAGCTTACTTATGCA 537
503 TrAsnValHisAlaSerGluIleSerTyrThrValIleLeuSerTyrA 520
538 AAAC..... 542
520 spProProValProArgGlyArgGluProLeuThrTyrPheIleGlyIys 536
543 .....TCTTCAGTGTAGAGAAAGAGATTGAATAATTTATTC... 581

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537 SerMetValGlySerGlySerTrpGlnArgValAsnAlaGlnValAlaVala 553
552 .....AGACATTAATTTATTAATTAACCTCCACAGAGACTACTAT 621
553 ILysSerProAlaGlyTyrAlaValAlaPheAspLeuAlaGlnGlyLysProTyrV 570
622 GCTCAAGTTAAAGCAGACACTACTAGCTCATGAGAAATGCTGTCTAT 671
570 alphaArgVal.....LeuSerAlaAsnLysHisGlyLysSer 582
672 AGTCCAGTACATTTGTATTAAGACACACAGTGGAAATGAACATA..... 713
583 AspProSerGlnIleThrGlnProIleGlnProGlnAspIleValaVala 599
714 ..CTCCACACAGAAATATGAAGTACAGTCCAAAT.....CAGAACT 756
599 LProSerAlaProGlyArgValAlaValAlaThrArgAsnThrLysThrSerV 616
757 ATGTTCTTAATGGGAT..... 773
616 alphaValGlnTrpAspLysProLysHisGlnGlnAsnLeuTyrGlyTyr 632
774 TATACATATGCAAAACATGACCTTTCAAGTCCAGTCCACGCTTTT 823
633 TyrIleAspTyrSerValAlaGlySerAsnGlnTrp..... 644
824 AAAAAGAGATCTGGAACACATTTGTATTAATGGAACAAATACCTGACT 873
645 .....GluProAlaAsnHis.....LysProIle..... 652
874 GTGAATAGTCAAAACTACCCAGTGTCTTCCCAAAAGCTTTCCAA 923
653 .....AspTyrAsnArg.....PheValAlaHisGlyLeuGlu 663
924 AAAGCA...ATTACCTTCTCCGCTACAGACATCTGATGCA..... 962
664 ThrGlyGlnGlnTyrIlePheArgValAlaValAlaValAlaValGlyPh 680
963 ..AATACACATCTTTTGTCTGGAAGAGATTAAGTTGATCTGCAATAC 1011
680 eSerGlnAsnSerGlnGlnSerGlnAlaIleLys.....ValG 693
1012 AAGCTTCTCTACTCTCCAGCTTT.....ACATTAAGATCCCTTGT 1055
693 IAlaIleAlaLeuThrCysProSerTyrProHisGlyIleThrLeuLysAsn 709
1056 ..GATTCATTCATATCTATATCGT.....GTCGAAAGACGCTGG 1096
710 CysAspArgLysLeuSerMetThrLeuGlyTyrPylAspAlaProLysTyrSerG 726
1097 AAACGCGCTGTGATCCAGATTAAT 1121
726 yGlySerProIleLeuGlyTyrTyr 734

```

```

RA Ohashi K., Honda S., Ichinomiya N., Nakamura T., Mizuno K.;
RT "Molecular cloning and in situ localization in the brain of rat sky
RT receptor tyrosine kinase."
RL J. Biochem. 117:1267-1275(1995).
CC -1- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY
CC IN THE CENTRAL NERVOUS SYSTEM.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN
CC OTHER TISSUES.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D37880; BAA07119.1;
DR HSSP: P11362; 1FGT.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PRAM: PF00041; fn3; 2.
DR PRAM: PF00047; lg; 2.
DR PRAM: PF00069; pkinae; 1.
DR Receptor: Glycoprotein; Tyrosine-protein kinase; ATP-binding;
KW transferase; Phosphorylation; Transmembrane; Signal; Repeat;
KW Immunoglobulin domain.
FT SIGNAL 1 30
FT CHAIN 31 880
FT DOMAIN 31 419
FT TRANSMEM 420 440
FT DOMAIN 441 880
FT DOMAIN 34 115
FT DOMAIN 131 200
FT DOMAIN 214 301
FT DOMAIN 305 401
FT DOMAIN 508 785
FT NP_BIND 514 522
FT BINDING 540 540
FT ACT_SITE 645 645
FT MOD_RES 676 676
FT CARBOHYD 53 53
FT CARBOHYD 75 75
FT CARBOHYD 181 181
FT CARBOHYD 220 220
FT CARBOHYD 230 230
FT CARBOHYD 283 283
FT CARBOHYD 356 356
FT CARBOHYD 370 370
FT SEQUENCE 880 AA; 95918 MW; C3751E86AE5FA5B CRC64;

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alignment scores:

Quality: 113.50 Length: 355
 Ratio: 0.701 Gaps: 17
 Percent Similarity: 45.634 Percent Identity: 22.254

alignment block:

us-09-240-675-1.x TYO3_PAT
 Align seg 1/1 to: TYO3_PAT from: 1 to: 880:

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33 GTCGCTCTCTGCGCGGAGACAGACCTAGTCTGCTCCCGTGGCCCATG 82
15 LeuLeuLeuAlaGlnAlaSerLeuLeuLeuProLys..... 27
83 GGTGTCTTCGCGACGCCAGCTGGAATAATCTTAATCTCTCAAAAG 132

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28 .....SerAlaAlaAlaGlyLeuLysLeuMetGlyAlaProValLysM 42
133 TR.....GAGGTCCAGCATC 146
42 eThValSerInclGlyInProValLysLeuAsnGlySerValGlyGly 58
147 ATGATGACAACTTATCTGAGCTGGAACAGAGAGATGCTGCTGG 196
59 MetAspAspProAspLeu...HisThrMetLysAspGlyAlaValGly 74
197 GAAT.....GTGACTTTTCATTCGATTATCAAAAAGTGGAGTCG 237
74 nAsnAlaSerGlnValSerIleSerIleSerGlnGln..... 86
238 ATAAATGGATAAATTTGCTGGTGCAGATAATTTACTAGTACCAATGC 287
87 ..AsnTrpIleGlyLeuLeuSerLeuLysSerAlaGlnArgSerAspAla 102
288 AACCTTTCTTCACTCAAGCTGAATGTTATGAGAAATTAATTTGGTAT 337
103 GlyLeuTyTrpCysGlnValLysAspGlyGlnGlnThrLysIle..... 117
338 AAGACGAGAAAAGAAAACACTTCTTCATGATGAGTGAAGTGAAGTCA... 383
118 .....SerGlnSerValTrpLeuThrValGlnGlyValAlp 129
384 .....TTTACACATTTTCCAAAGCTCAGATGGTCTCCAGAAAGTACAT 428
129 roPhePheThrValGlnProLysAspLeuAlaValProProAsnValPro 145
429 TTAGAAGCTGAAGATAAGCAATAGTATACATCTCTCTGGAACAAA 478
146 pheGlnLeuSerCysGlnAla.....ValGlyProProGlnLup 158
479 AGATAGCTTATGCTG.....GCTTGGATGCTTAAAGCT 513
158 ovalThrIlePheTrpTrpArgGlyProThrLysValGlyGlyProAlaS 175
514 TTACATATAGCTTACTATCTGAAAAAAGCTTCCAGGTAGAGAAAGG 563
175 eSerProSerValLeu.....AspValThrGlyValThrGlnArg 188
564 ATGAAATATTTATTCAGACATAAATTATTAATCTCCACAGAGAC 613
189 ThrGlnPheSerCysGlnAlaHisAsnIleLysGlyLeuAlaThrSerTr 205
614 TACTTATGCTTAAAGTTAAACGACACTACTAGTCAATGAAATTCG 663
205 gProAlaIleIleArgLeuGlnAla..... 213
664 GTGCTATATGTCAGTACATTTGATTAAGCACACATTTGAAATGAAGTA 713
213 ..... 213
714 CCTCCA.....CCAGAAATATAGAGTC..AGTGTCCAAATATCAGAA 754
214 ProProAlaAlaProPheAsnIleThrValThrThrIleSerSerSerS 230
755 CTATGTTCTTAATG.....GATTATACATATGCAACATG 792
230 nAlaSerValAlaTrpValProGlyAlaAspGlyLeuAlaLeuLeuHis 247
793 CCTTTCAGTTCAGTGCCTCCAGCCCTTTTAAAGAGATCCTGGAAAC 842
247 eGlySerThrValGlnValAlaHisAla.....ProGly... 257
843 CATTTGATTAATGAAACAAATACCTGACTGGAATATGCAAACTAC 892
258 .....GlnTrpGlnAlaLeuAlaValAlaValAlaProValProProPh 271
893 CCAAGTGTGCTTCCCAAAAGCTTTCCAAAAAGAAATTACTCTCTCC 942
..... 942

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271 eThCysLeuLeu...ArgAsnLeuAlaProAlaThrAsnTrpSerLeuA 287
943 GCGTACAGCATCTGATGGAATAATACACATCTTTTGGCTGAGAGATA 992
287 rGValArgCysAlaAsnAlaLeuGlyProSerProTyGlyAspTrpVal 303
993 AAGTTGATCTGAA 1007
304 ProPheGlnThrLys 308

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130 ytcglullealeglnlleglyproptoglullealeuglnserlleasn 146
444 AAGGCAATAGTGTACACATCTCTCGAACAAGATAGTGT ..... 488
147 GlyAlaIleLeuAlaLeuAlaSerProptoglulAlaSerValArgly 163
489 ATGGGGCTTGGAGTGTAAAGCTTACATTAACCTTACTTATGTGA 537
163 smetp...leuIleSerValPhePheLeuSerValValIleTpa 179
538 AAACCTTCAGCTGTGAAGAGATGAAATTTATTCACACAT 567
179 spasnSerSerVal...GluLeuValArgSerIleLeuProIleasp 194
588 AAAATTTATTAATCTCACAGAGACTTATGTCTAAAGTAAAGC 637
195 ValIleAsnAspLeuAlaProglutThrTyrCysLeuLysValGlnAl 211
638 AGCAGTACTTACGTCATGAAAAATGGTCTATAGTCCAGTACATGTA 687
211 atpThrValProleuGluAspLysGlyLeuPheSerProIleHisCysI 228
688 TAAGACACACAGTGA...AATGAACTACTCCACAGAAATATAGAA 734
228 IeUThrThrArgLysValAsnAspLeuLysCysProthrAsnValArg 244
735 GTGAGTGTCCAAATCAGAACTATGTCTTAAATGGATATATACAT 782
245 ValPheAlaLeuAsnMetLysPheTyrIleLeuThrAspAsnIleTyrAs 261
783 GCMAACAGACCTTTCAGTCAAGTCAAGGCTCCAGGCTTTTAAAGA 831
261 ngulHisValThrTyrThrValGlnTyrLeuThrGlyTyrLeuLysAsn 278
832 ATCTGGAAACCATTTGTATTAAGGAAACAATACCTGACGTGAAAT 881
278 eutTyrAspArgTyrSerSerLysTyrPoiLysValSerGlyCysGlnAsn 294
882 GTCAAAACTACCCAGTGT ..... GTCTTCCCTCAAAACGT 916
295 IleThrSerMetLysCysAsnLeuSerSerValIleLysProthrSer 310
917 TTTCGAAAAAGAAATTACCTTCCTCCGCTCAAGCATGTGAGGAATA 966
311 .....AlaSerTyrTyrPheArgValGlnAlaMetAsnGluTyrS 324
967 ACACATCTTTTGGTGTGAAGAGATAAGTTGATACTGAATAACAAAGT 1016
324 eutLysSerCysLeuSerLysAspValGluValAspProIleValThrAsn 340
1017 TTCTTACTTCCCTCAGCTTATTAACATTAAGCTTATGATTCATTC 1066
341 GluIleGlyProIleProAspValLysValAspIleSerAspValLeuAsn 357
1067 TATCTATATGGGTGCTCCAAACAGCTGTGAACACCCCTGTATCCAGG 1116
357 sIleLysIleThrProIleGlyProGlyAsnLysIleMetSerAspL 374
1117 ATATTCAGTCAATTTATGAATTTTGGGAAACACTGAAAGCT 1166
374 eutTyrAspPheSerTyrGlnIleLeuTyrTyrLysAsnSerSerAspAsn 390
1167 GAGAGAAAAATTTATCGAAAAAAATCATGAT ..... GTTACAGTCC 1207
391 GlnGlnIleValLysMetLysGluThrLysGlnThrIleAlaThrValSe 407
1208 TAATTTAAACCACTGATATATGTGTGAAGCAAGCAAGCAAGCA 1257
407 AspLeuAlaToseThrLeuTyrCysValLysValGlnAla.....P 422
1258 TGCATGAAAGCTGAATAAAGCAGTGTTTTACTGACGCTGATGTAG 1307
.....
422 heSerGluAlaTyrAsnLysSerSerAspPheSerArgGluGluCysIle 438
1308 AAACAAAAACACAGA 1322
439 GlyThrAlaGly 443
seq_name: sp_rdent:061190
seq_documentation_block:
ID 061190 PRELIMINARY; PRT; 349 AA.
AC 061190:
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE CYTOKINE RECEPTOR FAMILY 2, MEMBER 4 (CLASS II CYTOKINE RECEPTOR 4).
GN IL10RB OR CRFB4 OR CRF2-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
SEQUENCE FROM N.A.
RP MEDLINE; 97199375.
RA GIBBS V.C.; PENNICA D.;
RT *CRF2-4: Isolation of cDNA clones encoding the human and mouse
RT proteins.
RL Gene 186:97-101(1997).
DR EMBL; U53696; AAC53062.1;
DR MGD; MG1109380; IL10RB.
DR PFM; PFM0041; fn3.1.
SQ SEQUENCE 349 AA; 39774 MW; 4AC1802A CRC32;
alignment_scores:
Quality: 222.50 Length: 214
Ratio: 1.660 Gaps: 9
Percent Similarity: 62.617 Percent Identity: 26.168
alignment_block:
US-09-240-675-1 x 061190 ..
Align seg 1/1 to: 061190 from: 1 to: 349
711 CTACCTCCACAGAAATATAGAGTGTGCAAAATCAGACTATGT 760
21 IleProProglulysValArgMetAsnSerValAspPheLysAsnI 37
761 TCTTAATGGAT ..... TATACATATGCAACATGACCTTCAAG 801
37 eleuGlnTyrPoiLysValPheProLysThrAsnLeuThrPheIAs 54
802 TTCAGTGGCTCCAGGCTTTTAAAGAAATCTGGAACCATTTGTAT 851
54 IeGlnTyr ..... Glu 57
852 AAATGAAACAAATACCTGAC...TGTGAATATGCAAACTACCCAGG 898
58 SerTyrArgSerPheGlnAspIleCysLysArgGlnAlaSerThrGlnC 74
899 TGTCTTCCCTCAAAAGCTTTTCAAAAGAAATTAACCTTCCGCGTAC 948
74 AspPhe...SerHisLeuSerLysTyrGlyAspArgThrValArgVala 90
949 AAGCATGTATGAAATACACATCTTTTGGTGTGAAGATTAAGTT 998
90 GlnAlaIleLeuAlaAspGlnLysSerGluTyr...ValAsnValThrPhe 105
999 GATCTGAAATCAAGCTTCTTACTGCTCCAGCTTATTAACATTAAGT 1048
106 CysProValGluAspThrIleIleLeuTyrProIleGluMetGlnIleG 122
1049 CTTTACTGATTCATTCATATATATATGAGTGTGCTCCAAACAGTGTGA 1098
122 IleuAlaGlnSerLeuHisLeuArgPheSerAlaPro...GlnIleGlu 138

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1099 ACACCCCTGTATCCAGATTATCACTGATTATGAA..... 1136
1137 ..ATTATTTTGGGAAACCTTCAATGCTGAGAGAAATTTTCGA 1183
155 ArgValIGLTLyTrrPlySAsngLYThrsAngLulysPheGlnValIse 171
1184 GAAAAAATGATGATTACAGCTTCTAATTGAAACCATGACTGTATTT 1233
171 rProtyrAspSerGluValIleuValrAsnLeuGluProtyrThrTyrC 188
1234 GTGTGAACCCAGACACACACATGATGAGAAAGTGAATTAACCACT 1283
188 yAlIleGlnValIGlnGlyPheLeuValAspGln.....AsnArgThrGly 202
1284 GTTTTATGACGCTGTATGTGAGAAACAAACAGAAAT 1325
203 GluTrpSerGluProIleCysGluArgThr.....GlyAsn 214
seq_name: sp_rodent:063953

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seq_documentation_block:
ID 063953 PRELIMINARY: PRT: 332 AA.
AC 063953
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA RECEPTOR BETA SUBUNIT).
GN IFNGR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
NC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
SEQUENCE FROM N.A.
RX MEDLINE; 94170381.
RA HEMMI S., BOHNI R., STARK G., DI MARCO F., AGUET M.,
RT "A novel member of the interferon receptor family complements
RT functional of the murine interferon gamma receptor in human
RT cells."
RL Cell 76:803-810(1994).
[2]
SEQUENCE FROM N.A.
RP STRAIN-139SV/3.
RX MEDLINE; 97128072.
RA EBERSPERGER C., RHEE S., MUTHUKUMARAN G., LEMBO D., DONNELLY R.,
RA PESTKA S., DEMBIC Z.,
RT "Genomic organization and promoter analysis of the gene ifng2
RT encoding the second chain of the mouse interferon gamma receptor."
RL Scand J Immunol 44:599-606(1996).
DR EMBL; U65599; AAC52938.1; JOINED.
DR EMBL; U65594; AAC52938.1; JOINED.
DR EMBL; U65595; AAC52938.1; JOINED.
DR EMBL; U65596; AAC52938.1; JOINED.
DR EMBL; U65597; AAC52938.1; JOINED.
DR EMBL; U65598; AAC52938.1; JOINED.
DR EMBL; S69336; AB30165.1; JOINED.
DR MGD; MG1107654; Ifngr2.
DR PRAM; PF00041; fn3; 1.
SQ SEQUENCE 332 AA; 37471 MW; 0BF24E9E CRC32;

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alignment_scores:
Quality: 203.00 Length: 229
Ratio: 1.471 Gaps: 13
Percent Similarity: 60.262 Percent Identity: 30.131

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Alignment block:
US-09-240-675-1 x 063953

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Align seg 1/1 to: 063953 from: 1 to: 332

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87 TTGCGCAGCCGACGTGCA.....AAAATCTAAATCTTC 124
16 LeuGlyAlaAlaIleSerSerProAspSerPheSerGlnLeuAlaIlePr 32
125 TCAAAAAGTAGAGCTGACATCATGATCACTTATTCCTAGAGTGA 174
32 OleuAsnProAlaGluHisIleuValrAsnAspGlnIleLeuThrTrp 49
175 ACAGAGCCGATGAGTCT.....GTGCGAATGTGACT 206
49 IuProSerProSerSerAsnAspProArgProValIleGlyGlnValGlu 65
207 TTTTATTCGATTATCAAAAACCTGGATGGAT...AATGATTAAT 253
66 TyrSerPhe.....IleAspGlySerThrPheIleArgIle 76
254 G.....TCTGGGTGCAGATATATATAGTACCAATGCACTTTCT 297
76 IuLeuGluProAsnCysThrAspIleThrGluThrIleCysAspLeuThr 93
298 CA.....CTCAGCTGAATGTTATGAA...GAATTAATTCGCT 335
336 ATTAAGACGAGAAAAAGAAAC...ACTTCTATGCTATGAGCTGACTC 382
110 ValArgAlaLysArgGlyAsnLeuThrSerIleTrpValGlyLeuGluPr 126
383 ATTACACCATTTGCCAAGCTCAGATGGCTGCAGAA...GTACATT 429
126 OheGlnHisIleTyrGluAsnValThrValGlyProProLysAsnIleSerV 143
430 TGAAGCTGAAATAGGCAATAGATGATACATCTCTCTGAGAACAAA 479
143 alThrProGlyLysSerLeuValIleHisPheSerProPheAsp 159
480 GATATGTTATGTGGCTTTGATGTGTTAAGCTTACATATAGTTACT 529
160 .....ValPheHisGlyAlaThrPheGlnIleValLeuValH1 171
530 TATCTGAAAAACCTTCAGGTGTGAGAAAGATGAAATATATTT 579
171 sTyrTrpGluLysSerGluThrGlnGlnGlnValGluGlyProPhe 188
580 CCAAGCATTAATTTAT.....AAACTCACCAGACACTATTGT 623
188 ySerAsnSerIleValIleuGlyAsnLeuLysProTyrArgValIleCys 204
624 CTAAAGCTTAAGCGACCTA...CTTACGTCAGGAAAT 662
205 LeuGlnIleThrGluAlaGlnLeuIleuLysAsnLysIleAspProH1 221
663 GGTCTATAGTCCAGACATGATTAAGACCA 698
221 sGlyLeuLeuSerAsnValSerCysHisGluThrThr 233
seq_name: sp_vertebrate:09YGC8
seq_documentation_block:
ID 09YGC8 PRELIMINARY: PRT: 341 AA.
AC 09YGC8
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR 2.
GN IL10R2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
NC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
[1]
SEQUENCE FROM N.A.
RP REBOUD J., GARDINER K., MONNERON D., UZE G., LUTFALLA G.,
RT "Comparative genomic analysis of the Interferon/Interleukin-10

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RT	receptor gene cluster	..	
DR	Genome Res.	0:0-0.1(1993)	..
RL	EMBL:	AF082667	AD13678.1; ..
DR	EMBL:	AF082666	AD13671.1; ..
KM	Receptor		
SQ	SEQUENCE	341 AA:	35062 MW: 74330364 CRC32:

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alignment_scores:
    Quality: 189.50      Length: 221
    Ratio: 1.469         Gaps: 10
Percent Similarity: 58.371  Percent Identity: 27.149
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alignment_block:

Align seg 1/1 to: 09YGC8 from: 1 to: 341

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684 TGTATTAAAGACCAACAATTGAAAATGAACACTACCCTCCACCAAAAAATTAGA 733
      |||.....|||.....|||.....|||.....|||.....|||.....|||
12 CysLeuLeuLeuCysValSerGlyIleValProLysProArgAsnAlaMet 28
734 AGTACGTGTCCAAATATGAAAGCACTATGTCTTAATGGCAT ..... T 774
      :||||| | | | | | | | | | | | | | | | | | | | | | | | | |
28 gIleSerSerValAsnPheArgSerValIleLeuThrAspPropGluY 45
775 ATACATATGCAAACATGACCTTTCAAGTCAGTGCGTCCAGCGCTTTTAA 824
      :|||.....:|||.....|||.....|||.....|||.....|||.....|||
45 AlaGlyGlyAspLeuSerTyThrValGlnAlaIleSerIlePhePro 61
835 AAAAGGAATCCTGGAAACCACTTTGTATAAATGGAACAAATACCTGACTG 874
      |||.....|||.....|||.....|||.....|||.....|||.....|||
62 LysGlnAsnPheAsnPro ..... ValTh 69
875 TGAATATGTCAAATACCCACGTGT .. GTTCTCTCTCAAAACGTTTTCC 921
      |||.....|||.....|||.....|||.....|||.....|||.....|||
69 rThrIleAsnAsnValThrGluCysAspValSerSerLeuSerValTyLr. 85
922 AAAAAGAAATTACCTTCTCCGCGCTAACACATGTCATGAGAAATACACA 971
      |||.....|||.....|||.....|||.....|||.....|||.....|||
86 .. GJVAIeIyVAlIeUArIyValAdgTrIGlUTrGIuAspSGLInIs 100
972 TCTTTTGGTGTGAAGACATGAAGTAGTATACGTGAATATACAGCTTCT 1021
      |||.....|||.....|||.....|||.....|||.....|||.....|||
101 SerAspTrpAla .. ValValArPheUsPrometAlaSprIleValII 116
1022 ACTCTCTCCAGCTTTAAACATTAGATCCCTTACTGATTCATTCATATCT 1071
      |||.....|||.....|||.....|||.....|||.....|||.....|||
116 eGlyProSerValAsnValLysSerGluSerGlyThrIleHisValA 133
1072 ATATGGGCTGTCCA ..... AAACGTGTGGAAACAGCGCTGTATC 1112
      |||.....|||.....|||.....|||.....|||.....|||.....|||
133 sPrPheThcIyProAlaAlaAspArgGluHisAspLysTrpSerLeuLys 149
1113 CAGGATTAT .. CCACATATTATGAAATATATTTTGGGAAACACTCTC 1159
      |||.....|||.....|||.....|||.....|||.....|||.....|||
150 GluTYrTYrGlySetrPIleTYrGlnGlyIleLeuTYrTrpLysGlySe 166
1160 AATGCTGAGACAAAATATTCGAC ..... AAAAAATCTGATGTA 1200
      |||.....|||.....|||.....|||.....|||.....|||.....|||
166 rAsn ..... LysIleValIleHisIleAspThrLysHisAsnSerGluI 181
1201 CAGTTCSTAAATTGTGAACACAGTACTGTATATGTGGGAAAGCCAGAGCA 1250
      :|||.....|||.....|||.....|||.....|||.....|||.....|||
181 IeUeSerGlnIleuGlnUProTrpTrpIleTYrCysIleGlnValGlnGly 197
1251 CAACACATGAGAAAGAAAGCTGATATAAAGCAGTGCTTTTATGACGCTGT 1300
      :|||.....|||.....|||.....|||.....|||.....|||.....|||
198 ..... ValIleProGluTrpAsnLysThrGlyIleUarGserGlnGluLe 212
1301 ATGTGAGAAACA 1313
      :|||.....|||.....|||.....|||.....|||.....|||.....|||

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seq_name: sp-vertebrate:Q9W6U9

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seq_documentation_block:
ID Q9W6U9 PRELIMINARY; PRT; 918 AA
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AC Q9W609;
DT 01-NOV-1999 (TREMBlere). 12, Created)

DT	01-NOV-1999	(TIREMBLrel. 12, last sequence update)
DT	01-NOV-1999	(TIREMBLrel. 12, last annotation update)

DE GLYCOPROTEIN 130 PRECURSOR.

OS Gallus gallus (Chicken).

Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

RP SEQUENCE FROM N.A.
RN [1]

RC TISSUE-EMBRYONIC HEART PRIMARY CULTURE (E7, E8),
BY MEDLINE. 99026069

RA GEISSEN M., HELLER S., PENNICA D., ERNSBERGER U., ROHRER H.:

RT on gp130 cytokine receptor signaling

RL	Development 125:4791-4801 (1998) -
DR	EMBL: AJ011688: CAB42084.1: -

KW	Signal.	POTENTIAL.
1	36	

SQ SEQUENCE 918 AA; 102495 MW; 9DC128C3 CRC32;

alignment_scores:

Quality:	458.30	Gaps:	24
Ratio:	0.656	Percent Identity:	20.220
Percent Similarity:	46.374		

alignment_block:

Align seg 1/1 to: Q9W6U9 from: 1 to: 918

[illegible]

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468 CCTGACAAAGATAGTGTATGGCTTGCATGTTAGC... 512
331 .....SerlysglyProthrIlethrPargThrIleAspValSerProse 345
513 .....TTACATATAGCTTACTATCTGAAA.....A 540
345 rProalIaheThrIleValArgLeuMetThrPysAlaLeuGluProPheG 362
541 ACTCTTCAGGCTA.....GAGAA 560
362 IuAlaAsnGlyValIleLeuGluThrValThrIleArgAlaLysPro 378
561 AGGATGAAATATTTATTCAGACATAAATTTAACTCA... 605
379 ProLeuSerHisProProSerThrGlyAsnValThrThrThrSerLeuTh 395
606 .....CCAGAGCTACTTATGTCTTAAAGTTAAAGCAGCAGCTAC 645
395 rLeuLysLeuProAsnGlyThrTyf.....GluValThrValY 408
646 TTACGTATGGAATTTGCTGCTTATGCTCCAGTACATGTATTAAGACC 695
408 aAlaHisAsnArgValIleGlyAla...SerProProSerValLeuLeuIle 423
696 ACAGTTGAAATGAACTACCTCCACCAGAAATATAGAGTCAGTCCA 745
424 ProSerSerAsnSerLysAlaProValAsnIleArgThrLeuProLys 440
746 AAATAGACTATGTTCTTAATGGGATTATACATATGCAACATGACCT 795
440 sAspLysLysLeuThrPValGlyThrThrAlaProAsnValIleLysT 457
796 TTCAGTTCAGTGCCTCCAGCCTTTTAAAGAAATCCGGAACCAT 845
457 yValIleGluThrPys.....LeuMetSerAsnSerSerAspPys 470
846 TTGTTAATAGGAACAATACCTGACGTGAAATGCAAAATACCA 895
471 IleThrGluThrPglThrGluProLys...AsnIle..... 481
896 GTGTCTCTTCTCAAAAGCTTTCCAAAAGA..... 929
482 .....GlnGlyThrTyfLeuLysGlyAspIleLysProPheL 494
930 ATTACTCTCTCCGCTACAGCA...TCGTGGAATATACCA 971
494 yScyTyfLeuIleThrValTyfProLeuPheAlaAspLysGlnGlySer 510
972 TCTTTTGGCTGAGAGATTAAGTTGATCTGAAATACAGCTTCT 1021
511 GLy.....GlnSerValysAlaTyfLe 518
1022 ACTTCTCT.....CCAGCTTTACATTTAGATCCCTTA 1053
518 uGlnGlnIleLysProSerLysGlyProThrValGlnThrLysLysValG 535
1054 GTGATTCATTCATATC...TATATGGTGCCTCAAAACG 1091
535 IyLysAlaGlnAlaValLeuThrThrPAsnHisLeuThrValAspLysInd 551
1092 TCTGGAACAGCGCTGTATCCAGATATTCACATGATTATGAAATAT 1141
552 AsnGly.....PheIleArgSerTyfThrIleLeuTyfLysThVa 565
1142 TTTTGGGAAACACTTAATATGCTGAGAGAAAATTTATCGAGAAAAA 1191
565 IAspLysAsnGluThrAlaValSer.....ValAspProSerLysT 579
1192 CTGATGTACAGTCTCTAATTTGAACACATGACGTATATGTGTGAA 1241
579 hGluTyfThrLeuSerSerLeuThrSerAspThrLeuTyfThrValArg 595

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1242 GCCAGACGACACACC 1256
596 MetMetAlaTyfThr 600

seq_name: sp_human:014936
seq_documentation block:
ID 014936 PRELIMINARY PRT 484 AA.
AC 014936;
DT 01-NOV-1996 (TRENDEL. 01, Created)
DT 01-NOV-1996 (TRENDEL. 01, Last sequence update)
DT 01-NOV-1998 (TRENDEL. 08, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89003065.
RA AGUET M., DEMBIC Z., MERLIN G.;
RT "Molecular cloning and expression of the human interferon-gamma
RT receptor."
RL Cell 55:273-280(1988).
RN [2]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE: 97246734.
RA MERLIN G., VAN DER LEEDE B.-J.M., MCKRONE K., KNEZEVIC N.,
RA BANNARATH W., ROMQUIN N., VIEGAS-PEQUIGNOT E., KIEFER H., AGUET M.,
RA DEMBIC Z.;
RT "The gene for the ligand binding chain of the human interferon gamma
RT receptor."
RL Immunogenetics 45:413-421(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA DEMBIC Z.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBD databases.
DR EMBL: U19247; AAC52064.1; JOINED.
DR EMBL: U19241; AAC52064.1; JOINED.
DR EMBL: U19243; AAC52064.1; JOINED.
DR EMBL: U19244; AAC52064.1; JOINED.
DR EMBL: U19245; AAC52064.1; JOINED.
DR EMBL: U19246; AAC52064.1; JOINED.
SO SEQUENCE 484 AA; 53818 MW; EBC99D1F CRC32;

alignment_scores:
Quality: 132.00 Length: 350
Ratio: 0.714 Gaps: 15
Percent Similarity: 52.857 Percent Identity: 22.000

alignment_block:
US-09-240-675-1 x 014936
Align: seq 1/7 to: 014936 from: 1 to: 484

33 GTCTCTCTCGGGCGGACGACCTGATGCTGCTCCCTGGGCCCATG 82
1 MetAlaLeuLeuPheLeuLysProLeuValMetGlnIleValSerArgAl 17
83 GGTGTGCGCGCAGCC...GCAGGTGGAATAAATCTAAATCTCCCTCAA 129
17 aglMetGlyThrIleAspLeuGlyProSerSerValProThrProThrA 34
130 AAGTAGAGGTGACATATGATGACAACTTATCCCTGAGGTGGACAG 179
34 snValThrIleGlnSerTyfAsnMetAsnProIleValTyfThrGluTyf 50
180 AGCAGTAGCTGTGCGGAGATG...ACTTTTCATTCATATATCAAA 226
51 .....GlnIleMetProGlnValProValPheThrValGlnValLysAs 65
227 AACTGGATGGATTAATGATTAATAAATGCTGTGGGTGTCAGAAATATCTA 276

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01-NOV-1999 (TREMBLrel. 10, last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)
DE INTERFERON ALPHA/BETA RECEPTOR 2.
GN IFNAR2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauri
CC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RA REPOUT J., GARDINER K., MONNERON D., UZE G., LOTFALLA G.,
RT Comparative genomic analysis of the interferon/interleukin-10
RT receptor gene cluster.
RL Genome Res. 0:0-0(1999).
DR EMBL; AF082665; AAD13670.1; -
KW HSP; P13726; ITHF.
SQ SEQUENCE: 508 AA; 57049 MW; 2DC4E498 CRC32;

alignment_scores:
Quality: 131.00 Length: 502
Ratio: 0.567 Gaps: 29
Percent Similarity: 46.016 Percent Identity: 21.116

alignment_block:
US-09-240-675-1 x 09YHV9

Align seg 1/1 to: 09YHV9 from: 1 to: 508

30. ARGGTGCTCTCTGGGCGGAGC.....ACCTAGTGTCTGT 67
|||.....|
1 MetGlnThrLeuMetGlyGlyProLeuArgPheTyrGlnLeuValPheva 17
68 CGCGGCGGCCCATGGGTGTGTGCCAGCGCGGAGGTGGAAAAATGTA 117
|||.....|
17 Isertile.....LeucSalAlaCysTyrSerLeuSerGlu 31
118 AATGCTCTGAAAAAGTA.....GAGGTGCATCATGATGACAACTT 161
|||.....|
31 yellerProArgGluProProAspAsnLeuGlnMetThrSerAsnAspPhe 47
162ATCTGAGGTGGAAC..AGAGCGATGAGCTGTGGG.... 197
48 GlnHisIleLeuSerTyrPalaIleHisSerAspProThrValProThrTy 64
198AATGTCACCTTTTCATTCGATTATCAAAAAACAGGATGATTA 243
65 TTTAGTValLeuTyrSer.....SerHisSerant 75
244 GGGTAAATATGTTGGGTGCACAAATTTACTGACCAATGACATTT 293
75 TrpTyrIleAlaTyrGlnCysSerArgIleValGlnProPheCysAsnLeu 91
297 TCTTCTCAAGCTGATGATTTTGAAGA.....ATTAAAT 331
92 ThrAspAspPheLeuValValSerArgGluTyrSerAlaPheValGlnSe 108
332 GCGTATTAAGCGCAAAAAAGAAACCTTTTCATGATGATGAGTTACT 381
108 TrpPheValGluTyrGlnValPheAsnSerSerLeuLeuHis..... 121
382 CATTACACCATTTGCCAAAGCTCAGATTGGTCTCTCCAGAAAGTACATTA 431
122 PheSerProLeuSerGluThrPheLeuGlyProGluPheAsnLeu 137
432 GAAGCGAAGATTAAGCAATAGTATACATCTCT...CTGTGAAA... 476
138 SerSerCysValHisCysIleAsnIleThrIleLeuSerProProThrH 154
477AAGATAGCTTATCTGGGCTTTGGATGGTTTAAGCTTACAT 519
154 rleuArgTyrAsnGlyValSer.....L 162


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1210 ATTGTAACCACTGACT ..... GTATTATGTGTGAACCAAGA 1247
|||||
401 .. LeuserProteinUserTryValaIncysrThryrSerleuArgSerArg 416

1248 GCACAC 1253
417 SerAsn 418
|||||

seq_name: sp_rpodent:p97798

seq_documentation_block:
ID      p97798      PRELIMINARY;      PRT; 1493 AA.
AC      p97798;
DT      01-MAY-1997 (TREMblrel_03, Created)
DT      01-MAY-1997 (TREMblrel_03, Last sequence update)
DT      01-NOV-1999 (TREMblrel_12, Last annotation update)
DE      NEOGENIN (NEOGENIN PROTEIN).
OS      NEOL.
SS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE, 97407661.
RA      KEELING S.L., GAD J.M., COOPER H.M.;
RT      "Mouse Neogenin, a DCC-like molecule, has four splice variants and is
RL      expressed widely in the adult mouse and during embryogenesis.";
RL      Oncogene 15:691-700(1997).
DR      EMBL, Y09535; CAA70727.1; -.
DR      HSPF, P02751; IRTG.
DR      MGD; MGI:1097159; Neol.
DR      PFAM; PF00041; fn3; 6.
DR      PFAM; PF00047; Ig; 4.
DR      PRINTS; PR00014; FNTYPEPIT.
SO      SEQUENCE 1493 AA; 163159 MW; 98FF26676 CRC32;

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alignment scores:
      Quality: 130.00      Length: 415
      Ratio: 0.637      Gaps: 20
Percent Similarity: 49.157      Percent Identity: 21.446

alignment block:
US-09-240-675-1 x P97798 ...

Align seg 1/1 to: P97798 from: 1 to: 1493

      87  TTGTCGCGAGCGGAGCGATGGAAAAAAGCTAAATCTGCTCAAAAGACG 136
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
461  LKMLARGLALHTHTGGLGYPROLEIPROSEHARIPROLYGSPVALYA 477
      137  GGTGCACATCTACATGACAACTTTATC..CTGAGGTGAC.....A 177
      477  LALSERLEUVALERTHTMGRPELLEUYLEUHTPTDRTGTHPRO 494
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
494  LASETRPRONHISGLYASPSHNEUHTLYGTERVALPHEUTHTLYS 510
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
128  ACTGGAGATGATATTTGATGATAAATCTCTGGCTGCAGAAATTTACTAG 277
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
511  GLUGLYVALSPATY.....GLUAGVALGLASDHTSGERG 523
      278  T.....ACCAATGCAACTTTTCTTCACTAGACSTGA 309
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
553  nPROGLYGLMETGLVALYATHTEGLINSLEUSETPROIALTHVAL 540
      310  ATGTTTATGAAGAAATTAATTCGCTATAGACAGAAAAGAAACACT 359
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
540  YLLIEPHE.....LYVALMETALDELINSNLYSHISGLY 551
      360  TCTTCACAGTATGAGGTGACTCATATTTGACCACTTTCGCAAAAGCTCAGAT 409
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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552 SerGly..... GluSerSerAlaProLeuArgValGluThr.. 563
410 TGGTCTCCAGAGTACATTAGAAAGCTGAAAGATAGCAATAGCAAC 459
564 .... GluProGluValGlnLeuProGlyProAlaProAsnIleArgAla 579
460 ACATCTCTCCGGAACAAAGATAGTATTATGGGCTTG..... 500
579 yAlaThrSerProThrSerIleThrValThrTrpGluThrProLeuSer 595
501 ...GANGGTTAAAGCTTACATATAGCTTACTATCTGAAAACCTTC 547
556 GlyAsnGlyGlnIleGlnAsnTyrIleGlyTyrMetGlnGlyGly 612
548 AGGTGTAGAGAAAGAGATTGAAATTTATTCAGACATAAATTATA 597
612 rasPlysgluGlnAspIleAspValSerSerHisSerTyrThrIleAsn 629
598 AACCTCTACAGAGACTACTATTGTCTAAAGTTAAAGACACTACT 647
629 ILeuLysIleTyrThrGluTyrSerPheArgValAla..... Tyr 643
648 AGCTCATGGAATAATGGTCTATAGTCCAGTACATTGTATAAGACAC 697
644 AsnLysHisGlyProGlyValSerThrGlnAspValAlaValArgThr 660
698 AGTGAATAATGAACTACCTCCAGAAATAATAGAAAGTCACTGCCAA 747
660 uSerAspValProSerAlaAlaProGlnAsnLeuSerIleGluValArg 677
748 AT...CAGACTATGTCTTAATGC.....GATTATCATTTGCA 785
677 snSerLysSerIleValIleHisTrpGlnProProSerSerThrGln 693
786 AAC.....ATGACTTTCAGATTCAGTGGCTCCAGCCTTTTAA 826
694 AsnGlyGlnIleThrGlyTyrIleArgTyrArgLysAlaSerGly 710
827 AAGGAATCTGGAACCATTTGTATAAATGAAACAAATACCTGCTG 876
710 sSerAspValThrGluThrLeuValThrGlyThrGlnLeu..... 723
877 AAAATGTCAAACCTACCAGTGTCTTCCCAAAACCTTTCCAAA 926
724 .....SerGlnLeuIle.....GlnGlyLeuAspArgGly 733
927 GGAATTAACCTTCCGCTACAGATCGATGAAATACACA..... 971
734 ThrGluTyrAsnPheArgValAlaAlaIleThrValAsnGlyThrGly 750
972 ....TCTTTTGGCTGGAAGATTAAGTTGATGAAATACAGCTT 1017
750 oAlaThrAspTrpLeuSerAlaGluThrPheGluSerAspLeuAspGlu 767
1018 TCTTACTTCTCCAGTC.....TTTAACATGATGCCCTTACTGAT 1058
767 hArgValProGluValProSerSerLeuHisValArgProLeuValThr 783
1059 TCATTCATATCTATATCGTCTCCAAAACAGCTCGAAACAGCCTCT 1108
784 SerIle...ValValSerTrpThrProProGluAsnGlnAsnIle... 798
1109 GATCCAGATATTCACATGATTATGAAATTAATTTTGGAAAACACTT 1158
798 ValAlaGlyGlyTyrAlaIleGlyTyrGlyIle.....GlySer 811
1159 CAATAGCTGAGAGA...AAATATGAGAAAACAACTGATGTAAAGTT 1205
811 roHisAlaGlnThrIleLysValAspTyrIleGlnArgTyrTrpThr 827
1206 CCAATATTGAAACCATGACTGTATATGTGTGAAAGCCAGACCA 1250
828 GluAsnLeuAspProSerSerHisTyrValIleThrLeuLysAla 842

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seq_name: sp_invertebrate:094537

seq_documentation_block: PRELIMINARY; PRT; 1375 AA.

ID 094537;
AC 094537;
DT 01-FEB-1997 (TREMBLREL. 02, Created)
DT 01-FEB-1997 (TREMBLREL. 02, Last sequence update)
DT 01-NOV-1999 (TREMBLREL. 12, Last annotation update)
DE FRAXZLED.
GN FRAXZLED.
OC Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97015076.
RA KOLODZIEF P.A., TIMPE L., MITCHELL K.J., GOODMAN C.S., FRIED S.,
RA JAN L.I., JAN Y.N.;
RT "Triazolid encodes a Drosophila member of the DCC immunoglobulin
RT subfamily and is required for CNS and motor axon guidance."
RL Cell 87:197-204 (1996).
DR EMBL: U71001; AAC47314.1;
DR FLXBASE: FBgn0011592; fra.
DR PRAM: PF00041; fn3; 6.
DR PRAM: PF00047; 19; 3.
DR PRINTS: PF00014; FNTYPEIII.
SQ SEQUENCE 1375 AA; 151692 MW; 43806DBC CRC32;

alignment_scores:

Quality: 129.00 Length: 622
Ratio: 0.542 Gaps: 22
Percent Similarity: 38.264 Percent Identity: 16.399

alignment_block:

us-09-240-675-1 * 094537

Align seg 1/1 to: 094537 from: 1 to: 1375

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102 GGTGGAATAATCTPAAATCT.....CC 124
447 GlyGlyLysProLeuAspSerGlyLeuGlnAlaArgLeuProSerGlnPr 463
125 TCAAAAGTAAAGTGCACATCATAGATGACAACTTATC...CTGAGGT 171
463 oArgAspLeuValAlaGlnIleValLysSerArgPheValThrLeuSer 480
172 GGT..... 173
480 rPValGlnProLeuGlnAlaAsnAlaGlyAspValValTyrTyrThrValTyr 496
174 ....AACAGGAGGATGAGTCTGCGGAATGACTTTTCAAT 214
497 TyrLysMetAlaAsnSerGlnArgGlnGlnLysMetValThrLysSerH 513
215 CGATTATCAAAAACCTGGATGATTAATGTAATAATGTCTGGGTCTC 264
513 sAspAspGlnGlnValAsnIleGlnSerLeuLeuProGlyThrGlyTyrG 530
265 AGAATATCTAGTACGCAAAATGCAACTTTCTCA..... 299
530 LnpPheArgValGlnAlaAsnThrAsnPheGlySerGlyAlaSerSerAla 546
300 ...CTCAGCTGAATGTTATGAGAAATTAATTAATGCGT..... 335
547 ProLeuGluValSerThrGlnProGluValAsnIleAlaGlyProProAr 563
336 .....ATAAGACAGAAAACAAACCTTCTCATGCT 369
563 sAsnPheGluGlyTyrAlaAspSerHisLysGluIleTyrValLysTrp 580

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370 ATGAG..... 374
    |||
580 IugluprothValthrAsnGlyuileuLysTyrAlaValTyr 596
374 ..... 374
597 SerGluAsnAspSerGlyAlaAspLeuTyrHisAspSerThrAlaLeuG 613
375 ..... GTGACTCATTTA 387
613 uAlaValLeuThrGluLeuAspProHisThrAspTyrValIleSerVal 630
388 CACCATTTCCGAAAGCTCAGATTGCT..... 413
630 aIProPheAsnArgAsnGlyMetGlyAspSerSerAlaGluIleArgVal 646
414 ..... CCTCCAGAGTACATTGGA 433
647 LysThrPheSerSerThrProSerGluProPheAsnValThrLeuG 663
434 A.. GCTAAGATAAGCATAGTATGATACATCTCTCTCTGACAAAGA 480
663 uValThrSerSerSerIleThrValHisThrGluProAlaGluG 680
481 ATAGTGTATGTGGCTTGATGGTTAGCTTACATATACCTACTT 530
680 LuAspArgAsnGlyGlnIleThrGlyTyrLysIleArgTyrArgLys... 695
531 ATCTGAAAAAAGCTTTCAGGTGTAGAGAAAGATGAAATATTATTC 580
696 ... PheLysAspAlaProGluValLysSerThrProAlaAsnIle... Ar 710
581 CAGACATAAATTTTAACTCTCCAGAGACTTATGTCTTAAAG 630
710 gTyrPheGluLeuSerAsnLeuAspArgAsnAlaGluTyrGluValLysI 727
631 TTAAGCGACACTACTT..... AGCTCATGGAAT 662
727 leuAlaIleMetThrValAsnGlySerGlyProPheThrGluThrAsnArg 743
663 GGTGTCTATAGTCCAGTACATTGTTAAAGCCAGTGAATGAAGT 712
744 Ala..... AsnThrLeuGluAsnAspLe 751
713 ACCT..... 716
751 uAspGluThrGluValProGlyLysProIleThrIleSerIleHisProG 768
717 ..... CCACGAGAAATATGAGTGC 737
768 LyAlaAsnAsnIleAlaIleuHisThrGlyProProGluHisProGluIle 784
738 AGGTCCAAATTCAGAACTATGTTTAAAGC..... 770
785 LysIle..... ArgAsnTyrValLeuGlyTyrGlyArgGlyIleProAs 799
770 ..... 770
799 pGluAsnThrIleGluLeuLysGluThrGluArgTyrHisIleLeuLysA 816
771 ..... GATTAT 776
816 snLeuGluSerAsnMetAspTyrValValSerLeuArgAlaArgAsnVal 832
776 ..... 776
833 LysGlyAspGlyProProIleTyrAspAsnIleLysThrAspAspGluG 849
776 ..... 776
849 uProValAspAlaLeuProThrProLeuGluValProValGlyLeuArgAla 866
777 ACATATCAAAACATGACCTTTCAGAGTTCAGTGCCTCCAGCCCTTTTA 824

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||| ..... ||| ..... |||
866 IethrMetSerSerSerSerIleValValTyrThrIleAspThrMetLeu 882
825 AAAGAGAT..... 833
883 AsnLysAsnGlnHisValThrAspAsnArgIleTyrThrValSerTyrG 899
834 ..... CTGGAACCATTTGTATAATGGAACAAATACCTGACTGTAA 879
899 yIleThrGlySerAsnArgTyrArgTyr..... HisA 910
880 ATGTCAAAACATACCAGTGTCTTTCCTCAAAAGCTTTCCAAAAGA 929
910 snThrThrAspLeuAsnGlyMetIle... AsnAspLeuArgProAsnThr 925
930 ATTACCTTCTCCGTCACAGCATCTGATGGAATACATCATCTTTTG 979
926 GlnTyrGluPheAlaValLysValValLysGlyArgGluSerSerTr 942
980 GTCTGAAGAGTAAAGTTTGATCTGAATACAGCTTCTCTACTCTC 1029
942 PserMetSerValLeuAsnSerThrTyrGlnAsnValProValThrPro 959
1030 CAGCTTTAATATAGATCCCTGTAGTATTCATTCATATCATATAGG 1079
959 ro..... ArgGluValThrValArg 965
1080 GCTCCAAACAGTCTGGAACACGCTGTGATCCAGATTAATCA... 1124
966 LeuAspGluMetAsnProProThrValIleValGlnThrIleProPol 982
1125 ..... CTGATTATGAAATTTTGGAAACA 1155
982 shIleThrLeuGlyGlnIleThrGlyTyrAsnIleTyrThrThrAsp 999
1156 CTCAAAATGCTGAGAC..... AAATATGCAAAAAA 1190
999 hThrLysArgAspArgAspTrpSerValGluAlaPheAlaGlyGlu 1015
1191 ACTGATGTTACAGTCTTAATTGAAACACAGCTGATTAATGTTGAA 1240
1016 ThrMetLeuMetLeuProAsnLeuLysProTyrThrThrTyrTyrPhe 1032
1241 AGCCAGAGCACACACC 1256
1032 sValGlnAlaArgThr 1037
seq_name: sp_invertebrate:094538
seq_documentation_block:
ID 094538 PRELIMINARY; PRT; 1526 AA
AC 094538;
DT 01-FEB-1997 (TRENDArel. 02, created)
DT 01-FEB-1997 (TRENDArel. 02, last sequence update)
DT 01-NOV-1999 (TRENDArel. 12, last annotation update)
DE FRAZZLED.
GN FRAZZLED.
OS Drosophila melanogaster (Fruit fly)
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila
RN [1] FRAZZLED.
RP SEQUENCE FROM N.A.
RX MEDLINE: 97015076.
RA KOLODZIEJ P.A., TIMPE L., MITCHELL K.J., GOODMAN C.S., FRIED S.,
RA JAN L.Y., JAN Y.N.
RT "frazzled encodes a Drosophila member of the DC immunoglobulin
RT subfamily and is required for CNS and motor axon guidance."
RL Cell 87:197-204(1996)
DR EMBL: U71002; AAC47315.1;
DR FLXBASE: FBgn0011592; fra.
DR PFAM: PF00041; f03; 6.
DR PFAM: PF00047; f03; 3.

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DR PRINTS: PR00014: FNTYPE111
 SO SEQUENCE 1526 AA: 168787 MW: F17B1EC9 CRC32;

Alignment_scores:

Quality: 129.00 Length: 622
 Ratio: 0.542 Gaps: 22
 Percent Similarity: 38.264 Percent Identity: 16.399

Alignment_block:
 US-09-240-675-1 x 094538

Align seg 1/1 to: 094538 from: 1 to: 1526

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102 GGTGGAATAAATCTAAATCT...T.....CC 124
|||||  |||  |||
598 GlyGlyLysProLeuaspSerGlyLeuGlnAlaArgLeuProSerGlnPr 614
125 TCAAAAAGTAGAGTCGACATCATAGATGACAATTATC...CTGAGGT 171
|||  |||  |||  |||  |||  |||
614 CArgaspLeuValAlaGlnIleValLysSerArgpHeuValThrLeuSer 631
172 GG..... 173
||
631 rPValGlnProLeuGlnAsnAlaGlyaspValValTyrTyrThrValTyr 647
174 .....ACAGGAGCGATGAGTCGTGCGGAATGCACTTTTCATT 214
|||||  |||  |||  |||  |||  |||
648 TyrLysMetAsnAsnSerGlnArgGlnLysMetValThrLysSerHl 664
215 CGATTATCAAAAAGTGGATGATGATTAATGATAATGCTGCGGTGC 264
|||  |||  |||  |||  |||  |||
664 sAspaspGlnGlnValAsnIleGlnSerLeuLeuProGlyArgThrTyrG 681
265 AGAAATTAAGTACCAATGCAACTTTCTCA..... 299
||
681 InPheArgValGlnAlaAsnThrAsnPheGlySerGlyAlaSerSerAla 697
300 ..CTCAAGCTGAATGTTTATGAGAAATTAATGCGT..... 335
|||||  |||  |||  |||  |||  |||
698 ProLeuGlnValSerThrGlnProGlnValAsnIleAlaGlyProProAr 714
336 .....ATAAGAGCAAAAAGAAAACCTTCTCATGTT 369
714 gAsnPheGlnGlyTyrAlaArgSerHlLysGlnIleTyrValLysTrpG 731
370 ATGAG..... 374
|||
731 LngLInProThrValThrAsnGlyGlnIleLeuLysTyrArgValTyrTyr 747
374 ..... 374
748 SerGlnAsnaspSerGlyAlaaspLeuTyrHlAspSerThrAlaLeuGln 764
375 .....GTTGACGATTTA 387
764 uAlaValLeuThrGlnLeuArgProHlThrAspTyrValIleSerVal 781
388 CACCAATTCGCAAGCTCAGATTGT..... 413
|||||  |||  |||  |||  |||  |||
781 aLProPheAsnArgAsnGlyMetGlyAspSerSerAlaGlnIleArgVal 797
414 .....CTCCAGAAAGTACATTAGA 433
|||  |||  |||  |||  |||  |||
798 LysThrPheSerSerThrProSerGlnProProAsnAsnValThrLeuGln 814
434 A...CCTGAAGATTAAGCAATAGTATACATCTCTCGAAGAAAAG 480
|||  |||  |||  |||  |||  |||
814 uValThrSerSerSerSerIleThrValHlStrpGlnProProAlaGlnG 831
481 ATAGTGTATATGCGCTTGATGCTTAAGCTTACATATAGACTTACTT 530
|||  |||  |||  |||  |||  |||
831 LAspArgAsnGlnGlyGlnIleThrGlyTyrLysIleArgTyrArgLys... 846

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531 ATCTGAAAAAAGCTCTCAGGTGTAGAGAAAGATTGAAATATTATTC 580
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847 ..PheLysaspAlaProGlnValLysSerThrProAlaAsnIle...Ar 861
581 CAGACATTAATTTATTAACCTCTCACAGAGACTACTATTGCTTAAG 630
|||||  |||  |||  |||  |||  |||
861 gTyrPheGlnLeuSerAsnLeuAspArgAsnAlaGlnIleGlnValLysI 878
631 TTAAGCAGCACTACTT.....ACGTATGGAAT 662
|||||  |||  |||  |||  |||  |||
878 lAlaAlaMetThrValAsnGlySerGlyProPheThrGlnThrAsnArg 894
663 GGTGCTCTACTCCAGTACATTGTATTAAGCAAGCTGGAATGAACT 712
|||  |||  |||  |||  |||  |||
895 Ala.....AsnThrLeuGlnAsnAspLe 902
713 ACCT..... 716
902 uAspGlnThrGlnValProGlyLysProIleThrIleSerIleHlAspProG 919
717 .....CCACGAGAAATATAGAGTC 737
919 lYAlaAsnAsnIleAlaLeuHlStrpGlyProProGlnHlAspProGlnIle 935
738 AGTGTCAAAATCAGAACTATGTTCTTAATAG..... 770
|||||  |||  |||  |||  |||  |||
936 LysIle...ArgAsnTyrValLeuGlyTyrPglYArgGlyIleProAs 950
770 ..... 770
950 pGlnAsnThrIleGlnLeuLysGlnThrGlnArgTyrHlSileLeuLysA 967
771 .....GATPAT..... 776
967 snLeuGlnSerAsnMetLspTyrValValSerLeuAlaGlnArgAsnVal 983
776 ..... 776
984 LysGlyaspGlyProProIleTyrAspAsnIleLysThrArgaspGlnGln 1000
776 ..... 776
1000 uProValaspAlaProThrProLeuGlnValProValGlyLeuGlyAlaI 1017
777 ..ACATATGCAAAACATGACCTTCAAGTCAAGTCGCTCCAGCCTTTTA 824
|||||  |||  |||  |||  |||  |||
1017 lThrMetSerSerSerSerIleValValTyrThrPleAspThrMetLeu 1033
825 AAAGCAAT..... 833
1034 AsnLysAsnGlnHlSValThrAspAsnArgHlSValThrValSerTyrGln 1050
834 ..CTCGAAGAACATTTGTATTAAGAAACAAATACCTGACGTGAAA 879
1050 YLleThrGlySerAsnArgTyrArgTyr.....HlSA 1061
880 ATGCAAAACATACCAGGTGTCTTCTCCAAAAGCTTTCCAAAAGGA 929
|||||  |||  |||  |||  |||  |||
1061 snThrThrAspLeuAsnGlyMetIle...AsnAspLeuAsnProAsnThr 1076
930 ATTACCTCTCCCGCTACAGCATCTGAGGAATTAACATCTTTTG 979
|||||  |||  |||  |||  |||  |||
1077 GlnTyrGlnPheAlaValLysValValLysLysValArgArgLeuSerSer 1093
980 GTCTGAAGATTAAGTTGATGATGAATTAAGCAAGCTTCTACTCTCC 1029
|||||  |||  |||  |||  |||  |||
1093 pSerMetSerValLeuAsnSerThrTyrGlnAsnValProValThrPro 1110
1030 CAGCTTTTAACATTAGATCCCTTAGTATTCATTCATTCATTCATTC 1079
|||  |||  |||  |||  |||  |||
1110 TO.....ArgGlnValThrValArg 1116

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1080 GCTCCAAACAGCTGTGAAACAGCCCTGATCAGATATGCA... 1124
 1117 LeuAspGluMetAsnProProThrValIleValGlnTrpIleProProly 1133
 1125CTGATTATGAAATATTTTGGGAAAC 1155
 1133 SHLThrLeuGlyGlnIleThrGlyTyrAsnIleTyrIleThrThrAspT 1150
 1156 CTTCAANTCTGAGCAAAATATCGAAGAAAA 1190
 1150 hTrpTyrAsnGAspArgAspTrpSerValGlnAlaPheLeuGlyGlu 1166
 1191 ACTGATGTACAGTCTTAATTGAACACAGCTAGTATATGTGTGA 1240
 1167 ThrMetLeuMetLeuProAsnLeuPyrProTyrThrThrTyrThrLeu 1183
 1241 ACCGACAGCACACACC 1256
 1183 sValGlnAlaArgThr 1188

seq_name: sp_vertibrate:090610

seq_documentation_block:

ID 090610: PRELIMINARY; PRT: 1443 AA.
 AC 090610:
 DT 01-NOV-1996 (TREMBLrel. 01. Created)
 DT 01-NOV-1996 (TREMBLrel. 01. Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12. Last annotation update)
 DE NEOGENIN (FRAGMENT).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 NC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WHITE LEGHORN; TISSUE-BRAIN;
 RX MEDLINE; 95105243.
 RA VIELMEYER J., ROMAN J.M., DREYER W.J.;
 RT "Neogenin, an avian cell surface protein expressed during terminal
 RT neuronal differentiation, is closely related to the human tumor
 RT suppressor molecule deleted in colorectal cancer."
 RL J. Cell Biol. 127:2009-2020(1994).
 DR HSSP; P80362; 1MTL.
 DR PFM; PF00041; fn3; 6.
 DR PFM; PF00047; 19; 4.
 FT NON_TER
 SQ SEQUENCE 1443 AA; 158050 MW; 270877DC CRC32;

alignment_scores:

Quality: 127.50 Length: 415
 Ratio: 0.644 Gaps: 19
 Percent Similarity: 47.711 Percent Identity: 22.169

alignment_block:

US-09-240-675-1 x 090610

Align. seg 1/1 to: 090610 from: 1 to: 1443

87 TGTTCGCGACCGCGACAGTGAAGAAATCTAAATCTCCCTCAAAAGTAGA 136
 416 LeuAlaProAlaThrThrGlyProLeuProThrAlaPheArgAspValIle 432
 137 GGTTCGACATCATAGATGACAACTTATTCCTGAGGTGAACAGG... 179
 433 AlaThrLeuValSerThrArgPheIleArgLeuThrTrpArgThrProVal 449
 180 ..AGGATAGAGCTGTGCGGAATGCACTTTTCATTCATATATCAAAA 227
 449 aSerAspProGlnGlyAsnLeuThrTyrSerIlePheTyrThrLys 465
 228 ACTGGATGATTAATGATTAATATGCTGGGTGTCAGAAATATATCTAG 277

466 GlnGlyIleAsnTyrGluArgValGlnAsn...These 477
 278 TACCAATGCAACTTTCTTCACTCAAGCTGAATGTTATGAGAAATTA 327
 477 hArgProGlyGlnThrGlnValMetIleGlnAsnLeuMetProGlyThrVal 494
 328 AATGGGTATAGACAGAGAAAAGAAACACTTCTTCATGATGATGAGTT 377
 494 aTyrValPheArgValValAlaGlnAsnLysHisGlyIleGlyGlu 509
 378 GACTATTTCACCACTTTCGCAAGCTCAGATGCTCTCCAGAGTAGA 427
 510 ..SerSerAlaProLeuLysValAlaThrGlnProGluValIle 523
 428 TTTGAGAGCTGAAGTAAAGCAATGATGATACACATCTCTCTGACACA 477
 523 nLeuProGlyProAlaProAsnIleArgAlaTyrAlaGlySerProThrS 540
 478 AAGATAGTGTATNGGGCTTGGATGGTTATAGCTT 515
 340 eValThrValThrTrpGlnThrProLeuSerGlyAsnGlyIleGln 556
 516 ACATATAGCTTACTTATCTGAAAAACTCTGAGGTGAGAGAAAGAT 565
 557 AsnTyrLysLeuTyrTyrMetGluLysGlnAspSerGlnGlnAspVal 573
 566 TGAATATATTATTCACACATATAATTTATTAATCTCACACAGACATA 615
 573 LAspValAlaGlyLeuSerTyrThrIleThrGlyLeuLysTyrThrG 590
 616 CTTATGTCTTAAGATTAAGACAGCACTTACGTCATGAGAAATGTGT 665
 590 LutySerPheArgValValAlaTyrAsnLysHisGlyProGly 604
 666 GTCTATAGTCCAGTACATGTATTAAGACCAAGTGAAGAAAGACTAC 715
 605 ValSerThrGlnAspValValAlaArgThrLeuSerAspValProSerAl 621
 716 TCCACAGAAATATATAGAGTCAAGTCCAAAT...CAGAACTATGTC 762
 621 AlaProGlnAsnLeuThrLeuGlnAlaArgAsnSerLysSerIleMetL 638
 763 TTAATGGGATATACATATATGCAACATGACCTTCAAGTACGGCTC 812
 638 eunIleThrPheProProProAla 645
 813 CAGGCTTTTAAAGGAATCTGGAACCAATTG 848
 646GlyThrHisSerGlyGlnIleThrGln 654
 849 TATAATGGAACAAATACCTGACTGTGAAATGTCAAACTACCACT 897
 654 TyrLysIleArgTyrArgLysValSerArgLysSerAspValThrGlnS 671
 898 GTGCTCTTCCCAAAACCTTTCCAAAAGCAATT... 932
 671 eValGlyGlyThrGlnLeuPheGlnLeuIleGlyGlyLeuGlyGly 687
 933TACCTTCCGCGTACAGACATCTGTGGAATACACA... 971
 688 ThrGluTyrAsnPheArgIleAlaIleAlaMetThrValAsnGlyThrLys 704
 972 ...TCTTTTGTCTGAGAGATTAAGTTGATCTCAATATCAAGCTT 1017
 704 AlaThrAspTrpValSerAlaGlnThrPheGluSerAspLeuAspGlnS 721
 1018 TCCACTTCCTCCAGTCTTTACATTAGATCCCTTATGAT 1058
 721 eArgValProGluValProSerSerLeuHisValAlaProLeuValThr 737
 1059 TCATTCATATCTATATGCTGTCTCCAAAGATGTCGGAACACCGCTGT 1108
 738 SerIle...ValValSerTrpThrProProGluAsnGlnAsnIle...Val 752

1109 GATCCAGGATTATCCACTGATTATGAAATTTTGGGAAACACTT 1158
 1159 CAATGCTGAGCA..AAATATCGAGAAAAAACTGATGTTACGTT 1205
 752 lvalarglytyrallellytyglyle.....glyserp 765
 765 rohsalaglnthrllelyvalasptyrlysglnargtyrtythille 781
 1206 CCTAATTTGAACCACTGATGTTATGTTGTAAGCCAGAGCA 1250
 782 GlusnleuaspProserSerHstlyValleltheuysala 796

seq_name: sp_vertebrate:098949

seq_documentation_block:
 ID 098949 PRELIMINARY; PRT: 873 AA.
 AC 098949
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE AXL-RELATED RECEPTOR TYROSINE KINASE.
 GN REX.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 CC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97067156.
 RA BISCARDI J.S., DEMEYER F., RUEHLER G.F., CHESNUT D.A., BARAGONA S.C.,
 O'BRYAN J.P., DER C.J., FIODALISI J.J., FULTS D.W., MANESS P.F.;
 RT "Rex", a gene expressed in retina and brain, encodes a receptor
 tyrosine kinase of the Axl/Tyro3 family*;
 RL J. Biol. Chem. 271:29049-29059(1996).
 DR EMBL: U70045; AAC60041.1;
 DR HSSP: P00523; 2PTR.
 DR PROSITE: P00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: P00109; PROTEIN_KINASE_TYR; 1.
 DR PFAM: PF00047; fn3; 2.
 DR PFAM: PF00069; kinase; 1.
 DR SEQUENCE 873 AA; 96402 MW; 2918D550 CRC32;

alignment_scores:
 Quality: 123.00 Length: 453
 Ratio: 0.631 Gaps: 25
 Percent Similarity: 43.046 Percent Identity: 22.517

alignment_block:
 US-09-240-675-1 x 098949

Align seg 1/1 to: 098949 from: 1 to: 873

63 CTGTCGCCGCGGGCCGATGGGTG.....TCGCGAGC 97
 12 leuenuleuuglyleutrpalaialaleuargpslyalvalal 28
 98 CGCAGTGGGAAAAATCTAAATCTCTCAAAAAGTAGAGTC..... 140
 28 aalaglymetlysherhnglyserprollelyleuylvalsering 45
 141GACATCATAGATGACAACTTT 161
 45 lylglnprovallyleuasnlyserleuuglymetgluaspProglu 61
 162 ATCTGAGGAGGAGAGAGAGAGAGTCTGTGGGAGATGACTTTT 211
 62 metleu...triplelyshp.....glyalvalvalglinse 73
 212 ATTCGAT.....TATCAAAAATCGGATGATGATGATTAATGTT 255
 73 lvalasplvallytrileprovalaspluasphistriphe..... 87

256 CTGGTGTGAGATATTACTAGTACCAAAATGCACTTTCTTCACG 305
 88glyheleuserleuys 93
 306 CTGAATGTTATGAGAAATTAATTCGTTAAGGAGCAAAAAAGAAA 355
 94servalglut 97
 356 CACTGTCTCA.....TGATAGAGTTGACATTTACCACTTC 396
 97 glinaspserglytyrtyrtyrtyrtyrtyrtyrtyrtyrtyr 114
 397 GCAAGCTCAG.....ATTGCTCCGAGATACAT 428
 114 lglulseringlnlvaltrpleuilevalglulglulvalprotyrpheltr 130
 429 TTGAAGCTGAGATATAGGCAATAGTACATCTCTCTGGAACAAA 478
 131 valgluprogluasp.....valservalserproasphalapr 143
 479 AGATAGTATGTGGGCTTGGATGTGTTAAGCTTACATATAGCTTAC 528
 143 orphenismetalacysalalalvalalglyproprogluprovalthille 160
 529 TTATCTGAAA..... 539
 160 altriplemetglyaspserargvalglyleuproaspleserproser 176
 540ACTCTTCAGCTGAGAGAGAGATGAAATATTTATTCAG 583
 177 lileuasnvalserglyleuasnserthmePhsercysglul 193
 584 ACATAAATTTAAACTCTACACGAGATCTATGCTTAAAGTTA 633
 193 ahlsasnvallyglyleuasnserargthralathvalglitlile 210
 634 AACGACACTTACTAGTCATGGAATATGCTCATGTCAGTACAT 683
 210 ysalametProleu..... 214
 684 TGRTTAAGACCACTTGAATGAATGACCTCCACCAAAATTAAGA 733
 215Proleuasnvalth 220
 734 AGTCACTGCCAAATACAGACATGTTTAAATGAGATTATCATAG 783
 220 valiser.....Glnvalthser 227
 784 CAACATGACCTTCAAGTCAAGCTCCACGCTTTTAAAGAGAT 833
 227 erasnalaser.....Valvaltrpvalproglyheaspglyalga 241
 834 CC...GAAACATTTGTAAATGAAACAAATCTGCTGTA 880
 242 ProleuHiserctylheuglnvalalaguserproaspelylglol 258
 881 TGTCAAATACCAAGCTGCTTCTCCAAAAGCTTTCAAAAAGGA 930
 258 uvalserthnglu.....Valalaprovalproprophalalalygly 273
 931 TT.....TACCTTCGCGGTACAGATCT 956
 273 alglinlyleuysnliserthlnasrlyservalargvalglincys 289
 957 GATGGAATTAACACATCTTTGCTGCTGAGATTAATTTGATCTGA 1006
 290 asglumetglyserprophethngluhvaltyrph..... 303
 1007 AATCAAGCTTCTCACTCTCCAGCTTTTAAATTAAGTACCTTAGG 1056
 304Glnthrlleuaglnlealapro.....serserthnpro 315

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1057 ATTCATTCATATCTATATCGTCTCCA.....AAACAGCT 1094
1058 .....
315 LdaenlleHstVallelelnaIrgaspproGlyleuValleuglnurpdu 331
1095 GGAACACGCTT...GTATCCAGAGATTATCCAGATTATGAATAT 1141
332 GlyValAlaProAspValleuLysGlnAsnValleuglyTyArg..Le 347
1142 TTTTGG....GAAACACTTCAATGCTGAGAGAAAATATACGAGA 1185
347 uclurtrpleelnaspaenValthrglnGlyleuLlevalGlnAspT 364
1186 AAAACAGATTACAGTCTCTAT...TGAACCACTGACTGTA... 1229
364 hrlvsAlaAsnleuthrThrtrphenProleuLysAspLeulleArg 380
1230 TATGTGTG 1238
381 ValCysVal 383

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seq_name: sp_human:092859

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seq_documentation_block:
ID 092859 PRELIMINARY; PRT; 1461 AA.
AC 092859:
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE NEOGENIN.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC -Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MEYERHART J.A., LOOK A.T., BIGNER S.H., FEARON E.R.;
RL Oncogene 0:0-0(0).
RL EMBL: U61262; AAB17263.1;
DR HSSP: P02751; 1TTG.
DR PRAM: PR00041; fn3; 6
DR PRAM: PR00047; 19; 4.
DR PRINTS: PR00014; FNTYPEIII.
SQ SEQUENCE 1461 AA; 159958 MW; 0AB7247E CRC32;

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alignment_scores:

Quality	122.50	Length	421
Ratio	0.581	Gaps	20
Percent Similarity	50.119	Percent Identity	20.665

alignment_block:

us-09-240-675-1 x 092859

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Align-seg 1/1 to: 092859 from: 1 to: 1461
57 CTAGTGTGTCGTCGCCGCGCATGGGTGTGTCGCCGACGCGAGGTGG 106
425 LeuIlelleuGlnHsAlaPro.....AlaThrThrGln 436
107 AAAAATATMAATCTCTCAAAAAGTGAAGGTGCATATCATATGACA 156
436 yProleuProseAlaProArgAspValValAlaSerleuValSerTha 453
157 ACTTATG...CTGAGGTGGAAC...AGAGCGAGAGCTGTCGGG 197
453 rghelleyLysleuthrThrPArgThrProAlaSerAspProHsGlyAsp 469
158 AATGACTTTTTCATGATATCAAAAAGTGGAG...GATAA 241
470 AsnleuthrTySerValPheThrThrLysGlnGlylleAlaArgGlnAr 486
242 TTGATAAATATGCTGGGTGCACAAATTAATCAATCAAAATCAACT 291
486 gValGlnAsnThrSerHsAspProGlyGlnuWelGlnValThrIleGlnAsn 503

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292 TTTCTTCACTCAAGCTGAATGTTATATGAGAAATTAATTCGGATAGA 341
503 eumelProAlaThrValTyrllePhe.....AspValMet 514
342 GCAGAAAAAGAAACACTTCTTCATGATAGTGTGCTCATTTACAC 391
515 AlaGlnAsnLysHsGlySerGly.....GlnSerSerAlaPr 527
392 ATTTGGCAAGCTCAGATTGCTCTCCAGAAATCATTTAGAACCTGAG 441
527 OleuArgValGlnThr.....GlnProGlnValGlnLeuProGlyPro 542
442 ATAAGCAATGATGATACACATCTCTCTCGAAGAAAAAGATGATTG 491
542 lAProAsnLeuArgAlaTyrlAlaSerProThrSerIleThrValThr 558
492 TGGCTTTG.....GATGGTTAAGCTTTACATATGACTTACT 529
559 TrpGlnThrProValSerGlyAsnGlyGlnIleGlnAsnTyrlGlyLeu 575
530 TATCTGAAAAACTCTTCAGGTGAGAGAAAGATGAAATATTAATT 579
575 rTyrlMetGlnLysGlyThrAspLysGlnGlnAspValAspValSerSerH 592
580 CCAAGCATAAATTTATTAATCTTCACACAGACTACTATATGCTATAA 629
592 lSerTyrlThrIleAsnGlyLeuLysLysTyrlThrGlnTyrlSerPheArg 608
630 GTTAAGACAGCACTACTACTGCTGAGAAATGTTGTCCTATAGTCCAGT 679
609 ValValAla.....TyrlAsnLysHsGlyProGlyValSerThrProAs 623
680 ACATTGTTAAAGACACAGTGAATGAATGAATCTCCACACAAATA 729
623 pValAlaValArgThrLeuSerAspValPProSerAlaAlaProGlnAsnL 640
730 TAGAAGTACGTGTCCAAAAT...CAGAATATGCTTTAATGGAT... 773
640 euserleuGlnValArgAsnSerLysSerIleMetIleHsIleTyrlPro 656
774 .....TATCATATGCAACATGAC...TTTCAGTTCAGTG 808
657 ProAlaProAlaThrGlnAsnGlyGlnIleThrGlyTyrlSerArgTy 673
809 GCTCCAGCCTTTTAAAGAAATCTGGAACCATTTGTAAAGAGA 858
673 rArgLysAlaSerArgLysSerAspValThrGlnThrLeuValSerGlyT 690
859 AACAAATACGCTGCTGGAATATGCAAAATACCCAGTGTCTTCC 908
690 hrglnLeu.....SerGlnLeuIle..... 696
909 CAACAGCTTTTCAAAAAGATTTACCTTCCGCGTACAGCATGTA 958
697 GlnGlyLeuAspArgGlyThrGlnTyrlAspThrLeuSerAlaGlnThrPheG 730
959 TGGAAATACCA.....TCTTTGGCTCTGAAGATTAAGTTTG 999
733 rIleAsnGlyThrGlyProAlaThrAspThrLeuSerAlaGlnThrPheG 730
1000 ADATGAAATCAAGCTTCTCTACTCTCTCCAGTC...TTTAAC 1040
730 luserAspLeuAspGlnThrArgValProGlnValProSerSerLeuHsIle 746
1041 ATTAGATCCCTTAGTATTCATTCATATCATATTCGGTGTCCAAAC 1090
747 ValArgProleuValThrSerIle...ValValSerThrThrProProGly 762
1091 GTCGGAACACGCGCTGATCCAGATATTCACGATTAATGAATTA 1140
762 lAsnGlnAsnIle...ValValArgGlyTyrlAlaIleGlyTyrlGlyIle

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778 .....glyserprohnsalaglthrlleuylsalmsprtylys 790
1188 AAAACGAGTGTCACTGCTCCATTTGAAACGACGTACGCTATATGTGT 123
791 GlnArgTyrTyrThrIleGluAsnLeuAspProSerSerHisTyrValIi 807
1238 GAAAGCCACAGCA 1250
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      ::::|
807 etrlleuylsala 811
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seq_name: sp_vertebrate:Q91562

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seq_documentation_block:
ID      Q91562      PRELIMINARY;      PRT;      1427 AA
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DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE TMOR SUPPRESSOR.
GN XDCCA.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95113183.
RA PIERCEALL W.E., REALE M.A., CANDIA A.F., WRIGHT C.V., CHO K.R.,
RA FEARON E.R.;
RT "Expression of a homologue of the deleted in colorectal cancer (DCC)
RT gene in the nervous system of developing *Xenopus* embryos.";
RL Dev. Biol. 166:654-665(1994).
DR EMBL; U10986; AAA70168.1; -.
DR HSSP; P56276; ITLK.
DR PFAM; PF00041; fn3; 6.
DR PFAM; PF00047; 19; 4.
DR PRINTS; PR00014; FNTYPE11.
SO SEQUENCE 1427 AA; 156533 MW; E50B7475 CRC32;

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alignment_scores:
  Quality: 117.50      Length: 419
  Ratio: 0.596        Gaps:
Percent Similarity: 47.017  Percent Identity: 22.196
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alignment_block: 'US-09-240-675-1 x Q91562'

Align seg.1/1 to: Q91562 from: 1 to: 1427

[illegible]

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339 .....AAAGCTCAGTTGGCTCTCCAGAGTCAATTTAA 433
      :::::|||||
519 ValValThrGlnProGluLeuGlnValProGlyProValGluAsnLeu 555
      :::::|||||
434 AGCTGACATAAGGCATTAAGTATACACATCTCTCTCGACACAAAAGATA 483
      :::::|||||
535 n.....ValValSerThrAlaPro.....Thr 543
      :::::|||||
484 GTGTTATGCGGCGTTGCGATGGTTTAAGCTTTACA..... 518
      :::::|||||
543 erValLeuLeuSerThrIpsaProProCalaValAlaAsnGlyProValGln 559
      :::::|||||

```

519 ..TATAGCTTACTTATCTGGAAAACCTCTCAGGTGTAGAAGAAAGGAT 565

560 G l y t y r a r g l e u p h e c y s a l a g l u t h r p h e s e r g l y a r g l u g l i n a s n i l 576

576 egiValaspGlylleValTYRArgLeuGluGlyLeuArgGlySphThrG 593

616 CTTATTTGCTAAAGTTAAAGCAGCAGCTACTTACGTCATGGAATTGCT 665

666 GTCATAGTCCAGTACATTTGTATAAAGACCACAGTTGAAATGAACCTACC 715

608 ValSerSerGluGluHisThrValValThrLeuSerAspValProSerAla 624

624 ametProGlnasnValSerLeuGluValAlaasn..... 635

766 AATGGATTATACATATGCAACATGACCTTCAAGTTCAGTGCTCCAC 815
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050 .....serArgSerIleLysValSerIleP..... 043
816 GCCTTTAAAGGATCCTGGAAACCATTTG.....TA 850

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644LeuProProProGlyThrGlnAsnGlyPheIleThrGlyTyr 658

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851  TAATGGAACAATACCTGACTGTGAATGTCAAACTACC..... 893
|||||
658  rIvs      Tladythlsarclustbthravarrcc 669

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894CAGTGTGCTTCCCTCAAAACGTTTC..... 920

669 IygluIuengluthrleugluProasnasleuTpyrleuPhethrgly 685

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      ::|||
686 LeuGluGlySerGlnTyrSerPheGlnValAlaAlaMetThrValAs 702
      ::|||

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965 TAACACATCTTTTGGCTGAGAGATAAAGTTGATCT..... 100
|||||: |||::: ::|||

1005 GAATACAGCTTCTTACTTCTCCAGCTTTACATTAGA 104

719 spleuaspGlnSerGlnValProaspGlnProSerSerLeuHisValArg 735

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104/ 1ACCTAGGATTCATCCATAACIAAATCGGTCCTCCAAATCAGTCG 109
      ||::: ||::: ||::: :::::
736 ProLeuThrThrSerLeuIleMetSerTrpThrProProLeuAsnPr 751

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1097 AAACACGCGTGTGATCCAGGATTATCCACTGATTATGAATTTATTTTTT 114

751 oasnlle...ValValAlargglytyrillellelleglytyrilyVal..... 764

7653...GlySerProTyrAlaGluThrValArgValAspSerLysGlnArg 779

1194 GATGTACAGTCTATTTGAACCACTGACTGTATGTGTGAAGC 1243
::: |||||::: |||
780 TTTTYSerIleGluAsnLeuGluProSerSerHisTyrValIleSerIle 796
1244 CAGAGCA 1250
::: |||
796 ulysala 798

1251 GATGTACAGTCTATTTGAACCACTGACTGTATGTGTGAAGC 1299
::: |||||::: |||
1252 TTTTYSerIleGluAsnLeuGluProSerSerHisTyrValIleSerIle 1298
1299 CAGAGCA 1305
::: |||
1298 ulysala 1299